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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:41:58 ; Search time 34.2113 Seconds
(without alignments)

3179.172 Million cell updates/sec

Title: US-09-887-669-1
Perfect score: 7809
Sequence: 1 MDVAAAALPAFVALMILYPW.....EAPEQQYRFCDYVALEYLESS 1457

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74669064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cn2_6_ptodata/1/iaa/5A_COMB.pep:/*
 2: /cn2_6_ptodata/1/iaa/5B_COMB.pep:/*
 3: /cn2_6_ptodata/1/iaa/6A_COMB.pep:/*
 4: /cn2_6_ptodata/1/iaa/6B_COMB.pep:/*
 5: /cn2_6_ptodata/1/iaa/PCUTS_COMB.pep:/*
 6: /cn2_6_ptodata/1/iaa/backfles1.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	7809	100.0	1457	2	US-08-652-971-3	Sequence 3, Appli
2	7809	100.0	1457	2	US-08-449-644-1	Sequence 1, Appli
3	7809	100.0	1457	2	US-08-087-244A-1	Sequence 1, Appli
4	7809	100.0	1457	2	US-08-991-258A-3	Sequence 3, Appli
5	7809	100.0	1457	2	US-08-769-399-3	Sequence 3, Appli
6	7809	100.0	1457	3	US-08-991-953A-3	Sequence 3, Appli
7	7586	97.1	1439	2	US-08-449-644-2	Sequence 2, Appli
8	7586	97.1	1439	2	US-08-087-244A-2	Sequence 2, Appli
9	4812	61.6	1452	2	US-08-449-644-8	Sequence 8, Appli
10	4812	61.6	1452	2	US-08-087-244A-8	Sequence 8, Appli
11	4793	61.4	1452	2	US-08-652-971-4	Sequence 4, Appli
12	4793	61.4	1452	2	US-08-991-258A-4	Sequence 4, Appli
13	4793	61.4	1452	2	US-08-769-399-5	Sequence 4, Appli
14	4793	61.4	1452	3	US-08-991-953A-4	Sequence 4, Appli
15	4575	58.6	1436	2	US-08-652-971-2	Sequence 2, Appli
16	4575	58.6	1436	2	US-08-991-258A-2	Sequence 2, Appli
17	4575	58.6	1436	2	US-08-769-399-2	Sequence 2, Appli
18	4575	58.6	1436	3	US-08-991-953A-2	Sequence 2, Appli
19	4065	52.0	777	4	US-09-949-016-7158	Sequence 7158, Ap
20	3732	47.8	1075	4	US-09-949-016-6308	Sequence 830, Ap
21	1514.5	19.4	1501	2	US-08-447-464-3	Sequence 3, Appli
22	1514.5	19.4	1501	2	US-08-652-971-5	Sequence 3, Appli
23	1480	19.0	1911	2	US-08-348-006B-7	Sequence 5, Appli
24	1480	19.0	1911	2	US-08-800-825A-5	Sequence 5, Appli
25	1480	19.0	1911	3	US-09-158-657-5	Sequence 5, Appli
26	1480	19.0	1911	5	PCT-US94-0166-5	Sequence 5, Appli
27	1170.5	15.0	1099	1	US-08-015-985-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-652-971-3
; Sequence 3, Application US/08652971
; Patent No. 5814507

GENERAL INFORMATION:
 APPLICANT: Cheng, Jill
 ADDRESS: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd.
 CITY: South San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,971
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 225-3216
 TELEFAX: (415) 952-9881
 TELEX: 910 371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-652-971-3

Query Match 100.0%; Score 7809; DB 2; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0;

QY 1 MDVAAAALPAFVALWLYPWPLIGSALGSAGGCTEDDGPACDHYQDLYDDPEWVHVS 60
 Db 1 MDVAAAALPAFVALWLYPWPLIGSALGSAGGCTEDDGPACDHYQDLYDDPEWVHVS 60

Qy 61 AQEPHYLPPENFQGSTMVDPSSNNHDPGEKARILQLPTMKENDTHCIDFSYLYSOKGLNPG 120
 Db 61 AQEPHYLPPENFQGSTMVDPSSNNHDPGEKARILQLPTMKENDTHCIDFSYLYSOKGLNPG 120
 Qy 121 TLNLYRVNKGPLANPWNITGFTGRDWLRALBAVSTFWPEYQVIFEAEVSGGRSGYIA 180
 Db 121 TLNLYRVNKGPLANPWNITGFTGRDWLRALBAVSTFWPEYQVIFEAEVSGGRSGYIA 180
 Qy 181 IDDIQVLSYPCDKSPFLRLGDVEVNAQONATFOCIAIGRDAVHNLWLQRNGEDIPVA 240
 Db 181 IDDIQVLSYPCDKSPFLRLGDVEVNAQONATFOCIAIGRDAVHNLWLQRNGEDIPVA 240
 Qy 182 IDDIQVLSYPCDKSPFLRLGDVEVNAQONATFOCIAIGRDAVHNLWLQRNGEDIPVA 240
 Db 182 IDDIQVLSYPCDKSPFLRLGDVEVNAQONATFOCIAIGRDAVHNLWLQRNGEDIPVA 240
 Qy 241 QTKNINHRFAASERLQVETKTDQDLYRCVTOSERGGSVSNFAQLIVREPRPTAPPOL 300
 Db 241 QTKNINHRFAASERLQVETKTDQDLYRCVTOSERGGSVSNFAQLIVREPRPTAPPOL 300
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 Db 301 GVGPTVLLIQLNANSITIGDGPILKEVYRMTSGSWTEHANAFTYKLWHDPOTEYBI 360
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 Db 361 RVLTRPREGGTGLPGLPLITRTKCAEPMRPTKTLXIAEOTARRIAWDWESLGYNITRCH 420
 Qy 421 TENVTCIHYFHGNESRADCLMDPKAPQHVNHLPPYTNYSLKMLTNPEGRKESET 480
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 Db 541 GPOTVSNLWNSTHYFMHLHGTTYOFIRASTVKGFPATAINVTTNISAPSLSPDYEG 600
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 Db 601 VDSLNETATTITVLRLPAQAGAPISAQIVVEQLPHPRTKREAMECYQPVYQNA 660
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 Db 781 KKRKDANGNTROTMHNAMDRSYAQSOTLHAEDPLSLTMQDNFSPLNDPLVPTA 840
 Qy 841 VLDENHSATAESSRLIDPVRLCEGTESPYQTGQLHPAIRYADLQHNLMTSDSYGFK 900
 Db 841 VLDENHSATAESSRLIDPVRLCEGTESPYQTGQLHPAIRYADLQHNLMTSDSYGFK 900
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 Db 961 WLYRDGYORPSHYIATQGPVHETTYDFWRMWMQEQA S A C I V M N L Y E V G R Y C Y K W P D D 1020
 Qy 1021 TEVYGDPMKTVTCYMEPLAEYVVTFTLERRGYNETIREVKOPHTGWDHGVPYHATGLS 1080
 Db 1021 TEVYGDPMKTVTCYMEPLAEYVVTFTLERRGYNETIREVKOPHTGWDHGVPYHATGLS 1080
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 Db 1201 VTPRLOAEDCSIACLPRNHDKNRFMDLPDDRCLPFLITIDGESNYINALMDSYRQPA 1260
 Qy 1261 AFIVTOYPLINTVKEFWRLVYDGCCTSMILNEVLSQCGQYMWDEGMLRYGPQVEC M 1320
 Db 1261 AFIVTOYPLINTVKEFWRLVYDGCCTSMILNEVLSQCGQYMWDEGMLRYGPQVEC M 1320
 Qy 1321 SC5MCDVNRNIFRCNLTRPQEGTLMVOOPOYLWASHREBPGSKRSFLKLILQVEKWO 1380
 Db 1321 SC5MCDVNRNIFRCNLTRPQEGTLMVOOPOYLWASHREBPGSKRSFLKLILQVEKWO 1380
 Qy 1381 EECBEGEGRTIHCINGGRSGMFCAGIVEMVRQNVYDFHVAKTLYRNSKPNVNEAP 1440
 Db 1381 EECBEGEGRTIHCINGGRSGMFCAGIVEMVRQNVYDFHVAKTLYRNSKPNVNEAP 1440
 Qy 1441 EQYRCYDVALEYLISS 1457
 Db 1441 EQYRCYDVALEYLISS 1457

RESULT 2
 US-08-449-644-1
 ; Sequence 1, Application US/08449644
 ; Patent No. 5856162
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlessinger, Joseph
 ; APPLICANT: Sap, Jan M.
 ; APPLICANT: Ulrich, Axel
 ; APPLICANT: Vogel, Wolfgang
 ; APPLICANT: Fuchs, Miriam
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROLINE
 ; TITLE OF INVENTION: PHOSPHATASE-KAPPA
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/449,644
 ; FILING DATE: 24-MAY-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/087,244
 ; FILING DATE: 01-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7683-042
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-869-8844/9741
 ; TELEFAX: 212-869-8844/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1457 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-449-644-1

Query Match 100.0% Score 7809; DB 2; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 781 KCRKDANGNTQEMTHYNAQMSYADQSTLHAEDPLSLTMDOHNSPRLNDPLVPTA 840
 781 KCRKDANGNTQEMTHYNAQMSYADQSTLHAEDPLSLTMDOHNSPRLNDPLVPTA 840
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 841 VLDENHSATAESSRLDYPRLCEGTESTYQTGOLHPA1TRADLQH1QTMKTSDSYGFK 900
 841 VLDENHSATAESSRLDYPRLCEGTESTYQTGOLHPA1TRADLQH1QTMKTSDSYGFK 900
 961 WLYRDGYQRPShYIATQCPVHETTYDFKRMVMEQSACIVMTNLVEGRVKCYKWPDD 1020
 961 WLYRDGYQRPShYIATQCPVHETTYDFKRMVMEQSACIVMTNLVEGRVKCYKWPDD 1020
 1021 TEVYGDPKVTCYMEPLAEYVVRTFLEERRGNEIREVQFHFTGWPDHGVPTATHGLLS 1080

Db 1021 TEVYGDPKVTCYMEPLAEYVVRTFLEERRGNEIREVQFHFTGWPDHGVPTATHGLLS 1080
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 Db 1081 FIRRKVLNSNPPSAGIVVHCSAGAGRGTGCVIVIDIMLDAEREGVDIYNCVRLRSRR 114
 Qy 1141 NNVQTEBQYIFTHDAILEAACLGCBTAIPVCCEFAAYFDMRIDSOQNTHSHLKDDEQTLN 1200
 Db 1141 NNVQTEBQYIFTHDAILEAACLGCBTAIPVCCEFAAYFDMRIDSOQNTHSHLKDDEQTLN 1200
 Qy 1201 VTPRLOQAEDC5TACLPBNHDKRBFMDMLPPDRCLPLITIDGESSNYNAALMSYRQPA 1266
 Db 1201 VTPRLOQAEDC5TACLPBNHDKRBFMDMLPPDRCLPLITIDGESSNYNAALMSYRQPA 1266
 Qy 1261 APIVTOVPLPNVYKDFPLVLYDGCTSIVMLNEVDSLSCQPCQIWPEGMRLRYGP1QVEC 1332
 Db 1261 APIVTOVPLPNVYKDFPLVLYDGCTSIVMLNEVDSLSCQPCQIWPEGMRLRYGP1QVEC 1332
 Qy 1321 SC5MDDCDVNRIFRICNLTROPGYLMVQQFOYLGWASHREPVPGSKRSFSLKLILQVEK 1388
 Db 1321 SC5MDDCDVNRIFRICNLTROPGYLMVQQFOYLGWASHREPVESKRSFSLKLILQVEK 1388
 Qy 1381 ECECEGRTITHCLNGGRSMFCAGIVVENVKRNQVVDVTHAVKTLRNSKPNMVEAP 1444
 Db 1381 ECECEGRTITHCLNGGRSMFCAGIVVENVKRNQVVDVTHAVKTLRNSKPNMVEAP 1444
 Qy 1441 EOYRFCDVALLYLESS 1457
 Db 1441 EOYRFCDVALLYLESS 1457

RESULT 3
 US-08-087-244A-1
 ; Sequence 1, Application US/08087244A
 ; Parent No. 5862755
 ; GENERAL INFORMATION:
 ; Applicant: Schlessinger, Joseph
 ; Applicant: Sap, Jan M.
 ; Applicant: Ulrich, Axel
 ; Applicant: Vogel, Wolfgang
 ; Applicant: Fuchs, Miriam
 ; Title of Invention: NOVEL RECEPTOR-TYPE PHOSPHATASE-KAPPA
 ; Number of Sequences: 11
 ; Correspondence Address:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/087-244A
 ; FILING DATE: 01-JUL-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7683-042
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-869-8864/9741
 ; TELEFAX: 212-869-8864/9741
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 157 amino acids
 ; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-087-24A-1

Query Match	100 0% ; Score 7809 ; DB 2 ; Length 1457;	Db	961 WLYRDGYQRSHYIATQGPVHETVYDFWRMVWQEQSACIVMVTNLVEGRVKCYKWPDD 1020
Best Local Similarity	100 0% ; Pred. No. 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;	Qy	1021 TEVYDGFKVTCVEMPLAEVTVRTTLERRGYNEREVQFHFTGWPDHGVPHETVYDFWRMVWQEQSACIVMVTNLVEGRVKCYKWPDD 1080
Matches 1457; Conservative 0;		Db	1021 TEVYDGFKVTCVEMPLAEVTVRTTLERRGYNEREVQFHFTGWPDHGVPHETVYDFWRMVWQEQSACIVMVTNLVEGRVKCYKWPDD 1080

Qy 1 MDVAALPAFALWLLYPWPLGSALQFSAAGCTFDGPGACDWHQLDDEWHS 60
Db 1 MDVAALPAFALWLLYPWPLGSALQFSAAGCTFDGPGACDWHQLDDEWHS 60
Qy 61 AQEPHYLPPEMFQSYMVVDSSNHDGEKARLQLPMTKENTHC1DFSYLILYSQKGLNPG 120
Db 61 AQEPHYLPPEMFQSYMVVDSSNHDGEKARLQLPMTKENTHC1DFSYLILYSQKGLNPG 120
Qy 121 TLNLYRVNKGPLANPIWNTGFTGRDWLRALAVSTFWPEYQVIFEAEVSGGRSGYIA 180
Db 121 TLNLYRVNKGPLANPIWNTGFTGRDWLRALAVSTFWPEYQVIFEAEVSGGRSGYIA 180
Qy 122 AFITVQYPLNTVQDFKWRLYDYGGTSIVMLNEVDSLQSGCPQYWPEEGMRLRYGPQVECML 1320
Db 122 AFITVQYPLNTVQDFKWRLYDYGGTSIVMLNEVDSLQSGCPQYWPEEGMRLRYGPQVECML 1320
Qy 123 VPRLOAEDSIAICPRNHDKRNFMMLPPDRCLPLITDGESESYINALMDSYRQPA 1260
Db 123 VPRLOAEDSIAICPRNHDKRNFMMLPPDRCLPLITDGESESYINALMDSYRQPA 1260
Qy 124 AFITVQYPLNTVQDFKWRLYDYGGTSIVMLNEVDSLQSGCPQYWPEEGMRLRYGPQVECML 1320
Db 124 AFITVQYPLNTVQDFKWRLYDYGGTSIVMLNEVDSLQSGCPQYWPEEGMRLRYGPQVECML 1320
Qy 125 SCSDMCDVNRIFRICNLTRPOEGYLIVMQOFOYLGMASHREVPGGSKRSFLKLILQVEKWQ 1380
Db 125 SCSDMCDVNRIFRICNLTRPOEGYLIVMQOFOYLGMASHREVPGGSKRSFLKLILQVEKWQ 1380
Qy 126 BECEBEGRTIHCLNGGRSGMFCAIGIVVEMVRQNVYDVHFHVKTLRNSKPNNVEAP 1440
Db 126 BECEBEGRTIHCLNGGRSGMFCAIGIVVEMVRQNVYDVHFHVKTLRNSKPNNVEAP 1440
Qy 127 EQYRFCDYDALEYLSS 1457
Db 127 EQYRFCDYDALEYLSS 1457

RESULT 4
US-08-991-258A-3
; Sequence 3, Application US/0891258A
; Patent No. 592887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOMBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; PRIORITY/DOCKET NUMBER: A-63478-3/WHD/MTK
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (415) 781-1989
; TELEX: (415) 398-3249

Qy 128 KTKCVRATKAATAEDEVIPAKQTDRVKIAGISAGILYVILLVVVIVKSKLA 780
Db 128 KTKCVRATKAATAEDEVIPAKQTDRVKIAGISAGILYVILLVVVIVKSKLA 780
Qy 129 KTKRDANGNTROEMTMVNAMRSYADQSTLHAEDPLSLTMQHNSPRLNDPLVPTA 840
Db 129 KTKRDANGNTROEMTMVNAMRSYADQSTLHAEDPLSLTMQHNSPRLNDPLVPTA 840
Qy 130 LGGGAPYFAELPPGNLPEPAPFTYDNRTYKGFVNPLAPRKGYNIYFQAMSSEKET 720
Db 130 LGGGAPYFAELPPGNLPEPAPFTYDNRTYKGFVNPLAPRKGYNIYFQAMSSEKET 720
Qy 131 KTQCVRATKAATAEDEVIPAKQTDRVKIAGISAGILYVILLVVVIVKSKLA 780
Db 131 KTQCVRATKAATAEDEVIPAKQTDRVKIAGISAGILYVILLVVVIVKSKLA 780
Qy 132 EYESFFEGQSASWDVAKDQNAKQYGNITAYDSRSLVQVEDPSSDYYINANYIDI 960
Db 132 EYESFFEGQSASWDVAKDQNAKQYGNITAYDSRSLVQVEDPSSDYYINANYIDI 960
Qy 133 WLYRDGYQRSHYIATQGPVHETVYDFWRMVWQEQSACIVMVTNLVEGRVKCYKWPDD 1020

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 STRANDEDNESS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-991-258A-3

Query Match 100.0%; Score 7809; DB 2; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0;

Qy	1 MDVAALAPAFVALWLYPPFLGSGALGFSAGGCTFDGPAGCDYHQLYDDPEWVHS	60	Qy	901 EYESEFFEGOSASWDVAKKDQNRAKRNRYGNIIAYDHSRVLQPVEDDPSSDYINANYIDI	960
Db	1 MDVAALAPAFVALWLYPPFLGSGALGFSAGGCTFDGPAGCDYHQLYDDPEWVHS	60	Db	901 EYESEFFEGOSASWDVAKKDQNRAKRNRYGNIIAYDHSRVLQPVEDDPSSDYINANYIDI	960
Qy	61 AEPEPHYLPEMPQGSYMWDSNHDPGEKARLQLPMTKENDTHCDFSYLISQKGLNPG	120	Qy	961 WLYRDGYQRPSHYIATOGPYHETTYDFWRMVMWQOSACIVMTNLVEGRVKCYKXWPDD	1020
Db	61 AEPEPHYLPEMPQGSYMWDSNHDPGEKARLQLPMTKENDTHCDFSYLISQKGLNPG	120	Db	961 WLYRDGYQRPSHYIATOGPYHETTYDFWRMVMWQOSACIVMTNLVEGRVKCYKXWPDD	1020
Qy	121 TINLILVRVNGPLANPIWNTGFTGRDWAELAVSTFWNNEYQVTFEAEVSGERSGYA	180	Qy	1021 TEVYDFKTYTCVEMPLAKYVRFETLERRGYNEREVQHFTGWPDIHGVPHTTGLLS	1080
Db	121 TINLILVRVNGPLANPIWNTGFTGRDWAELAVSTFWNNEYQVTFEAEVSGERSGYA	180	Db	1021 TEVYDFKTYTCVEMPLAKYVRFETLERRGYNEREVQHFTGWPDIHGVPHTTGLLS	1080
Qy	181 IIDDQVLSYPCDKSPHFLRLGIDVETNAQQNATFOCIATGRDAVINKLMLQRNGDEPIYA	240	Qy	1081 FIRYVKLSNPPSAGPPIVHCISAGRTGCYIVIDIMLDNAEREGVTDIYNCVKALRSRI	1140
Db	181 IIDDQVLSYPCDKSPHFLRLGIDVETNAQQNATFOCIATGRDAVINKLMLQRNGDEPIYA	240	Db	1081 FIRYVKLSNPPSAGPPIVHCISAGRTGCYIVIDIMLDNAEREGVTDIYNCVKALRSRI	1140
Qy	241 QTKNINHRFAASPRQLQETKTDQDLYRCYTOSERGSYNSNPAQIIVRSPRPIAPPOL	300	Qy	1141 NMVQTEQFBIQFIHDIAIBACLGETAIPYCEFKAYAFDMTRIDSQTNSSHLDKEFQTTLNS	1200
Db	241 QTKNINHRFAASPRQLQETKTDQDLYRCYTOSERGSYNSNPAQIIVRSPRPIAPPOL	300	Db	1141 NMVQTEEQTIFHDIAIBACLGETAIPYCEFKAYAFDMTRIDSQTNSSHLDKEFQTTLNS	1200
Qy	301 GVGPYLLQINANSITGDSPIILKEVERMTSGSWTETHVNAPTYKWHLDDETEYI	360	Qy	1201 VTPRQIAEDCSIAICPRNDKPNRPMMLPPDRCLPLFTIDGESSNYINAALMDSYRQPA	1260
Db	301 GVGPYLLQINANSITGDSPIILKEVERMTSGSWTETHVNAPTYKWHLDDETEYI	360	Db	1201 VTPRQIAEDCSIAICPRNDKPNRPMMLPPDRCLPLFTIDGESSNYINAALMDSYRQPA	1260
Qy	361 RVLITRPGEGGTGLPGPPPLTRTKCAEPRTPTKTLKIAEQARRTAIWESLGYNITRCH	420	Qy	1261 AFIVTYQPLPNTVDFWRLVYDYGCTSIVMLNEVDSLSCGPQTMPEEGMLRYGPQVECML	1320
Db	361 RVLITRPGEGGTGLPGPPPLTRTKCAEPRTPTKTLKIAEQARRTAIWESLGYNITRCH	420	Db	1261 AFIVTYQPLPNTVDFWRLVYDYGCTSIVMLNEVDSLSCGPQTMPEEGMLRYGPQVECML	1320
Qy	422 TENVTCYHYFRGNESRADCLMDPKAPKOHVNHLPPTNVSKMLTNPGRKESET	480	Qy	1321 SC5MCDVNRIFCNCNLRPQEGLYMLVQFQVLYGASHREVPGSKRSFPLKLIQVEKMQ	1380
Db	422 TENVTCYHYFRGNESRADCLMDPKAPKOHVNHLPPTNVSKMLTNPGRKESET	480	Db	1321 SC5MCDVNRIFCNCNLRPQEGLYMLVQFQVLYGASHREVPGSKRSFPLKLIQVEKMQ	1380
Qy	481 IIQTBDBVPGPVPVSLOGTSFENKFLPKWKEPLEPGNLTQYEVSYSSIRSFDPAVPA	540	Qy	1381 EECSEGEGTITHCLNGGRSGMCIAIGIVVEMYKRONTVDYFAVKTLRNSKPNMVEAP	1440
Db	481 IIQTBDBVPGPVPVSLOGTSFENKFLPKWKEPLEPGNLTQYEVSYSSIRSFDPAVPA	540	Db	1381 EECSEGEGTITHCLNGGRSGMCIAIGIVVEMYKRONTVDYFAVKTLRNSKPNMVEAP	1440
Qy	541 GPPOTVSNLWNSTHVFMLHPGTTQFIRASTYKFGSPATAINVTTNISAPSPLDYG	600	Qy	1441 EQYRCYDALEYLESS 1457	
Db	541 GPPOTVSNLWNSTHVFMLHPGTTQFIRASTYKFGSPATAINVTTNISAPSPLDYG	600	Db	1441 EQYRCYDALEYLESS 1457	
Qy	601 VDASLINEATTITVLLRPAQAKGAPISAYQIIVVOLHPRTKREGAMCYQPVTVYQA	660			
Db	601 VDASLINEATTITVLLRPAQAKGAPISAYQIIVVOLHPRTKREGAMCYQPVTVYQA	660			
Qy	661 LSGGAPYPPAELPPGPNLPEAPFTVGDRTYKAGISAGILYFILLIVIVIVKSKLA	720			
Db	661 LSGGAPYPPAELPPGPNLPEAPFTVGDRTYKAGISAGILYFILLIVIVIVKSKLA	720			
Qy	721 KTOQCVRIATKAATTEPEVTPDPAKOTDRTVYKTAGISAGILYFILLIVIVIVKSKLA	780			
Db	721 KTOQCVRIATKAATTEPEVTPDPAKOTDRTVYKTAGISAGILYFILLIVIVIVKSKLA	780			
Qy	781 KKRKDAMGNTROEMTHMVAMDRSYADQSTLHAEDPLSLTFMDQHNSPRLPNDPLVPTA	840			
Db	781 KKRKDAMGNTROEMTHMVAMDRSYADQSTLHAEDPLSLTFMDQHNSPRLPNDPLVPTA	840			
Qy	841 VLDENHSATAESESSLRUDVPRYLCESTESEPTQGQLHPARVADLQHINLMKTSDSYGFK	900			
Db	841 VLDENHSATAESESSLRUDVPRYLCESTESEPTQGQLHPARVADLQHINLMKTSDSYGFK	900			

RESULT 5

US-08-769-399-3

; Sequence 3, Application US/08769399
 ; Patent No. 5976552
 ; GENERAL INFORMATION:
 ; ADDRESSEE: Genentech, Inc.
 ; APPLICANT: Cheng, Jill
 ; APPLICANT: Lansky, Laurence A.
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 ; PHOSPHATASE, PTP LAMBDA.
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 460 Point San Bruno Blvd.
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; APPLICATION NUMBER: US/08/769, 399
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreicer, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P1033
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 225-3216

TELEFAX: (415) 952-9881
 TELEX: 910 371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOGY: linear
 MOLECULE TYPE: protein

JJS-08-769-399-3

Query Match	Score	Length	DB	Match	Score	Length	DB				
Best Local Similarity	100.0%	1457		100.0%	7809	1457					
Matches 1457:	Conservative	0;	Pred. No.	0;	Mismatches	0;	Indels	0;	Gaps	0;	
1	MDYAAAALPAVALWLLPWPLIGSALGFSAGCTFDGPGACDYHDLDDFEWVVS	60	1	MDYAAAALPAVALWLLPWPLIGSALGFSAGCTFDGPGACDYHDLDDFEWVVS	60	1	MDYAAAALPAVALWLLPWPLIGSALGFSAGCTFDGPGACDYHDLDDFEWVVS	60	1	MDYAAAALPAVALWLLPWPLIGSALGFSAGCTFDGPGACDYHDLDDFEWVVS	60
2	AQEPHYLPEMPQGSYMDSSNHDPGEKARQLQPTMKENDTHCIDEPSYLYSQKGPNP	120	61	AQEPHYLPEMPQGSYMDSSNHDPGEKARQLQPTMKENDTHCIDEPSYLYSQKGPNP	120	61	AQEPHYLPEMPQGSYMDSSNHDPGEKARQLQPTMKENDTHCIDEPSYLYSQKGPNP	120	61	AQEPHYLPEMPQGSYMDSSNHDPGEKARQLQPTMKENDTHCIDEPSYLYSQKGPNP	120
3	TNLTVRNGKPLANPTNWTGFGRDWRAELAVSTPNEQVIFAEVSGCRGTYIA	180	121	TNLTVRNGKPLANPTNWTGFGRDWRAELAVSTPNEQVIFAEVSGCRGTYIA	180	121	TNLTVRNGKPLANPTNWTGFGRDWRAELAVSTPNEQVIFAEVSGCRGTYIA	180	121	TNLTVRNGKPLANPTNWTGFGRDWRAELAVSTPNEQVIFAEVSGCRGTYIA	180
4	IDDIQVLSPYCDKSPPHFLRLGDEVNAGGNAATFOCIATGDRDATHKLWLQRNGEDIV	240	181	IDDIQVLSPYCDKSPPHFLRLGDEVNAGGNAATFOCIATGDRDATHKLWLQRNGEDIV	240	181	IDDIQVLSPYCDKSPPHFLRLGDEVNAGGNAATFOCIATGDRDATHKLWLQRNGEDIV	240	181	IDDIQVLSPYCDKSPPHFLRLGDEVNAGGNAATFOCIATGDRDATHKLWLQRNGEDIV	240
5	QTKNINHERRFAASFLRQLQETKTQDLYRCVTOSERGSGYNSNFAQLIVREPPTAPPOL	300	241	QTKNINHERRFAASFLRQLQETKTQDLYRCVTOSERGSGYNSNFAQLIVREPPTAPPOL	300	241	QTKNINHERRFAASFLRQLQETKTQDLYRCVTOSERGSGYNSNFAQLIVREPPTAPPOL	300	241	QTKNINHERRFAASFLRQLQETKTQDLYRCVTOSERGSGYNSNFAQLIVREPPTAPPOL	300
6	GVGTTTLLQLNANSIIGGPILIKEVPRMTSCSWTETHAVNAPTYKLWHLDDPTEYEL	360	301	GVGTTTLLQLNANSIIGGPILIKEVPRMTSCSWTETHAVNAPTYKLWHLDDPTEYEL	360	301	GVGTTTLLQLNANSIIGGPILIKEVPRMTSCSWTETHAVNAPTYKLWHLDDPTEYEL	360	301	GVGTTTLLQLNANSIIGGPILIKEVPRMTSCSWTETHAVNAPTYKLWHLDDPTEYEL	360
7	RVLTRPGGGTGLPGPPILTRTCACPRTPKTLKIAIQARRIAYDWLSLGYNITRCH	420	361	RVLTRPGGGTGLPGPPILTRTCACPRTPKTLKIAIQARRIAYDWLSLGYNITRCH	420	361	RVLTRPGGGTGLPGPPILTRTCACPRTPKTLKIAIQARRIAYDWLSLGYNITRCH	420	361	RVLTRPGGGTGLPGPPILTRTCACPRTPKTLKIAIQARRIAYDWLSLGYNITRCH	420
8	TENNTICYYFRGHNESRADCCLMDPKAPOHVNNPHLPPTVNSLKMILNPGRKESET	480	421	TENNTICYYFRGHNESRADCCLMDPKAPOHVNNPHLPPTVNSLKMILNPGRKESET	480	421	TENNTICYYFRGHNESRADCCLMDPKAPOHVNNPHLPPTVNSLKMILNPGRKESET	480	421	TENNTICYYFRGHNESRADCCLMDPKAPOHVNNPHLPPTVNSLKMILNPGRKESET	480
9	IIQIDEDVGPVPVKSLQSTSFKENIKFLNKWKEPLEPNGLITQEVSYSSIRSFDPAVPA	540	481	IIQIDEDVGPVPVKSLQSTSFKENIKFLNKWKEPLEPNGLITQEVSYSSIRSFDPAVPA	540	481	IIQIDEDVGPVPVKSLQSTSFKENIKFLNKWKEPLEPNGLITQEVSYSSIRSFDPAVPA	540	481	IIQIDEDVGPVPVKSLQSTSFKENIKFLNKWKEPLEPNGLITQEVSYSSIRSFDPAVPA	540
10	GPPOTVSNIWNSTHVPMLHPGTYQFTRASTVKGPFPATINTVNISAPLPDVEY	600	541	GPPOTVSNIWNSTHVPMLHPGTYQFTRASTVKGPFPATINTVNISAPLPDVEY	600	541	GPPOTVSNIWNSTHVPMLHPGTYQFTRASTVKGPFPATINTVNISAPLPDVEY	600	541	GPPOTVSNIWNSTHVPMLHPGTYQFTRASTVKGPFPATINTVNISAPLPDVEY	600
11	VDA5NETATTITVLLRPQAOKGAPISATOIIVVQLPRTKREAGAMCYQVPTVYNA	660	601	VDA5NETATTITVLLRPQAOKGAPISATOIIVVQLPRTKREAGAMCYQVPTVYNA	660	601	VDA5NETATTITVLLRPQAOKGAPISATOIIVVQLPRTKREAGAMCYQVPTVYNA	660	601	VDA5NETATTITVLLRPQAOKGAPISATOIIVVQLPRTKREAGAMCYQVPTVYNA	660
12	LSGGAPYYFAELPGNLDEPAPTVGDRTYKCFWMNPPLAPRKGNYIQMSSVKEF	720	661	LSGGAPYYFAELPGNLDEPAPTVGDRTYKCFWMNPPLAPRKGNYIQMSSVKEF	720	661	LSGGAPYYFAELPGNLDEPAPTVGDRTYKCFWMNPPLAPRKGNYIQMSSVKEF	720	661	LSGGAPYYFAELPGNLDEPAPTVGDRTYKCFWMNPPLAPRKGNYIQMSSVKEF	720
13	KTKQCVRIATAAAEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	780	721	KTKQCVRIATAAAEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	780	721	KTKQCVRIATAAAEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	780	721	KTKQCVRIATAAAEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	780
14	TTQCVTRIAKAAATEEEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	840	781	TTQCVTRIAKAAATEEEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	840	781	TTQCVTRIAKAAATEEEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	840	781	TTQCVTRIAKAAATEEEPEVTPDPAKQTVKPFATINTVNISAPLPDVEY	840
15	VLDENHSATAESSLLDVRYLCGETESTYQGQHPARVADLQHNLIMKTSYGFK	900	941	VLDENHSATAESSLLDVRYLCGETESTYQGQHPARVADLQHNLIMKTSYGFK	900	941	VLDENHSATAESSLLDVRYLCGETESTYQGQHPARVADLQHNLIMKTSYGFK	900	941	VLDENHSATAESSLLDVRYLCGETESTYQGQHPARVADLQHNLIMKTSYGFK	900

RESULTS

US-08-991-953A-3

Sequence 3, Application US/08991953A

; Patent No. 6083748

; GENERAL INFORMATION:

; APPLICANT: Cheng, Jill

; APPLICANT: Lasky, Laurence A.

; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE PHOSPHATASE, PTP LAMBDA

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR, HOIBACH, TEST, ALBRITTON & HERBERT, LLP

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111

; COMPUTER READABLE FORM: FLOPPY disk

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,953A

FILED: 16-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/652,971

FILING DATE: 24-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H. 100 |||||
 REGISTRATION NUMBER: 24,190 100 |||||
 REFERENCE/DOCKET NUMBER: A-63478-3 /WHD/MTK 100 |||||
 TELEPHONE: (415) 781-1989 100 |||||
 TELEFAX: (415) 398-3249 100 |||||
 TELEX: 100 |||||
 INFORMATION FOR SEQ ID NO: 3 : 100 |||||
 SEQUENCE CHARACTERISTICS: 100 |||||
 LENGTH: 1457 amino acids 100 |||||
 TYPE: amino acid 100 |||||
 STRANDEDNESS: 100 |||||
 TOPOLOGY: Linear 100 |||||
 MOLECULE TYPE: protein 100 |||||
 US-08-991-95A-3 100 |||||

Query Match 100 0%; Score 7809; DB 3; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MDVAAAALPAFVALMLYPPPLGSSAGGTGCGTDDPGACDYHQIYDDPEWVHS 60	Db	1 MDVAAAALPAFVALMLYPPPLGSSAGGTGCGTDDPGACDYHQIYDDPEWVHS 60	Qy	1081 FIRRKVLNSPPSAGPPIVWHCSAGAGRGTGCYIVIDIMLDMAEREGRVDTYNCVKARLSRRI 1140
Db	1 MDVAAAALPAFVALMLYPPPLGSSAGGTGCGTDDPGACDYHQIYDDPEWVHS 60	Db	1081 FIRRKVLNSPPSAGPPIVWHCSAGAGRGTGCYIVIDIMLDMAEREGRVDTYNCVKARLSRRI 1140	Qy	961 WLYRDGYQRPSHYATOGPYHETTYDFWRMWQDQSACIYVMVNLEVEGRVKCYXWPDD 1020
Qy	61 AEQPHYLPPMPQGSYMMVDSNHDGEKARLQLQPTMKENDTHCIDSFTLISOKGLNPG 120	Db	961 WLYRDGYQRPSHYATOGPYHETTYDFWRMWQDQSACIYVMVNLEVEGRVKCYXWPDD 1020	Qy	1021 TEVYDFKVTYCVCNEPLAAYVVRFTTLERGYNBIREVKOFHFTGWPDEGVYHTATGLLS 1080
Db	61 AEQPHYLPPMPQGSYMMVDSNHDGEKARLQLQPTMKENDTHCIDSFTLISOKGLNPG 120	Qy	1021 TEVYDFKVTYCVCNEPLAAYVVRFTTLERGYNBIREVKOFHFTGWPDEGVYHTATGLLS 1080	Db	1021 TEVYDFKVTYCVCNEPLAAYVVRFTTLERGYNBIREVKOFHFTGWPDEGVYHTATGLLS 1080
Qy	1221 TLNLILVRNGKPLANPIWNTGFTGRDWLRAELAVSTFNPNKEYQVIFAEVSGGRSGYIA 180	Db	1221 TLNLILVRNGKPLANPIWNTGFTGRDWLRAELAVSTFNPNKEYQVIFAEVSGGRSGYIA 180	Qy	1081 FIRRKVLNSPPSAGPPIVWHCSAGAGRGTGCYIVIDIMLDMAEREGRVDTYNCVKARLSRRI 1140
Db	1221 TLNLILVRNGKPLANPIWNTGFTGRDWLRAELAVSTFNPNKEYQVIFAEVSGGRSGYIA 180	Qy	1141 NMVQTEEQVIFHDAILEACLGCTEAIPIVCFKAAYFMDMIRIDSQTNSHLKEFQTUNS 1200	Db	1141 NMVQTEEQVIFHDAILEACLGCTEAIPIVCFKAAYFMDMIRIDSQTNSHLKEFQTUNS 1200
Qy	1811 IDDIQVLSYPCDKSPHFLRGDVEINAGQNTFCQIATGRDAVINKLWTQRRNGEDIPVA 240	Db	1811 IDDIQVLSYPCDKSPHFLRGDVEINAGQNTFCQIATGRDAVINKLWTQRRNGEDIPVA 240	Qy	1261 AFIVTQYPLPNTVKDFWLILYDYGCTS1IMLNEDLSQGCPQWMPPEGMLRYGP1QVECML 1320
Db	1811 IDDIQVLSYPCDKSPHFLRGDVEINAGQNTFCQIATGRDAVINKLWTQRRNGEDIPVA 240	Db	1261 AFIVTQYPLPNTVKDFWLILYDYGCTS1IMLNEDLSQGCPQWMPPEGMLRYGP1QVECML 1320	Qy	1321 SCSDMCDVNRIFRICNLTRPQEGLMYQOFOQLGWASHREVPSSRSFKLKLQVEKWQ 1380
Qy	2441 QTKNINHRFAASPRLOQEVTKTDQLYRCVTSQSERGSGTSNFAOLIVRSPRPTAPPQL 300	Db	2441 QTKNINHRFAASPRLOQEVTKTDQLYRCVTSQSERGSGTSNFAOLIVRSPRPTAPPQL 300	Qy	1321 SCSDMCDVNRIFRICNLTRPQEGLMYQOFOQLGWASHREVPSSRSFKLKLQVEKWQ 1380
Db	2441 QTKNINHRFAASPRLOQEVTKTDQLYRCVTSQSERGSGTSNFAOLIVRSPRPTAPPQL 300	Qy	1381 EECBEGEGTIHICNGGERSGMFCAGIVVEMVRQNVTDVFAVKTLRNSKPNMVEAP 1440	Db	1381 EECBEGEGTIHICNGGERSGMFCAGIVVEMVRQNVTDVFAVKTLRNSKPNMVEAP 1440
Qy	3041 GVGPTYLILQNLANSITIGGPILLKEVEYKRTMTCSSWTEATHVAPTYKWLHDPDTEYI 360	Db	3041 GVGPTYLILQNLANSITIGGPILLKEVEYKRTMTCSSWTEATHVAPTYKWLHDPDTEYI 360	Qy	1441 EQYRFCDYALEYLESS 1457
Db	3041 GVGPTYLILQNLANSITIGGPILLKEVEYKRTMTCSSWTEATHVAPTYKWLHDPDTEYI 360	Db	1441 EQYRFCDYALEYLESS 1457		
Qy	3641 RVLTRPGEGTGTGLPGPPLTRTCGAEPRTPTKTLKIAQARRIAVDWSLGNITRCH 420	Db	3641 RVLTRPGEGTGTGLPGPPLTRTCGAEPRTPTKTLKIAQARRIAVDWSLGNITRCH 420		
Qy	4241 TENVTCITYFRGNESRACLMDPKAPOHVNHLPPTNVSLKMLTNPGRKESEET 480	Db	4241 TENVTCITYFRGNESRACLMDPKAPOHVNHLPPTNVSLKMLTNPGRKESEET 480		
Qy	4841 IIQTDDBVPGPVPVKSLQGTSSENKFLWKEPLEPNGLTTOVEVSYSIRSFSDPAVPA 540	Db	4841 IIQTDDBVPGPVPVKSLQGTSSENKFLWKEPLEPNGLTTOVEVSYSIRSFSDPAVPA 540		
Qy	5441 GPPQTVSNLWNSTHEVFMHLHPGTYQFTRASTVKGFPATAINTVNISASLPDYG 600	Db	5441 GPPQTVSNLWNSTHEVFMHLHPGTYQFTRASTVKGFPATAINTVNISASLPDYG 600		
Qy	6041 VDASLINEATTITVLLRPAQAKGAPSAYQIVVEOLHPRHTKREAGAMCYQVPTVYNA 660	Db	6041 VDASLINEATTITVLLRPAQAKGAPSAYQIVVEOLHPRHTKREAGAMCYQVPTVYNA 660		
Db	6041 VDASLINEATTITVLLRPAQAKGAPSAYQIVVEOLHPRHTKREAGAMCYQVPTVYNA 660	Qy	661 LSGGAPYYFAELPGCNLPPAPPTVPGDNRTYKGFNNPLAPLKPGNYNIFQAMSSVKEET 720		
Qy	661 LSGGAPYYFAELPGCNLPPAPPTVPGDNRTYKGFNNPLAPLKPGNYNIFQAMSSVKEET 720	Db	661 LSGGAPYYFAELPGCNLPPAPPTVPGDNRTYKGFNNPLAPLKPGNYNIFQAMSSVKEET 720		
Qy	7241 KTQCYRIATAAAATEPEVTPDPAKQTDVVKTAGISAGILVFLULLVVIVVKSKLA 780	Db	7241 KTQCYRIATAAAATEPEVTPDPAKQTDVVKTAGISAGILVFLULLVVIVVKSKLA 780		
Qy	7841 KKRKDAMGNTRQEMTMVNAMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA 840				

RESULT 7
 US-08-449-644-2 ; Sequence 2, Application US/08449644
 ; Patent No. 5856162
 GENERAL INFORMATION:
 APPLICANT: Schlesinger, Joseph
 ADDRESS: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449, 644
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/1933
 FILING DATE: 01-JUL-1993
 ATTORNEY /AGENT INFORMATION:
 NAME: COZZI, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE DOCKET NUMBER: 7683-042
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEX/FAX: 212-869-8864/9741
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1439
 TYPE: amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US -08-449-644-2

Query Match 97.1%; Score 7586; DB 2; Length 1439;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 1421; Conservative 12; Mismatches 5; Indels 20; Gaps 4;

Qy	1	MD-VAALARPAVALWLYPWLGSAGGCFDDPGACDYHQDLYDDFEWVHV	59
Db	1	MDTAAALARPAVALLSPWLGSAGGCFDDPGACDYHQDLYDDFEWVHV	60
Qy	60	SAQEPHYPPEMPGSTMVDDSSNNHDFGEKARLOQLPTMKENDTHC1DFSYLLYSOKGLNP	119
Db	61	SAQEPHYPPEMPGSTMVDDSDHDFGEKARLQLPTMKENDTHC1DFSYLLYSOKGLNP	120
Qy	120	GTLNLYVRNKPLANPIWNTGFTGRDWLRAELAVSTFWNEQVIFEAEGSGRSGYI	179
Db	121	GTLNLYVRNKPLANPIWNTGFTGRDWLRAELAVSTFWNEQVIFEAEGSGRSGYI	180
Qy	180	AIDDIQVLSYPCDKSPHFLRLGDVEVAGONATFOCIATGRDAVNLKLWLRNGEDIPV	239
Db	181	AIDDIQVLSYPCDKSPHFLRLGDVEVAGONATFOCIATGRDAVNLKLWLRNGEDIPV	240
Qy	240	AOTKINHRRFAASFRILQEVTKTDQDLXRCYTOSERSGSVSNFAQLIVREPPRTPAPQL	299
Db	241	AOTKINHRRFAASFRILQEVTKTDQDLXRCYTOSERSGSVSNFAQLIVREPPRTPAPQL	300
Qy	300	LGVGPTYLQNLQNLANSIIGDGPITLKEYEYMRMTSGSWTETHAVNAPTYKLWHDPTDEYE	359
Db	301	LGVGPTYLQNLQNLANSIIGDGPITLKEYEYMRMTSGSWTETHAVNAPTYKLWHDPTDEYE	360
Qy	360	IRVLTRPREGGTGLPGLPLTRTKCAEPMTPTKTLKIAEQARRAIDWLSGNITRC	419
Db	361	IRVLTRPREGGTGLPGLPLTRTKCAEPMTPTKTLKIAEQARRAIDWLSGNITRC	420
Qy	420	HTFNVNTICHYFRGHNESRADCLMDPKAPOHVNHLPPYTNVSLKMLTNPEGKESEE	479
Db	421	HTFNVNTICHYFRGHNESRADCLMDPKAPOHVNHLPPYTNVSLKMLTNPEGKESEE	480
Qy	480	TIIQTDEDPGPVPPVKSLSQGTSFENKLFLNKEPLEPNQITQYEVSYSIRSFSDFAPV	539
Db	481	TIIQTDEDPGPVPPVKSLSQGTSFENKLFLNKEPLEPNQITQYEVSYSIRSFSDFAPV	540
Qy	540	AGPPQTVSNLWNSTHAYMHLLPQGTYQFIRASTVKGFGPATIAINTNTSAPSLEPDYE	599
Db	541	AGPPQTVSNLWNSTHAYMHLLPQGTYQFIRASTVKGFGPATIAINTNTSAPSLEPDYE	600
Qy	600	GYDASLNETATTITVLLRPAQKAPISAYQIVBOLPHRTKREAGMECYQVPVYQN	659
Db	601	GYDASLNETATTITVLLRPAQKAPISAYQIVBOLPHRTKREAGMECYQVPVYQN	660
Qy	660	ALSGGGAPYYFAAELPPGNLPEPAPFTYQDFNRKGFNNPLAPRKGYNYFOAMSSVEKE	719

RESULT 8

US -08-087-244-A-2
 ; Sequence 2, Application US/0808724A
 ; Patent No. 5863755

GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph
 APPLICANT: Sap, Jan M.
 APPLICANT: Ullrich, Axel
 APPLICANT: Vosel, Wolfgang
 APPLICANT: Fuchs, Miriam
 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York

COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 COMPUTER: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/087,244A
 FILING DATE: 01-11-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-042
 TELEPHONE: 212-790-9050
 TELEFAX: 212-869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1439 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US - 08-087-244A-2

Query Match 97.1%; Score 7586; DB 2; Length 1439;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 1421; Conservative 12; Mismatches 5; Indels 20; Gaps 4;

Db 1 MD-VAAALPAFVALMLYPPLGSSALQFSAGGCTFDPGACDYHDLDDFEWAV 59
 Db 1 MD-TAAALPAFVALLSPWPLJSAQQGTSAGCFTDIDGCA 60
 Qy 60 SAQEPHYLPPEPMPOGSYMMVDSNHDPGKEARLQLPMTMKENDTHCIDFSTLYSQKGIMP 119
 Db 61 SAQEPHYLPPEPMPOGSYMMVDSHDGPKEARLQLPMTMKENDTHCIDFSTLYSQKGIMP 120
 Qy 120 GTLNIVLRVNRKGPLANPIWNTGFTGRDWIRAELEVTPNEYQVIFAEVSGRSGTI 179
 Db 121 GTLNIVLRVNRKGPLANPIWNTGFTGRDWIRAELEVTPNEYQVIFAEVSGRSGTI 180
 Qy 180 ADDIQVLSYPCDKSPHFLRGLDVEVNAGONATFOCIATGRDAVINKLWLQRNGEDIV 239
 Db 181 ADDIQVLSYPCDKSPHFLRGLDVEVNAGONATFOCIATGRDAVINKLWLQRNGEDIV 240
 Qy 240 AQTKNINHRFAASRLQEQTKTODLYRCYTOSERGSGVSNPAOLIVEPRPIAPPOL 299
 Db 241 AQTKNINHRFAASRLQEQTKTODLYRCYTOSERGSGVSNPAOLIVEPRPIAPPOL 300
 Qy 300 LGVGPTYLQLQNLANSITGGDPITLKEVETRMISCTWTHAVNAPTYKLWHDDETE 359
 Db 301 LGVGPTYLQLQNLANSITGGDPITLKEVETRMISCTWTHAVNAPTYKLWHDDETE 360
 Qy 360 IRLVLTTRGEGRTGTLGLGPPLIITRKCAEPMRTPKTLKIAEQARRIAVDESLCGYNITC 419
 Db 361 IRLVLTTRGEGRTGTLGLGPPLIITRKCAEPMRTPKTLKIAEQARRIAVDESLCGYNITC 420
 Qy 420 HTENVTICHYFRGHNESRADCLMDPKAQOHNNHLPPYTNSLKMILTNPEGRKESSE 479
 Db 421 HTENVTICHYFRGHNESRADCLMDPKAQHVNNHLPPYTNSLKMILTNPEGRKESSE 480
 Qy 480 TI IQTDEDVPCPVPSLQGTSFENKIFLAWKEPLPGLTQEVSYSSIRSDFPAVY 539
 Db 481 TI IQTDEDVPCPVPSLQGTSFENKIFLAWKEPLPGLTQEVSYSSIRSDFPAVY 540
 Qy 540 AGPPOTVSILWNSTHVFMLHPGTITYQFFTRASTVKGFGPATAINVTTNISAPSLPDXB 599
 Db 541 AGPPOTVSILWNSTHVFMLHPGTITYQFFTRASTVKGFGPATAINVTTNISAPTLPDXB 600
 Qy 600 GVDASLINEATTITIVLRLPAQAKGAPISAYQIVVLEHPRTRKEAGAMECYQVPVTYQN 659

Db 601 GVDASLINEATTITIVLRLPAQAKGAPISAYQIVVLEHPRTRKEAGAMECYQVPVTYQN 660
 Qy 660 ALSGGAPYPAEELPGPNLBPBAPPTVGDNRTYKGFWNPPLAQKGYNYFOAMSSVKE 719
 Db 661 AMSGGAPYPAEELPGNLBPBAPPTVGDNRTYQOFWNPLAQRKGYNYFOAMSSVKE 720
 Qy 720 TKTQCVRIATKAATEEPEVITDPKQTDRVKLAGISAGILQFLILLVVTVTKSKL 779
 Db 721 TKTQCVRIATK-AAPEPEVITDPKQTDRVKLAGISAGILQFLILLVVTVTKSKL 779
 Qy 780 AKKRKDAMGNTROQENTHMYNAMDRSYADQSTLHAEDPLSLTEMQDNHESPRLPNDPLVPT 839
 Db 780 AKKRKDAMGNTROQENTHMYNAMDRSYADQSTLHAEDPLSLTEMQDNHESPRY----- 831
 Qy 840 AVLDNHSATAESELLDVPYLCGETESPYQTGQLHPAIRVADLQHNLQHNLMKTSDSYGF 899
 Db 832 --- ENHNSATAESELLDVPYLCGETESPYQTGQLHPAIRVADLQHNLQHNLMKTSDSYGF 887
 Qy 900 KEKEYSFEEQGSASWDACKDQRKAKRNYGNIAWDHSRVTLQPVEDDPSSDYINANYYD 959
 Db 888 KEKEYSFEEQGSASWDACKDQRKAKRNYGNIAWDHSRVTLQPVEDDPSSDYINANYYD 946
 Qy 960 IWLYDGKQRPSPHYTATQGPVHETYDFWRMWQEOQSACIVMVTNLVEGRVCKCYKWPD 1019
 Db 947 -----DGQYQRPSPHYTATQGPVHETYDFWRMWQEOQSACIVMVTNLVEGRVCKCYKWPD 1001
 Qy 1020 DTEVYGFDTYKVTCVEMPLEYVVRTFTLERRGVNEIREVKQHFHTGPDPGVPYHATGLL 1079
 Db 1002 DTEVYGFDTYKVTCVEMPLEYVVRTFTLERRGVNEIREVKQHFHTGPDPGVPYHATGLL 1061
 Qy 1080 SFIRVKLNSNPPSAGPIVHCSAGAGRGTGIVIDIMLNAEREGVTDYNCVKALRSRR 1139
 Db 1062 SFIRVKLNSNPPSAGPIVHCSAGAGRGTGIVIDIMLNAEREGVTDYNCVKALRSRR 1121
 Qy 1140 INMYCTEEQYIFIHDAILEACLGCTTAIPVCEFKAYFDMIRIDSQTNSHLDKFQFTLN 1199
 Db 1122 INMYCTEEQYIFIHDAILEACLGCTTAIPVCEFKAYFDMIRIDSQTNSHLDKFQFTLN 1181
 Qy 1200 SVTRPLQADPSCSIALCPRNHDKNFMDMLPPDRCLPFLITDGESSNYNAALMSYROP 1259
 Db 1182 SVTRPLQADPSCSIALCPRNHDKNFMDMLPPDRCLPFLITDGESSNYNAALMSYROP 1241
 Qy 1260 AAFTVTOYPLNTYRDFWRLVYDGCSTIWMNEVDLSQSCPCQWPEBGMRLRGFIQVEC 1319
 Db 1242 AAFTVTOYPLNTYRDFWRLVYDGCSTIWMNEVDLSQSCPCQWPEBGMRLRGFIQVEC 1301
 Qy 1320 MSCSMDCDVINRIFICNLTRPQEGYLMYQFOYLGWASHREVPGSKRSFLKL11LQVEK 1379
 Db 1302 MSCSMDCDVINRIFICNLTRPQEGYLMYQFOYLGWASHREVPGSKRSFLKL11LQVEK 1361
 Qy 1380 QBECBEGEGRTIILCNGGRSGMFCAGIIVENVMKRNQVVDVFAVTLRNSKPNMVEA 1439
 Db 1362 QBECBEGEGRTIILCNGGRSGMFCAGIIVENVMKRNQVVDVFAVTLRNSKPNMVEA 1421
 Qy 1440 PEQYRFCDVALEYLESS 1457
 Db 1422 PEQYRFCDVALEYLESS 1439

RESULT 9
 US-08-419-644-8
 Sequence 8, Application US/08449644
 ; Patent No. 5856162
 GENERAL INFORMATION:
 ; APPLICANT: Schlessinger, Joseph
 ; APPLICANT: Sap, Jan M.
 ; APPLICANT: Ulrich, Axel
 ; APPLICANT: Vogel, Wolfgang
 ; APPLICANT: Puchs, Miriam
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROLINE
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449, 644
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/087, 244
 FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE DOCKET NUMBER: 7683-042
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEX: 212-869-9864/9741

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown

MOLECULE TYPE: Protein
 US-08-449-644-8

Query Match 61.6%; Score 4812.5; DB 2; Length 1452;
 Best Local Similarity 61.4%; Pred. No. 0;
 Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;

Qy 22 LIGSALGFFSAGGCTFDGPGACDYHQLYDDPEWVSAQPHYLPPMFGSTMVDS 81
 Db 14 LLLTAAGETPSGGCLPDEPYSTCGYSQSEGDDENWQVNTLTKPTSDPMPGSLMLVNVA 73

Qy 82 SNHDPEKAROLQPTMKENDTHCIDFSYLYSQSGKLNGPTLNILVRVNGKGPLANPIWNT 141
 Db 74 SGPPEGQAHLLPQLKENDTHIDFHVVSSGSNSPGLLNVVVKVNGPAGNP IWNIS 133

Qy 142 GFPGRDWRMRLAELAVSTFPNPEQYQFVEREVSGGRSGCYTAIDIOVLSPCDKSPPHELRG 201
 Db 134 GDPTTRNRAELAISTFPNFQYQFIVEV-ITSCHGQYLAIDEVKLHPCTRTPHELR IQ 192

Qy 202 DVEVNAGQNAATFOCIATGDAVENKLWLRQRNGEDIPVQATQNINHRPASFRLOEVTK 261
 Db 193 NVEVNAGQFATFCQSATGRTVAGDRNLQGIDVRAKEIKVTSSEFRFENVNTTK 252

Qy 262 TDODLYRCVTOSERGSVNSNFAOLIVREPRRAPPOLLGVSPHTYLI QLNANSITIGDGP 321
 Db 253 RDGKYKMRITRGVGGSNAYBLVKEPPVPAPOQASGATYLM QLNANSINGDGP 312

Qy 322 ILILKEYEVRMTSGSWTETHAVNAPTYKWLHDPPTEYEIRVLTTRPGEGTGLPGLPLIT 381
 Db 313 IVAREVEYCTASGSWNDRQPVDSYKIGHLDDETEYEISVLTTRPSEGTCSPGPALRT 372

Qy 382 RTKCAEPRTPKTLKIAEQARRIAWDLSGLGNITROCHTFNTVICHYFRGHNESRD- 440
 Db 373 RTKCADPMPGPRKLEVVKPSRQITVBPFGNVTRCHSYNUTVHYCQVGQEOQVRE 432

Qy 441 -CLDMDPKAPOHVNHLPPHTYSLKMLLTNPGRKSESETIQTDEDVPGVVPVKSLOG 499
 Db 433 VSMDTENSHQHTITNLSPYTNVSKLLMNPPGRKESQELIVQTDELPGAVPTSIG 492

Qy 500 TSPENKIFLNWKPEPLEPGLITQYEVSYSIRSFSDFPAVPGPQTVNSLNNSTHAFMFH 559
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :

Db	493 STFEEKIFLOWREPTQTYGVITLYBITYKAVSSFPPEIDLSNQSSRVSULKGNETHPLFFG 552
Qy	560 LHPGTTYQFPIBASTVYKGFOPATAINVNTNISAPSLPDYEGVDASUNETATTITVLRPA 619
Db	553 LYPGTTYSFTIRASTAKGFGPPATNQFTKVISAPMPAYB-LETTLNQTONVTVMLKPA 611
Qy	620 QAKGAPIASAYQIVVEQLHPTKREAGAMBCYQFVTYKONALSGAPYKPAELPGNLP 679
Db	612 HSRGPVSVQIVMEVSEKSTKTOCVRIATAKAAFTPEPEV 739
Qy	680 EPAPFTVGUDRTRYKGFWNPPLAPRKGNTYQFAMSVEKSTKTDYKCPVIFHQNQASLNSQYFAAEPADSUQ 671
Db	672 AAQPFITGDNKNTYQGWTNPLPFSYRIVFQAASRANGEKTKIDQVATKGAATPKP-- 729
Qy	740 IPDPAKOTDPRVKLAGISAGLIVLILLYVIVKSKLAKKCKRDAKGNTROEMTHMVN 799
Db	730 VPEPEQTDHTVKIAGVIAIGLFLIFTGLSVLYMKRKLAKCCKETMSSTROENTVMVN 789
Qy	800 AMDRSYADQSTLHAEDPLSLTFMDORNFSPLPNPD-----LYPTAVL_DENH 846
Db	790 SMDKSYAEQQGTCNCDE -- ASFEMDTHNLNGRSVSSPSSFTMKNTLSTSVPNSVYDPETH 846
Qy	847 SATASSRULDVPRY-LCEGETSPYOTGOLHPATVADLQHINLMKTSDSYGFEBEYES 905
Db	847 TMASDTSLSVQSHTYKREPADVPTQGOLHPAIRVADLQHITOMKCARGYGFEEYES 906
Qy	906 FFEQGOSASWDVAKKQNBKRNBYGNLIAJDHSRSRVTLQPYVEDPSSDYYINANYIDDIWLYRD 965
Db	907 FFEQGOSAPWDSAKKENRMKNRYGNLIAJDHSRSVLTQDGTNDSYDINGNYI-----D 960
Qy	966 GYQRPHYIATQGPVHETVDFWNTWQEQSACTIMVNLVEGVYKCYKWPDDTEVYG 1025
Db	961 GYHRPHYIATQGPQETI DFWRYWHENTAIIIMVNULEGVYKCCKYWPDDTEIYK 1020
Qy	1026 DFKVTCVEMEPLAETVVRTPLERGYNIREVKOFHFTGMPDHGPVYHATGLLSPTRRV 1085
Db	1021 DIKVTLJETELLAEVTRPAVEKGVHEIREIQHTFMPDHGPVYHATGLLGTVRQV 1080
Qy	1086 KLSNPPSPSAGPITYVHCSAGAGRTGCIVIDIMDMAEREQVUDIYNCVAKLRSRRINMVOT 1145
Db	1081 KSKSPSPSAGLIVHCSAGAGRTGCIVIDIMDMAEREQVUDIYNCVREIRSRRINMVQT 1140
Qy	1146 BEQYIPTHDALEACLGCETAIPVCEFKAAFYDMRIDQSQTNSHILKDEFOTINSYTPRL 1205
Db	1141 BEQYIPTHDALEACLGDISVPSAQRSYLQYDMMKLDPQNSQKEEPTLNWYPTL 1200
Qy	1206 QAEDCSTACLPRNHDKRNFMDMLPPDRCLPLITDGESSNYINAALMDSYRPAFAFIVT 1265
Db	1201 RVEDCSTAILPRNHDKRNCMDLPPDRCLPLITDGESSNYINAALMDSYQPSAFIVT 1260
Qy	1266 QYPLPNTYKDFWRLYDYGCTSIVMLNEVLDLSQGCPQWPEEGMLRYGPJOVECMSCSMID 1325
Db	1261 QHPLPNTYKDFWRLYDHYCTSVMLNDVDAQLCQYWPQWVHHGPJOVEFSADLE 1320
Qy	1326 CDVNRIFRICNLTRPQEGYLIVMQOFOYLGMASHREVPGSKRSFELKLILQVEKMWQRECEC 1385
Db	1321 EDIISRFYRNAARQDGTMVBMQOQFLGPMPYRDTPSKRSEPLKLURQDWMQBEYNG 1380
Qy	1386 GEGTRIHCUNGGRGSGMCAIGIVEMVKQNVVDVFHAVKTLLNSKPNVTEAPQOYRF 1445
Db	1381 GEGPTVTHCLNGGRSGTFCNISIVCEMLRHQRTDVPHAVKTLLNSKPNMVDLDDQYKF 1440
Qy	1446 CYDVALYLES 1456
Db	1441 CYEVALYLENS 1451

RESULT 10
 US-08-087-244-A-8
 ; Sequence 8, Application US/08087244A
 ; Patent No. 583755
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlessinger, Joseph

APPLICANT: Sap, Jan M.
 APPLICANT: Ullrich, Axel
 APPLICANT: Vogel, Wolfgang
 APPLICANT: Fuchs, Miriam
 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
 TITLE OF INVENTION: PHOSPHATASE-KAPPA
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE S. EDMONDS
 CITY: 1155 Avenue of the Americas
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/087, 244A
 FILING DATE: 01-JUL-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-042
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864/9741
 TELEX: 66141 PENNIE
 TELEFOR: FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US - 08-087-244A-8

Query Match Score 4812.5; DB 2; Length 1452;
 Best Local Similarity 61.4%; Pred. No. 0;
 Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;

Qy 22 LIGSALGQQSSAGGCTPDDGCGACDHYQHDLYDDFWHVAQAEPHYLPPMPQGSYMWDS 81
 Db 14 LLTAAAGETSGGCFLDEPYSTCGYSQSBDDEWEQVNTLTKPTSDPMPGSSMLVNA 73
 Qy 82 SNHDFGEKARQLQPLTMKENDTHCIDFSYLLYSQSGLNPLNTLVVNGKPLANPIWNT 141
 Db 74 SGRPGQRAHILLPOLKENTHC1DFHYFVSSKNSNPGLNVTVNGNGLPNPIWNS 133
 Qy 142 GFTGRDWJLRAELAYSTEWNPNEYQVIFEAEGGRSGYIAADDIQVLSYCPDKSPHELG 201
 Db 134 GDPTKTWNRAELAISTFWNPFYQVIFEV_ITSGHGYLLADEVKLGHECTRTHFLR1Q 192
 Qy 202 DVEINAGQNTFOCATGRDAVHNKLWLQRNGEDIPVQTKNINHRPAASPLQEVTK 261
 Db 193 NVEVAGQAFATFOCSAIGRTVAGDRWLQGIDVRDAPLKEIKVTSSRRTIASPVNNTK 252
 Qy 262 TDQDLYRCUTQSERGSGVSNFAOLIVREPREPPIAPPOLGVGPTYLQIOLANANSIIGDCP 321
 Db 253 RDAGKVRMWRTEGGGINSYAAELVKEPPVPIAPPQLASVGATLWQIOLANANSINGDP 312
 Qy 322 IILKEVEYRMISGSMWTEHAWNAPTYKLWHDPTOEYERTRVLTRPGBGTGLGPPLIT 381
 Db 313 IVAREVEXCTAGSNNDRQFDSTSYSKIGHLDPTOEYELSVLTRPGEKGTSGPALRIT 372
 Qy 382 RTKCAEPMRTPKTLKIAEIQARRIAWDWSLGYNTRCFENVTCYHFRGNESRAD- 440
 Db 373 RTKCADPMRGPRKLEVEVEYKSROITIRWEPFGNVTRECHSYNLTHYCQVGQEOVRE 432
 Qy 441 -CLMDPKAQHQVYNHLPPPTNVSLKMLTNPEGRKESSETIQTDEDPGPVVKSLQ 499

Db 433 VSWDTENSHPQHTITNLSPYTNVSKLILMNPGRKESQELIVQTDEDLPGAVPTESIQ 492
 Qy 500 TSFENKIFUNWKPEPLPQNGLITOEVSYSSIRSFRPAVAGPPCTVSILAWNSTHVFHM 559
 Db 493 STFEKIFLQWRREPQTYGVTILFBITYKAQSSPFRSUSKGNETHFLFFG 552
 Qy 560 LHPCTTYQFPIRASVTKGFPATAINVTNISAPS LPDYEVDASLNEFATTITLRLPA 619
 Qy 553 LYPTGTYSFPIRASVTKGFPATNQFTKISAPSMPAYE-LETFLNQTDNTVTLMLKPA 611
 Db 620 QAKGPAPISAYQIVVQLHPTKRBAGAMBCYQVPTVNONALSGGAPYFAAEELPGNLP 679
 Qy 612 HSRGPBVPSVYQIVVBEERPRTKTTEILKCYPVIFHQNASLINSQYFAAEFPADSLQ 671
 Db 680 EPAPPTVGDNRTYKGFNNPLAPRKPGKQNYFOAMS SVEEKETKOCVRLAKAKRDAMGNTQEMTHMTN 739
 Db 672 AAQPPTGDKNTKINGWNTPLPKSYRIFQQAASRANGEKTDKVQVATKGATPKP-- 729
 Qy 740 IPDPAKQDTRVUKLAGISAGLIVPILLWVTKSKLAKRKDAMGNTQEMTHMTN 799
 Db 730 VPEPEKOTDHTVKLAGVLAGILFVTTIFGVVLWMKRKLAKRKETMSSTROEMTMVN 789
 Qy 800 AMDRSYADOSTLHAEDPLSLTFMWHQNFFPRLPNDP-----LVPTAVL-DENH 846
 Db 790 SMDSXSAEQGTCNDE--AFSEMDTMHNGLNGSVPSSFTMKINTLSTSVNPNSYYPDETH 846
 Qy 847 SATABSSRLLDVPRY-LCIGCTESPYQTGOLHPATRADILQHNLMKTSDSYGRKEEYRS 905
 Db 847 TMASTDSSVLSQSHYTKKREPADVYQTGOLHPATRADILQHNLQHNTQMKCAGBGGPRKEEYRS 906
 Qy 906 FPEQGOSASHDVAKDQNZAKRKNRYGNMIIAYDHSSRVLQPYEDDSSDYINANYIDIWLYRD 965
 Db 907 FFEQGQAPDSDAKKDENRMKNRGCNIIAYDHSSRVLQFQLEGDTNSDYZNGNYI----D 960
 Qy 966 GYQRPHYIATQGPVHETVYDFWMWWQEQSACTIVMVNLVEVGRKCYKWPDDTEVYV 1045
 Db 961 GYHRPHYIATQGPMEIYDFWMWHTENTASIMVTLNVEVGRVCKCKYWPDDTEIYK 1020
 Qy 1026 DFKVTCVNEPLAEYVVRIFTBLERGRYNEIREYQFHFTGWPDGVPYHATGLLSFIRR 1085
 Db 1021 DIKVLTIELBLASVIRTAVERGVHVBIRETRQHFHTGWPDGVPYHATGLGTVRQV 1080
 Qy 1086 KLSNPNPSAGPVIYHOSAGAGRGTGYYIVIDMLDMAEREQVDIYNCVKALESBRINNMVQT 1145
 Db 1081 KSKSPPSAGPVIYHOSAGAGRGTGCFIVIDMLDMAEREQVDIYNCVRLRSRBRINNMVQT 1140
 Qy 1146 EQQVFIHDIALELCGETAIPVCEKAYFDMIRISQTNSSHLKDEFQTONSVPBL 1205
 Db 1141 EQQVFIHDIALELCGETAIPVCEKAYFDMIRISQTNSSHLKDEFQTONSVPBL 1200
 Qy 1206 QAEPICSIACLPRHNDKPRFMDMIPPDRCLPFLITDGESENLYNAALMDSYROPAFIVT 1265
 Db 1201 RVEBCSIALLPRNBKRNCMDLIPDRCLPFLITDGESENLYNAALMDSYKQSAFIVT 1240
 Qy 1266 QYPLPNTVKDFMPLVYDYGCTSIVMLNEVDSLQGCPQTWPEEGMLRYGPQIQCMSCSMD 1325
 Db 1261 QHPLPNTVKDFWRLVLDYHTCSVMLNDYDPAOLCPQYWPGNGTHRGFIQVERVSADL 1320
 Qy 1326 CDVNRIPRICNLTROBEGYLMYQFOYLGWASHREVEPSKRSPLKL1LQEVKNQECB 1385
 Db 1321 EDISIRIFRINYAARPDGYRMQFQFLGWPMYRDTFVSKRSFLKL1RQVDKRNQEYNG 1380
 Qy 1386 GEGRTIHLNGGGRSGMFCAGIGIVENYKRONVVDYHAWKTLRNSIENPMYTAPEQYRF 1445
 Db 1381 GEGPTVHHLNGGGRSGTFCASIVCEMLRHQRTDVFHAWKTLRNSIENPMYTAPEQYRF 1440
 Qy 1446 CYDVALEYLES 1456
 Db 1441 CYEVALLEYLNS 1451

US-08-652-971-4

; Sequence 4, Application US/08652971

; Patent No. 5844507

GENERAL INFORMATION:

APPLICANT: Cheng, Jill

APPLICANT: Lasby, Laurence A.

TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE

PHOSPHATASE, PTP LAMBDA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: 10

ADDRESSSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd.

CITY: South San Francisco

STATE: California

ZIP: 94080

COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,971

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1033

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 225-3216

TELEFAX: (415) 952-9881

TELEX: 910 371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1452 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-971-4

Query Match 61.4%; Score 4793.5; DB 2; Length 1452;

Best Local Similarity 61.3%; Pred. No. 0;

Matches 889; Consensus 208; Mismatches 325; Indels 29; Gaps 9;

Qy 22 LIGSALGOFSGAGCTFDGPACDYHODLYDDFWTHVSAQEPhYLPEMPOGSYXWDS 81

Db 14 LLTAAGTTFSGCLFDPPYSTCGYSDAEDDFENWEGVNTLTKPTSDPMMPSGSFLVNT 73

Qy 82 SNHDPEKARLQLOPTMKENDTCIDESYLISQSKGLNPGTINLIVRUNKGLANPNTWNT 141

Db 74 SGKPEGORAHLLPQLKENDTHC1DHFYVSSKSNSAAGLNLNVYVCKNGPLGNPNTWNT 133

Qy 142 GFPGRDWIRAEALAVSTFWPNENQVIFEALESVSGRSGYIAIDDIQVLSYPCDKSPHFLRG 201

Db 134 GDPTRTHPRRAELISTFWPNFQVIFTY-VTSGHQGIADEKVLPCHPTPHFLRQ 192

Qy 202 DVEVNAGGONATFOCIATGRDAHYNKWLQRNRNGDITPACTNNINHRFAASFRLOEVTK 261

Db 193 NVEVNAGGOFATFOCSAIGRTVAGDRLWQIDVRDAPKEIKVTSSRFRIASFNVNTK 252

Qy 262 TDDLYRCVTSQSRGSSNSNEQLIUVEPPIRAPPOLQGSGPTYLQIQLANNSILGDGP 321

Db 253 RDAGKVRMTCIEGGVGNSYNAELVVEPPVAPPOLASGATYLIQLANNSINGDGP 312

Qy 322 LIKEVEPRMTSSSWTEHAVNAPTYKWHLDPTTEYIULTRPSEGTTGLPGPLLT 381

Db 313 IVAREVETCTSSWWNDQPVDSYKIGHLDPTTEYIULTRPSEGTTGLPGPLLT 372

Qy 382 RTKCAEPRTPKTLKIAQARRIAYDWEWSLGYNITRCHTNTYFRGHNESRAD- 440

Db 373 RTKCADPRTGPRKLEVVETVKRSQQTIRWEFGNIVTRCHSYNLTVHYQVGGQEVREE 432

441 -CLMDMPKAQPHVYVHLPPYTNTVSLKMLTNPCEGRKESEETIOTIDEDYEGPVPKSLOG 499
 Qy Db 433 VSWDDTDSHSQHTTINLSPATNSVSKLIMNPCEGRKESEQLTVDDEDLGAVPPESIQ 492
 Qy 500 TSPENKIFLWKPEPLEPGNLTQYVSYSSISRSPEPAVAGPPPTVSNLWNSTHVNEMH 559
 Db 493 SAFBKSKIPLOWREPTOYGVITLYEITYKAVSSPFPEIDLSNOSGRVSXLGNETFLFFG 552
 Qy 560 LHPGTTYQFPTRASTVKGFSPATAINVNTNISAPLPDVGDASLNEPATTTVLRLPA 619
 Db 553 LYPTGTTYSFTIRASTAKGFSPATNQFTKISASMPATE-ETFLNQIDNTVTLKPA 611
 Qy 620 QAKGAPISSAYQIVVQLPHRTKREBAGAMCYQVPTVYONALSGGAPYFAAEFPGNLIP 679
 Db 612 QSRGPAPSVYQIWVEBERPRTKCTEILKCYPVJHFQNASILNSQYFAAEFPADSLQ 671
 Qy 680 EPAPPTVGDNRTYKCFWNUPPLAPRKGYNYQFAMSVEKETKTQCVTRAKAAATPEPEV 739
 Db 672 AAQPTTIGDNKTYNQSYWNTPLPHKSYRYYQAAGRANGEETKIDCVRVATKGAVTPKP-- 729
 Qy 740 IPDPKQTDREVVKLAGISAGILVFLILLVIVTRKSKLAKRKDAMGNTROENTHMVN 799
 Db 730 VPEPEKQTDHTVKZAGVTAGILFLVPLGWLVNLKGRKLAKRKETMSSTROENTVMN 789
 Qy 800 AMDRSYADOSTLHARDPLSLTMDHOHNSPRLNPDP-----LYTAVLU-DENH 846
 Db 790 SMDKSTAEOQTNCDE--AFSMGTHNLNERSVSPSSFTMKTINTLSTSVPNSYYPDETH 846
 Qy 847 SATASSRLLDVPRY-LCGETTESPYQTQGOLHPAIRVADLQHINLMKTSDSYGFKEYES 905
 Db 847 TMASDTSLLAQPTYKREAADVPQTQGOLHPAIRVADLQHITQMKCAEGYGFKEYES 906
 Qy 906 FFEQQGASWYAKQDNRAKNRGNIAIDHSRVLQFVTPYDPPSDYINANYIDWLYRD 965
 Db 907 FFEQQGAPWDPSACKDENRMKRNQYGNIAIDHSRVLQMLEGDNNSDINGNYI----D 960
 Qy 966 GYQRPSHYIATQGPHYTHETYDFWRKMWQEPOSACTVNTNLIVEGVKVKYWPDPDTEVYG 1025
 Db 961 GHRRHNYIATQGPQETIDFWRNWHENTASIMVNLYEVGRYKCCYWPDPDEIYK 1020
 Qy 1026 DFKVTCVEMPLAEYVTRPTELERGYNEIREVKQFHFTGMPDHGVPYHATGLLSFIRR 1085
 Db 1021 DIKVLTIDTELLAETVTPAVEKGTHEIREIQHFTGMPDHGVPYHATGLLSFVRQV 1080
 Qy 1086 KLSNIPSAGIIVRHSAGAGRTGCVTVIDMLDMAREGVYDINYCTKALSRRNIMVOT 1145
 Db 1081 KSKSPNAGLPLVHSSAGRTGCFVIDIMLDMAEREGVYDINYCVRELRSRNVNMVOT 1140
 Qy 1146 BEQYIPTHDALCICGETAIPIVCEPKFAAYFDMRIDTSQTNSHLKDFTOTLNSTYTPRL 1205
 Db 1141 BEQYIPTHDALCICGDTISPAQSVRLYDMMKLDPQINSSQIKEFPTLNWYPTPL 1200
 Qy 1206 QAEDCSIACLPRNHDKNRFEDMLPPDRCLPFLITDGESSIONYINAALMDSYRQPAPFIVT 1265
 Db 1201 RVEDCSIAALLPRNHDKNRCMIDLPPDRCLPFLITDGESSIONYINAALMDSYKQPSAFIVT 1260
 Qy 1266 QYPLPNITYKDWLVDYDGTSIVMLNEUDLSQGQYWPBEGMLRYGPQVECMSCSM 1325
 Db 1261 QHPLENTVKDFWRLDHYHTCITSVVMNDVAQLCQWPFQYWPVHGPQYEVFSADL 1320
 Qy 1326 CDVINRIFRICNLTRPQEGTLMVOQFQLGMASHRREVPGSKRSFLKLQILOVEKQWBECCE 1385
 Db 1321 ED1SRIFRTNASHQDGHMRMVQQLQGLPMPYRDTPVSKRSFLKLIRQDVKWQEEYNG 1380
 Qy 1386 GEGRTLHCINGGRSGMFCAIGTYVEMVKRQNVYDVFHVAKTLLRNSKPNVVEAPCQYRF 1445
 Db 1381 GEQPTVHCLNGGRSGCTFCASIVCBLRQHQTVDLQYKF 1440
 Qy 1446 CYDVALEYLES 1456
 Db 1441 CYBVALEYLN 1451

RESULT 12
 US-08-991-258A-4
 Sequence 4, Application US/08911258A
 GENERAL INFORMATION:
 Patent No. 5928887
 APPLICANT: Cheng, Jill
 APPLICANT: Lasky, Laurence A.
 TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 STREET: FLEER, HOBACH, TEST, ALBRITTON & HERBERT, LLP
 CITY: San Francisco Center, Suite 3400
 STATE: California
 COUNTY: United States
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/991.258A
 FILING DATE: 17-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PILING DATE: 24-MAY-1996
 TELECOMMUNICATION INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE DOCKET NUMBER: A-63478-3/WHD/MTK
 TELEPHONE: (415) 781-1989
 TELEX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid
 STRANDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-991-258A-4

Query Match Score 4793.5; DB 2; Length 1452;
 Best Local Similarity 61.3%; Pred. No. 0;
 Matches 899; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

QY 22 LLGSALGQSAGGGTFDDSGACDYHODIYDDEPYSTCYSQADDFEWQNTLKEFSDPMPSSFMLNT 73
 QY 82 SNHDPGKEKARLQLQPTMKENDTHCIDFSYLLSQGKLNPGTLLNLYRWNKGPLANPINNT 141
 QY 74 SGKPEGQRHLLPKLNDTHCIDFSYLLSQGKLNPGTLLNLYRWNKGPLANPINNT 133
 Db 14 LLDTAAGETFGGCLFDEPYSTCYSQADDFEWQNTLKEFSDPMPSSFMLNT 73
 QY 23 LLGSALGQSAGGGTFDDSGACDYHODIYDDEPYSTCYSQADDFEWQNTLKEFSDPMPSSFMLNT 81
 Db 142 GFTGRDWLRELAVSTFWNEYQNTFEEVSGGRSGYIADDIQVLSYFCDSKPHFLRG 201
 Db 134 GDPTRTWHRLAISTFWPNFYQVIFEV-VTSCHGQGLAIDEVKLGHTCTRIPHFLRIQ 192
 QY 202 DVEYNAQONATFOCIATGRDAVNKLWLRNNGTIVPQTKNINHRRFAASPLQEVTK 261
 Db 193 NVEVNAQGPAFQCSAIGRTVAGDLWLQIDVERDAPLGIKVTSRRIASFNVNNT 252
 QY 262 TDQDLYRCQTOSERSGSVMNAQJLIVREPRPRIAPPOLQGVGPTYLICQLNANSIIGCOP 321
 QY 253 RDAKYRCMTCCTEGGGINSYAEIUVKEPPIAPPOLQASVGATLWQLNANSINGCOP 312
 QY 322 LIKEVEYRMTSGSMYETEHAVNAPTYKWLHDPTDEYERVLTRPGEGTGLGPPLT 381

Db 313 IVAREVEYCTASGSWNDRQPVDSYSKIGHLDPTDEYEISVLLTRPGEGTGSPPGPALRT 372
 QY 382 RTKCAEPRTPKLIAEIQARRIAVDMESLGNTIRCHTNTCTHYFRGNEISRAD- 440
 Db 373 RTKCADPREGPRKLEVEVKSRQITIREPFQGNTVRCHSYNLTVHYQVQGQEOVRBES 432
 QY 441 -CLJDMDPKAPQHVNHLPPYTNSLKMILTNPGRKESSEETIOTDEDVPGPVVKSLQG 499
 Db 433 VSWDDDSHAPQHTTINLSPYTNSVSKLILMNPERKESDELTVQDDEDPGAVETEISQG 492
 QY 500 TSEPNKIFLNWKBRPLEPNGLIIQTYEVSSYSSIRSFDPAVVAQPPQTIVSNLWNSTHVFEMH 559
 Db 493 SAFFEKIFQWREFTQTYGVTILETYKAVASSFDPERDSLNSQGSRVSKLGNETHFLFG 552
 QY 560 LHPPTTQOFFIRASTVKGGPATANNTNISAPSPLPDYGVDAISLNNETATTIVLRLRA 619
 Db 553 LYPTTYSFTTRISTAKFGPPATNQFTTKISAPSMPAYE-FETPLNQTDNTVYMLRPA 611
 QY 620 QAKSAPASAYQIVQEVLPHRTKREAGAMECYOVPVYQNALSGGAPYQFAAELPPGNNLP 679
 Db 612 QSRGPAPVSYQIVBEEPRRPTKTTBLKCPVPHFQNQASLNSQYFAAEPADSLSQ 671
 QY 680 EPAPPTVQEDNRTYKGFMNPLAPRKGMNYFOAMSIVEKETKTQCVRIATAKAATEEPEV 739
 Db 672 AAQPFITGDNKTYQYNTPLPKSYRILYQQASRANGEKLDCRVATKGAVTPKP- 729
 QY 740 IPDPAKQD9D9VVKAGISAGSLVPLLLLIVVTKSKLAKRKRDKAMGNTROEMTMVN 799
 Db 730 VPEEEKQDHTVKIAGVIAQGILFVUFLGVVLMKPKRKLAKERKETMSSTRQEMTVVN 789
 QY 800 AMDRSYADOSTLHAEDPLSLTMDQHNFSPRLPNDP-----LVPTAVL-DENH 846
 Db 790 SMDKSAYAEGTNCD--AFSFGTHTNLRGVSYSSPSSFTMKTNTLSFVSPNNSYPDETH 846
 QY 906 FFEQQSASWDVAKKDQNRAKKNRGNMAYDHSRVLQPVEDPSSSYDANYIDWLYRD 965
 Db 907 FFEQQSAPMDSAKKDENRMKRNTRGNMAYDHSRVLQMLEGDNNSDYINGNYI----D 960
 QY 966 GYQRPSHYTATQGHETTYDFWRMWWQEQSACTIVMTNLVEGRVKCYKWPDDTEYYG 1025
 Db 961 GHPRPHHTATQGMQETIYDFWRMWWHENTASTIMVTLNVEGRVKCCYKWPDDTEYK 1020
 QY 1026 DFKVTCVMEPLAEYVPTFTLERGYNEIREVKQFHETGWPDHGPVYHATGLLISFIRR 1085
 Db 1021 DIKVTLIDTELAEYVIRTFAVEKRGTHEIRETRQFHETGWPDHGPVYHATGLLGFVRQV 1080
 QY 1086 KLSNPSPSAPIVVCAGRTGCVYIDIMLDMAERCVVDLYNCVAKLRSRINMVQT 1145
 Db 1081 KSSSPNAGPLVTHCSAGAGRTGCFIVDILMDMAERCVVDLYNCVAKLRSRINMVQT 1140
 QY 1146 EEOYTFIHDAILEACLGCTETAIPVCEFKAYFDMIRPSQTNSHLDKFQTLNSVTPRL 1205
 Db 1141 EEOYVFIHAILEACLGCTSPASQVSLYDVKNLQDQTNSSQIKEFRUNMVTPL 1200
 QY 1206 QAPDQSIACLPRNHDKRNMDFMLPPDRCLPFLITIDGESSSYNINAALMDSYRQPAAFVYT 1265
 Db 1201 RVEPDSIALPRNHEKRNCMDILPPDRCLPFLITIDGESSSYNINAALMDSYKOPSAFVYT 1260
 QY 1266 QYPLPNTKADFWEVLYDYGCTSVMNVEYDLSQCCPQWPEEGMLRYGPIQVECMSCMD 1325
 Db 1261 QHPLPNTKDFWRLVLDHTCSTMVNLNDYDPAQLCQWPMENGVRHRGPQVBFVSADIE 1320
 QY 1326 CDYTRIPRICNUTRPQEGSYLQOFQYLGASHREVPGSRSKFLKL1QVEKMQECEB 1385
 Db 1321 ED1SRIFRIFYNAISRPQDSEHRYTQFQFLGPWPMTRDPSKRSPLKLQRQDVQWKEQYNG 1380
 QY 1386 GEGRTIHLHCLNGGSGRCMFCAGITVEMYKRONVYDFHAKVKTLRNSKPNMVEAPEQYRF 1445
 Db 1381 GEGPTVHVCLNGGSGRCMFCASIVCEMLHQRTVDFHAKVKTLRNNKPNMVDLQZKF 1440

Qy 1446 CYDVALEYLES 1456
 Db 1441 CYEVALEYLNS 1451

RESULT 13-
 US-08-769-399-4
 Sequence 4, Application US/08769399
 Patent No. 5976852
 GENERAL INFORMATION:
 APPLICANT: Cheng, Jill
 APPLICANT: Labey, Laurence A.
 TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 NUMBER OF SEQUENCES: 10
 TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
 CORRESPONDENCE ADDRESS:
 STREET: 460 Point San Bruno Blvd.
 CITY: South San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/769,399
 FILING DATE: 435
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 225-3216
 TELEX: 910 371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid
 STRANDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

us-08-769-399-4

Query Match Similarity 61.3%; Score 4793; DB 2; Length 1452;
 Best Local Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

Db 1322 ILIKEVEYRMTSGSWTETHAVNAPIYKLWHDPPDEYEIRVLLTPEGGTGLPQPPLIT 381
 Db 313 IVARVEYCTAGSKMNDQRQVDSYSKIGLDPDEYEISVLLTPEGTGSPPALRT 372
 Db 382 RTKCAEPMRPTPKLMAIEIQARRIAVDWESLGYNTRCHTFNVTLCYHYFRGHNESSRAD- 440
 Db 373 RTKCDPMPREPRKLGVEVEYRSRQITRWEFGYNTRCHSYNLTHYGRGGQBQVRE 432

Db 441 -CLDDPKAQHUVNLPPTVNSKMLTNEGRSESEETIQLQDEDPGPVPKSLOG 499
 Db 433 VSWDDTDNSHPHQHTTNLSPYNTVSKLMMNPEGRKESQELTVQDDELPGAVPESIOQ 492

Db 500 TSFENRIFLNKWPKEPBPNGLITQEVSYSSIRSFSPPAVPAGPPQVSNLWNSTHVFMH 559
 Db 493 SAFEXPLLOWREPOTQYGVITLITYKAVSSPEIDISNRVSKLGNETHFLFEG 552

Db 560 LHPGTTOFFTRASTVKGFGPATAINVNTNISAPSLPDYEGVDAISINETATTIVTLRRA 619
 Db 553 LYPGTTYSPTRASIAKGFGSPATNQFTKISAPMPAY-FETLNUQTONTVTLKPA 611

Qy 620 QAKGAPISAYQIUVFOLHPFRTKRAGAMECYQVUTYQHALSGGAPYPAELLPGNLP 679
 Db 612 QSRGPAPSVYQIVWEEBEPRTKTCTEILKCPVPHFQNASILNSQYYAAEFADSLQ 671

Qy 680 EPAPPFTVGDNRTYKGFWNPPLAPRKGNYNFOAMSVERKETKTQCVRATKAATBEPV 739
 Db 672 AAQPFITIGENKTYNGWNTPLPHSYRYYQAARANGEKIDCVRATKGAVTPKP-- 729

Db 740 IPDPAKQTDRVVKLAGISAGILVFLILLVVIVTKSKLAKKRKDAMGNTROENTHMVN 799
 Db 730 VPEPEQTDITVKIAGILFTIFLGVVLWKKRKLAKKRKETMSSTRQETVMVN 789

Qy 800 AMDRSYADQSTLHAAPLSLTMQDNFSSPLRNPD-----LYPTAVD-DENH 846
 Db 790 SMDKSYAEOCTNCDE--AFSFMGTHNLNCRVSPPSSFTMKNTNLSTSBNNSYYPDETH 846

Qy 847 SATABECSRLLDVPRY-LCEGTEESPYOTGOLHPATIVADLQHINMKTSDSYGFBEYES 905
 Db 847 TMASDPTSSLLAQPHTYKKREADDPVQTQHPMPAIRVADLQHITQMCKABEGYGFBEYES 906

Qy 906 PFEQGQASWDYVAKKONRAKKNRYGNNTIAYDHSHRVLIQPPVEDDPSYDINANYIDIWLYRD 965
 Db 907 PFEQGQAPWDSAKDDENRMKNRYGNNTIAYDHSHRVLQMLEDDNSSYINGYI----D 960

Qy 966 GYORPSHYIATQGPHETIVDEMRMWOEQSACTIVMNTNLVEGRKCYKWPDTDEVYG 1025
 Db 961 GHYRPNHYIATQGPQETIYDFWRNWHENTASIMVNTNLVEGRKCKYWPDTDEBYK 1020

Qy 1026 DEKVTCVEMPLAEVVRTFLERCGYNEREVQFHFTGMPDHGYPHATGLLSFIRR 1085
 Db 1021 DIKVYLIDTELAEVIRTPAVEKGTHEFREIQPHETGMPDHGYPHATGLLSFIRRQV 1080

Qy 1086 KLSNNPPSAGP1VWHCSAGAGRTGCTVIDIMLDMAREGVYDIYCYKALSRRIINQVOT 1145
 Db 1081 KSKSPPNAGPLVHCSAGRTGCFIVIDIMLDMAREGVYDIYCYRELRSRRVNMVQ 1140

Qy 1146 EQYIIRHDATEACLCGETAIPVCEFKAYEDMIRIDSQTNSSHLKDEFQTLNSVTPRL 1205
 Db 1141 EEQYVFTHDALLEACLGDTSTPASQVRSLYDMKLDPQTNSQIKEEFTLNWYPTPL 1200

Qy 1206 QAEDCSTACLPNHNIDKRFMMLPDRCLPLITDGESSNTINAALMDSKRQAPAFIVT 1265
 Db 1201 RVEDCSTALLPRNHEKRCMDILPDRCLPLITDGESSNTINAALMDSKRQAPAFIVT 1260

Qy 1262 QYPLPNPTVKDFWLRYDGTISIVMLNEVDLSQGPQYWPBEGMRYGPIOVECMSCMD 1325
 Db 1261 QPBLPENTVKDFWLVDYHCTSVMLNDVPAQLCQYWPPENGVRHGPQIVEFVSADL 1320

Qy 1326 CDVNPBFRICLUTRPOEGGLMVOQFOYLGASHREVPGSKRSFSLKILLOVEKWWOEECE 1385
 Db 1321 EDIISRFIYTNAISPRDGHHRVQOQFLGPMPYRDTPVSKRSFLKLIRQDVQWBEBYNG 1380

Qy 262 TDDLYRVCCTQSBERGSCTGSNPAOLIVTEPPRPIAPPOLLGVPYTLIQLQANSITGDP 321
 Db 253 RDAGKYRCMICTEGGVG-SNYAELVVKRPPVPTAPPQLASGATYLIQLQANSINGDGP 312

Qy 1386 GEGRTIITHCLNGGSGMFCAIGIVVEMVKRQNVDVFDHAKTLLRNSKPNVYEAPEQYRF 1445

RESULT 14

US-08-991-953A-4

Sequence 4, Application US/0891953A

Patent No. 6083748

GENERAL INFORMATION:

APPLICANT: Cheng, Jill

APPLICANT: Lasky, Laurence A.

TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE PHOSPHATASE, FTP LAMBDA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, AUBRITTON & HERBERT, LLP

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,953A

FILING DATE: 16-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/652,971

FILING DATE: 24-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-633478-3/WHD/MTK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1452 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-991-953A-4

Query Match Score 4793.5; Length 1452;

Best Local Similarity 61.3%; Pred. No. 0;

Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

YQ 22 LLGSALQFSAGGGCTFDGPGACDTHQDLYDDFENVHSAQEPhYLPPMPOGSYMWDS 81

Db 14 LLLTAGTGGCGLDEPYSTCGYSQAEDDFNWEQNTLKTETSDPMPNGSFMLYNT 73

YQ 82 SNHDGEKAQLQPLMKENDTHC1DFSYLLIYSQRCLNPGTLNLYVNUKGPLANPIWNT 141

Db 74 SGKPEGQRAHILLPKKENTHC1DFHYSSKSNAAPGILNNTYKVNNNGPLGPNTWNS 133

YQ 142 GFTGRDWLRAABLAESTFWNPNEYQVTFEAEVSGGRGSSYCDKSPHFLRG 201

Db 134 GDPRTWHRHLAISTFWNPFYQVIFEV-VTSGHGOLAIDEVKVLGHPTTRPHFLRG 192

YQ 202 DVEVNAGQWATFOCIATGDAVHNKLWLQRNGEDIPVAQTKNINHRRPAASFRQLQEVTK 261

Db 193 NVEVAGQFATFOCSAIGRTVAGDRMLWQDIDVRDPLKEIKVTSRRIASFNVNNTK 252

QY 262 TDQDLYRCUTQSBERSGSVSNPAQLIIVREPRPRIAPPQLLGYPPTXLIQIWNANS1IGDGP 321

Db 253 RDAGGYRCMICTEGGYGSISYAELVKEPPVPIAPQASGVATLWIQIWNANS1NGDGP 312

YQ 322 TILKEYEYTRNTSGSSTEAVNAPPYKLWELDPDPEYEIRVLLTPBEGGTGGLPGPPLIT 381

Db 313 IVARVEYCTASGSNDROPVDSTSJKLGHLDPDPEYEISVLLTRPGEGETGSPGPALRT 372

QY 382 RTKCAEPMRPTKLTIAEQARTRAVDWSLGYNTTRCHFNVTCYHYFRGNHSBRAD-440

Db 373 RTKCAFPMRGPRKLEVEVKSRQITIRWEPGGINTRCHSYNLTHYQVQGQZQVRE 432

QY 441 -CLMDPKAOPQHVVNHLPPPTNVNSKMLTNPEGRKESSEBTIOTDVEDYGPVPVYKSLOG 499

Db 433 VSWDDDNSHFQHTTINLSPPTNVSYKLILMNPNEGRKESQLTVOQDLEDLFGAVPBESIQG 492

QY 500 TSFENKIFLWKPEPLEPGLTQYEVSYSSIRSPPDPAVPGPPOTVSNLWNSTHVFHM 559

Db 493 SAFEERKIFLQWRPEPQTYGVITLBYTAVSSPFPEIDLSNQSGRSVSKGNETHFLFFG 552

QY 560 LHPGTYQFTRASTVKGRSPATAINVNTNISAPLPDVEGVDSLNEPATTTVLLRPA 619

Db 553 LYPTGTYSFTRASTAKGRSPATNQFTKISASPMPE-FETFLNQDNTNTVIMLKPA 611

QY 620 QAKGAPISAYQIVVYOLPHRTKREAGAMECYQVPTVYONALSGGAPYFAAELPGNLP 679

Db 612 QSRGAPVSYQIVVVEERPRTRKCTTEILCKYPIFHQNASTLINSQYFAAEFFADSLQ 671

QY 680 EPAPPTVGDNRTYKGFWNPLAPRKQNYFQAMSVERETKTOCVRITKAATPEPEV 739

Db 672 AAQPTTIGDKNTKYQWNTPLPHIKSYRYYQASRANGEKTKIDCURVATKGAVTPKP-- 729

QY 740 IPDPKQTDKRVKLAGISAGLVPLVTKLQVIGVILFIFGQVILWKKRQKETMSTRQENTVMN 799

Db 730 VPEPKQTDHTVKLAGVIGVILFIFGQVILWKKRQKETMSTRQENTVMN 789

QY 800 AMDRSYADQSTLHAEDPLSIITEMQHNFSPLRNPDOP-----LYPTAVL-DENH 846

Db 790 SMDKSYABEQGTCNCDE---AFSMGTMHNLRGSVSPSSFTMKTNLTSVPSNPSYDPETH 846

QY 847 SATAESRRLDVPRY-LCBGTESPQQTGOLHPAIRADLQHINMKTSYGFKEYES 905

Db 847 TMASMTSSLAQPHTKRKEAADPVYOTQLHHPAIRADLQHITOMKCAEGYGPKEYES 906

QY 906 FPEGGASNDVAKDQNRKRNRYGENIIADHSRVTLOPVEDPSSDYDITVANYIDIWLYRD 965

Db 907 FPEGGASPDSSAKDDENRMKRNRYGMIIADHSRVLQMLEGDNNSDYINGNYI----D 960

QY 966 GYQRFSHYATOGPVTHETYDPMAMWQEOSACTIVMNTLVEGRVKCYKWPDTDEVYG 1025

Db 961 GHRENHYATOGPMQETYDPMWMMHNTAS1IMVTLVEGRVKCCWKPDTTEIYK 1020

QY 1026 DKYOTCVEMEPLARYVVRPTTLERGYNBIREVCFHFTGWPDHGYPYHATGLSFIRR 1085

Db 1021 DIKVTLIDTELLAVRIFAVERGIHEIRTRQHFHGWPDRGVPYHATGLLGFVRQV 1080

QY 1086 KLSLNSPSAGPVIWHCSAGRTGCTYIVDMLDAERGVUDINCRALSRINMVQT 1145

Db 1081 KSKSPPNAGPLVWICSGAGRTGFIVDMLDAERGVUDINCRERSRINMVQT 1140

QY 1146 EBOQFIFHDAILEACLGCTAIPYCEFKAYFDMRIDSQTNSSHLKDEFQTLNSTPRL 1205

Db 1141 EEQYTFIHDAILEACLGCTAIPYCEFKAYFDMRIDSQTNSSHLKDEFQTLNSTPRL 1200

QY 1206 QAEDQSIACLPNEDKRNTPMDMLPDRCLPPLTIDGESSNYINAALMDSYRQPAFIVT 1265

Db 1201 RVEDQSIALLPRNHEKRNCDMLIDPDRCLPPLTIDGESSNYINAALDSYKQSAFIVT 1260

QY 1266 QPAPNTVQDFWRLVYDGCSTSWMNLEYDLSOCGPQWPEEGMLRYGPQVECNCSMDS 13225

Db 1261 QHPLNTVQDFWRLVLDXHCTSVMLNDVDAQLCPQTMWENGVRHGPQVEFVSADEL 13220

Db	204	QNASQCMAGRAAEAEHFFLQRQSQVLFPAAGYHISRRFLATPLASVGSRSEODLYR	263
Qy	269	CYTOSERGSGVSNPAQLIVREPPPTIAPPOLLGCGPTYLJLQLQNLNTSIIQGDPIILKEVE	328
Db	264	CVSOPRGAVSNPAELIVREPPPTIAPPOLLRAGPTYLQNLNTSIIQGDPIVKEIE	323
Qy	329	YMTSGSWTETHANAPTYKLWHLDPDTEYEIRVILTRPGEGTGIGPQPPLITRCKAEP	388
Db	324	YMRARGPWLEHVATNLXTYKLWHLDPDTEYEISVILTRPGEGTGIGPQPPLISRTCKAEP	383
Qy	389	MRTPKTLKAEIQARRIAVDWEISLGYNITRCHTFNVTICHTYFRG - HNESTRADLIDMDP	446
Db	384	TRAPGLAFAIQARQLQWEPLYNVTRCHTAVSLCYTRYLGGSHNQTIRECYKMER	443
Qy	447	KAPQHVNWHLPPTVNSLKMILNTNPEGRKESEETI1QTQDDEPGVPVKSLQGTSENKI	506
Db	444	GASRYTIKQNLPPFNRINHVRLLNTNPEGRKEGKTVFTQDDEPGGIAAESLTFTPLEDMI	503
Qy	507	FLNWKPLEPNGLITQEVNSYSSTSFDPAVPVAGPPQTVSNLWMSTHYFNMHLHPTTY	566
Db	504	FLKWPBEPQEPNGLITQVEISQSISSDPAVNPVPEPRRTISKLNRTETHYFNSNLHPTTY	563
Qy	567	QFFIRASTYKGFPATAINTTNISAPSPLDYEQYDASLINEATTITVLRPAQAKAPI	626
Db	564	LFSVARTSKFGFQGALETTNSAPSFDYADNPSPLGSESENTITVLLPAQGRGAPI	622
Qy	627	SAYQTVVEQLHPHRKTKEAGAMECQVPTYQNALSGGAPYFAEELPPGNLPEPARPTV	686
Db	623	SVYQVTVVEBRPRLRREPAQDCSVPLTFETALLARGLYHFQGELAAASSLEAMPFTV	682
Qy	687	GDNRYTKGFWNPPLAPRKGYNTIYFOAMSSVKEKETIQCVRILATAATEPEVIVDPAQK	746
Db	683	GDNQTYRGFWNPPLPEPKAYLIVFOAASHLKGETRLNCIRKACKESKRPL-EVSQR	741
Qy	747	TDRVYKLAGTSA-GILVFILLLVVVIVVKSKLAKRKDAMGNTQEMTMVNAMDTSY	805
Db	742	SEEMLILIGIACGGAVLILLGAIVTIVRKGPKYPMTK-ATVNTRQEKTNNMSAVDRSF	800
Qy	806	ADQSTLHAEDPLSLTFMDQHNFSPPLPNDPLVPTIAVLDENHSATAESRLL-DVPRYLC	864
Db	801	TDQSTLQEDERLGLSFMDAPEGYSPR-----GDQRSGGTVEASSLJGGSPRPGC	849
Qy	865	GTESSPYQTGOLHPAIRVADLQHNMKTSDSYGFKEEYESFFEGOSASWYDVKDGNRA	924
Db	850	RKGSSYHTGOLHPAIRVADLQHNMQMKTAEGYFGQEYESFFEG---WDATKDDKLK	905
Qy	925	KNRVGNLIAYDHSRVILQPVQEDPSSDYMANYIDIWLYRDGYQRPHYIATQGPVHETV	984
Db	906	GGRQEPVSAYDRAHHTYKLHPMLADPADIYISANYI-----DGYHRSHNHFIAIQGPKPEMI	959
Qy	985	YDFWMWQDQSAUVMVNLIVEGRVKCYKWPDDTEVYGFPTVTCVMBPLATEYVRT	104
Db	960	YDFWMWQBOCAStVMTKLVEVGRVKCSRYWPESDMYGDIKITLVKTKTELAEYVRT	101
Qy	1045	FTLERRGNEBIREVKOFHETCPDPHCVPHATGLLSFIRRYKLSNPPSAGIVWHSAGA	110
Db	1020	FALERGYSARHEVQFHFTAWPHEGVPHATGLLAIRYKASTPPDAGPVWHSAGT	107
Qy	1105	GRTGYIVIDIMLDMAEREGVYDINYCNVKALRSRINMVOTEQYQFHDIALEAQLGE	116
Db	1080	GRTGCVYIVDMLDVAECGEGVYDINYCNVKLCSRSRNMQEQYFHDIALEAQLGE	113
Qy	1165	TAIPCYCEFKAYFDIIRIDSTNSHILQDEQTLNSVTPRQADESIACLPRNHDKRF	122
Db	1140	TTIPNEFRATYREMIRIDPOSSNSQLREEQTLNSVTPPLDVECSIALPPRNDRKNS	119
Qy	1225	MDMLPDPDRCLPLFLITDGESSNYINALMDSYRQAAFIOTOYLPNTVKDFWRLVYDYG	128
Db	1200	MDVLPPDRXLFLFLISSDGPNNYINALTDTSYTRIASAFVTLHPLQSTTPDWFRLVYDYG	125
Qy	1285	CTSTMVLMNEVLSQG -- CPOYWPFGMLRYGPQIVBCMSCSMDCVINRIFCINLJTRP	134
Db	1260	CTSTMVLMNOONOSNAMPCLOVWPEPGRQOGLMEYFVUSGTANEDIVSRPVLQNSRL	131

Qy	1342	QEGYIMVQQFQYLGASHREYPGSKSFLKLILQEVKQEECEGEGRITIHLNGGGRS	1401
Db	1320	QEGLHLVRHFQLMSAYRDPSRKAFLHLIAEVKWO - AESGDGRTVVCLNGGGRS	1377
Qy	1402	GMFCAGIVVEMVKRQNVDVFHAVENTLNSKPNMVAPEQYRFCYDVALEYLS	1456
Db	1378	GTECCATVLEMIRCSLVDYFFAACTLRLNPKNMVETMDOYHFCDVAVIYEVIA	1432

Search completed: June 1, 2005, 13:57:37
Job time : 41.2113 secs

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OM protein - protein search, using sw mode1

Run on: June 1, 2005, 13:31:52 ; Search time 147.411 Seconds
(without alignments)

Title: US-09-887-669-1

Perfect score: 7809

Sequence: 1 MDVAAAALPAFVALWLYPW.....EAPEQYRFCYDVALLYLESS 1457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

(without alignments)

3822.724 Million cell updates/sec

Add47019 Human Pro

Add47015 Human Pro

Aay81785 Human pro

Aay56100 LAR tyros

Aab19712 Human pro

Add18740 Human dis

Adj33670 Human leu

Adp18674 Human PTP

Adq66041 Novel hum

Aau14143 Human nov

Adn02662 Liver dis

Adr40183 Human pro

Aar1726 Human PTP

Aaw7225 Human pro

Aaw94027 Human pro

Aau01459 Human pro

Abb57380 Rat mucoc

Abb57380 Rat

mucous

ADD18742 Human dis

ALIGNMENTS

RESULT 1
1 ABB57308 standard; protein; 1457 AA.

1 ID ABB57308
XX AC ABB57308;

XX DT 07-MAR-2002 (first entry)

XX DB Mouse ischaemic condition related protein sequence SEQ ID NO: 862.
XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX OS Mus musculus.

XX PN WO200188188-A2.
XX PD 22-NOV-2001.

XX PP 18-MAY-2001; 2001WO-JP004192.
XX PR 18-MAY-2000; 2000JP-00145977.

XX PA (UNI-) UNIV NIPPON SCHOOL JURIDICAL PERSON.

XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX DR WPI; 2002-034733/04.
DR N-PSDB; AB19774.

XX PT Examining the ischemic condition (e.g. occlusive ischaemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

XX Claim 2; Page 2155-2161; 2650pp; English.

CC The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method

CC is useful for examining the ischaemic condition (e.g. compressive

CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABB59202 to AB19912, encoding the

CC protein sequences in ABB57030 to ABB57374) or by determining the

CC expression profile of a gene group comprising these genes. The expression

CC levels or expression profiles produced by these genes are used as an

CC indicator when screening for ischaemic condition-improving drugs or

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description	
1	7809	100.0	1457	5	ABB57308	Abb57308 Mouse isc	
2	7762	99.4	1457	2	AAR63633	Aar3633 Murine re	
3	7586	97.1	1439	2	AAR63632	Aar3632 Human rec	
4	7582	97.1	1439	7	ADJ68478	Adj68478 Human hea	
5	7567	96.9	1440	2	AAY29591	Aay29591 Human pro	
6	7567	96.9	1440	8	ADJ23886	Adj23886 Human PTP	
7	7412	94.9	1407	2	AAR63631	Aar3631 Murine re	
8	4823	56.5	61.8	1452	4	AAM79159	Aam79159 Human pro
9	4812	56.5	61.6	1452	6	ABR58629	Abr58629 Human can
10	4812	56.5	61.6	1452	8	ADI80761	Adi80761 Human pro
11	4789	56.5	61.3	1452	7	ADJ68277	Adj68277 Human hea
12	4783	61.2	1455	4	AAM80143	Aam80143 Human pro	
13	4591	58.8	1436	7	ADB79775	Adb79775 Rat putat	
14	4577	58.6	1436	4	AAM25768	Aam25768 Human pro	
15	4575	58.6	1436	2	AAW41261	Aaw41261 Receptor	
16	4545	58.2	1462	5	ABB97521	Abb97521 Novel hum	
17	4542	58.2	1463	6	ABJ37035	Abj37035 Human bre	
18	4542	58.2	1463	7	ADB75519	Adb75519 Prostate	
19	4542	58.2	1520	5	ABJ05584	Adj05584 Breast ca	
20	4359	55.8	1442	7	ADJ68999	Adj68999 Human hea	
21	4271	54.7	1430	2	AAW49907	Aaw49907 Human pan	
22	2471	31.6	623	4	AAM25675	Aam25675 Human pro	
23	2216	28.4	815	4	AAM28875	Aam28875 Human pro	
24	1514	19.4	1501	2	AAR72858	Aar72858 Rat recep	
25	1495	19.2	1948	7	ADD18742	Add18742 Human dis	

therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.

Sequence 1457 AA:

Query Match	100.0%	Score 7809;	DB 5;	Length 1457;	
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 1457;	Conservative 0;				
CC	MDVAAALPAVALWLYPPWLGSAQFQSAGGCTFDGPGACDYHQDLYDDFEWVHVS 60				
CC	MDVAAALPAVALWLYPPWLGSAQFQSAGGCTFDGPGACDYHQDLYDDFEWVHVS 60				
SQ	Sequence 1457 AA:				
Qy	1 AQPFLPPEMFGSMMUDSSNHHDPEKARLQLPMTKENDTHC1DFSTYLISQKLNPG 120				
Db	61 AQPFLPPEMFGSMMUDSSNHHDPEKARLQLPMTKENDTHC1DFSTYLISQKLNPG 120				
Qy	121 TLNLLVRVKNGPLANPTWNTGTPGDRWLRLAELAVSTFWPNBYQVIFEAEVSGGSGSYIA 180				
Db	121 TLNLLVRVKNGPLANPTWNTGTPGDRWLRLAELAVSTFWPNBYQVIFEAEVSGGSGSYIA 180				
Qy	181 IDDIQVLSYPCDKSPHFLRGLPVEVNAQGQATFOCIATGRDAVHNKLWLQRNGEDIPVA 240				
Db	181 IDDIQVLSYPCDKSPHFLRGLPVEVNAQGQATFOCIATGRDAVHNKLWLQRNGEDIPVA 240				
Qy	241 QTKNINHRFAASERPLQETKTDQDLYRCUTQSERGGSNSHAQILIVREPRPIAPPQI 300				
Db	241 QTKNINHRFAASERPLQETKTDQDLYRCUTQSERGGSNSHAQILIVREPRPIAPPQI 300				
Qy	301 GVGPTLILQLQANSIIQDGFLILKEVYRMTGSWTEHVNAPTYKLWLDPDEYEI 360				
Db	301 GVGPTLILQLQANSIIQDGFLILKEVYRMTGSWTEHVNAPTYKLWLDPDEYEI 360				
Qy	361 RVLLTRPREGGTGLPGPPLITRTKCAEPMRTPKTLKIAETARRIAIDWESLGYNTRCH 420				
Db	361 RVLLTRPREGGTGLPGPPLITRTKCAEPMRTPKTLKIAETARRIAIDWESLGYNTRCH 420				
Qy	421 TENUTICHYPHGHNSRPAADCCLMDRKAPQTVVNLHPPPTVNSLMLITNPEGRKESET 480				
Db	421 TENUTICHYPHGHNSRADCCLMDRKAPQTVVNLHPPPTVNSLMLITNPEGRKESET 480				
Qy	481 IIQTDEDVPGPVPPVKSLQGTSPENKFLWKEPLPENGITQVEYSYSRSFDPAVVA 540				
Db	481 IIQTDEDVPGPVPPVKSLQGTSPENKFLWKEPLPENGITQVEYSYSRSFDPAVVA 540				
Qy	541 GBPQTYSNLWNSTHAYFMHLHGTTYOFIRASTVKGFPATAINTVNISAPSILPDYEG 600				
Db	541 GBPQTYSNLWNSTHAYFMHLHGTTYOFIRASTVKGFPATAINTVNISAPSILPDYEG 600				
Qy	601 VDASLNETATTITVLJLRPAQKGAQAPISAQYIIVVEQLHPPHTKRAGAMECYQPVYQNA 660				
Db	601 VDASLNETATTITVLJLRPAQKGAQAPISAQYIIVVEQLHPPHTKRAGAMECYQPVYQNA 660				
Qy	661 LSGGAPYKFAAEPLPGNLPERPAPFTYQKGFNPPLAPRKGYNNIYQAMSSVKEET 720				
Db	661 LSGGAPYKFAAEPLPGNLPERPAPFTYQKGFNPPLAPRKGYNNIYQAMSSVKEET 720				
Qy	721 KHQCVRATKAALATEEPVIPDPAKOTDRVVIAGTSAGLIVFILLLWVIVKSKLA 780				
Db	721 KHQCVRATKAALATEEPVIPDPAKOTDRVVIAGTSAGLIVFILLLWVIVKSKLA 780				
Qy	781 KKRKDANGNTROBMTHNMVNMDSRYSADQSTLHAEDPLSLTMDQHNSPRLPNDPLVPTA 840				
Db	781 KKRKDANGNTROBMTHNMVNMDSRYSADQSTLHAEDPLSLTMDQHNSPRLPNDPLVPTA 840				
Qy	841 VLDENHSATAESSRLDVPRYLCBGTESPYQTGQLHPAIRADLQHNMKTSDSYGFK 900				
Db	841 VLDENHSATAESSRLDVPRYLCBGTESPYQTGQLHPAIRADLQHNMKTSDSYGFK 900				
Qy	901 EEEYESPPFQGSASWDVAKDQNRAKNEYGNITAYDHSRVILQPVEDPSSDYINANYIDI 960				
Db	901 EEEYESPPFQGSASWDVAKDQNRAKNEYGNITAYDHSRVILQPVEDPSSDYINANYIDI 960				

Qy	961 WLYRGCGYQRPSHYATQGPVHETVYDFFWRMVWQEQSACTVMTNVNVEGRVCKCYWPDD 1020				
Db	961 WLYRGCGYQRPSHYATQGPVHETVYDFFWRMVWQEQSACTVMTNVNVEGRVCKCYWPDD 1020				
Qy	1021 TEVIGDFKVTCVEMPLAETYVVRTTLEERRGYNELREVQFHFTGMPDHGVYHATGTLIS 1080				
Db	1021 TEVIGDFKVTCVEMPLAETYVVRTTLEERRGYNELREVQFHFTGMPDHGVYHATGTLIS 1080				
Qy	1081 FIRYKLSNPPSAGPJVVHCSAGARTGCVIVIDMLDMAERGVVDIYNCVKAARSRI 1140				
Db	1081 FIRYKLSNPPSAGPJVVHCSAGARTGCVIVIDMLDMAERGVVDIYNCVKAARSRI 1140				
Qy	1141 NMVCTEEQYIPTFHDAILEACIICGETAIPVCEFKAYFDMRIDTSQTNSSH1KDEFOTLNS 1200				
Db	1141 NMVCTEEQYIPTFHDAILEACIICGETAIPVCEFKAYFDMRIDTSQTNSSH1KDEFOTLNS 1200				
Qy	1201 VTPRLOAQEDCSIACPRNHDKNRFDMLPPDRCLPLITDGESSIONYINALMDSYRQA 1260				
Db	1201 VTPRLOAQEDCSIACPRNHDKNRFDMLPPDRCLPLITDGESSIONYINALMDSYRQA 1260				
Qy	1261 AFIVTQYPLPNTVDFWRLVYDGGTSIYVLINEVLIUSQGPQYWBEGLMRYGPLOVECIM 1320				
Db	1261 AFIVTQYPLPNTVDFWRLVYDGGTSIYVLINEVLIUSQGPQYWBEGLMRYGPLOVECIM 1320				
Qy	1321 SC5MCDVINVTRIFRNLCNLTRPQEGLYTMVQOFGYIQLGWASHREVPGSKRSFLKLQLOEKWQ 1380				
Db	1321 SC5MCDVINVTRIFRNLCNLTRPQEGLYTMVQOFGYIQLGWASHREVPGSKRSFLKLQLOEKWQ 1380				
Qy	1381 EECBEGEGRTIHCLNGGGRSGMPCAGIIVYEMVYRQNYYDVFHAVKTLRNSKPNNVEAP 1440				
Db	1381 EECBEGEGRTIHCLNGGGRSGMPCAGIIVYEMVYRQNYYDVFHAVKTLRNSKPNNVEAP 1440				
Qy	1441 EQYRFYDVALEYLESS 1457				
Db	1441 EQYRFYDVALEYLESS 1457				
RESULT 2					
	AAR61633	standard; protein; 1457 AA.			
ID	AAR61633				
XX					
AC	AAR61633;				
XX					
DT	21-OCT-2004 (revised)				
DT	25-MAR-2003 (revised)				
DT	08-JUN-1995 (first entry)				
XX					
DE	Murine receptor-type protein tyrosine phosphatase precursor protein.				
XX					
KW	Receptor-type protein tyrosine phosphatase protein; cellular signal; RPTase-kappa; enzyme.				
KW					
XX					
OS	Mus musculus.				
OS	Unidentified.				
XX					
FH	Key				
FT	Peptide	1..25			
FT	label= signal				
FT	33..189				
FT	/label= A5 surface protein homology				
FT	733..774				
FT	/label = Transmembrane				
FT	926..1156				
FT	/label = PTBase I				
FT	1218..1455				
FT	/label = PTBase II				
PN	WO942161-A1.				
XX					
PD	27-OCT-1994.				
XX					
PF	20-APR-1994;				
PF	94WO-US004377.				

XX	21-APR-1993;	93US-00049384.
PR	01-JUL-1993;	93US-00087244.
XX	(DYN-) UNIV NEW YORK MEDICAL CENT.	
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
PA	XX	
P1	Schlessinger J, Sap JM, Ulrich A, Vogel W, Fuchs M;	
XX	WPI: 1994-341769/42.	
DR	Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k) protein and DNA - useful to identify ccds which bind to RPTP-k and modulate enzymatic activity. Also inhibition of type II RPTP homo:philic binding (Eng).	
PS	PS	Claim 2; Fig 1; 144pp; English.
XX	The novel receptor-type protein tyrosine phosphatase protein or glycoprotein is termed RPTP kappa (also known as RPTase-Kappa). The first approx. 170AAs of RPTP kappa show similarity (26% overall identity) to a region in the Xenopus cell surface protein A5 with features of Ig-like domains. There are four putative fibronectin type III-like repeats residues 236-681. The tandem repeat of two fibronectin type III-like repeats for most RPTases. A feature of RPTP kappa is the extended distance between its transmembrane domain and the start of the first phosphatase homology domain. The RPTP kappa cDNA sequence comprises a 5' UTR of 1072 bpS and a 3' UTR of 388 bpS. The translational initiation codon is identified by a start environment for initiation of translation (Kozak) and by the existence of an upstream in-frame stop codon, and is followed on by a hydrophobic region that may serve as a signal peptide. (Updated on 25-MAR-2003 to correct PN field.)	
CC	CC	Revised record issued on 21-OCT-2004 : Correction to feature table key .
CC	CC	Sequence 1457 AA;
SQ	Query Match 99.4%; Score 7762; DB 2; Length 1457; Best Local Similarity 99.5%; Pred. No. 0; Mismatches 6; Indels 0; Gaps 0;	
Matches 1449; Conservative 2; Mismatches 6; Indels 0; Gaps 0;		
Qy	1 MDYAAALPAFAVMLLYPWPLLSALGFSAGCTTDDPGACDYHDLYDDEWHTS 60 1 MDYAAALPAFAVMLLYPWPLLSALGFSAGCTTDDPGACDYHDLYDDEWHTS 60	
Db	Qy 61 AQEPHYLPPEMPQGSYMMVDSNNHDPGEKARLQLPTMKENDTHCIDFSTLLYSOKGLNG 120 61 AQEPHYLPPEMPQGSYMMVDSNNHDPGEKARLQLPTMKENDTHCIDFSTLLYSOKGLNG 120	
Db	Qy 121 TLTFLVRVKGPLANPINWNTGTGRDMLRAELAVSTFWNEYQVIFAEVSGRSGYIA 180 121 TLTFLVRVKGPLANPINWNTGTGRDMLRAELAVSTFWNEYQVIFAEVSGRSGYIA 180	
Db	Qy 241 QTINNHRFAASFRLOQEVTKTDDLYRCVTOSERGSVSNFAOLIVREPPIAPPOLL 300 241 QTINNHRFAASFRLOQEVTKTDDLYRCVTOSERGSVSNFAOLIVREPPIAPPOLL 300	
Db	Qy 181 IDDIQVLSPYPCDKSPHFLRGDVENVAGONATFOCIATGRDAVINKLWLRQRNGEDIPVA 240 181 IDDIQVLSPYPCDKSPHFLRGDVENVAGONATFOCIATGRDAVINKLWLRQRNGEDIPVA 240	
Db	Qy 301 GVGPTYLJQLNANSIIGCPILKEVKEYVMTSGSWTETHAVNAPTYKLWHLDDDTVEI 360 301 GVGPTYLJQLNANSIIGCPILKEVKEYVMTSGSWTETHAVNAPTYKLWHLDDDTVEI 360	
Db	Qy 361 RVLTRPGEGTGCGPPLTRTCAEPMTPKTLKIAEQARRIAEVMSLGNITRCH 420 361 RVLTRPGEGTGCGPPLTRTCAEPMTPKTLKIAEQARRIAEVMSLGNITRCH 420	
Qy	421 TENVITYCHYFRGINESRACLMDPKAQPHVNHLPPPTVNSLMLTNPEGREKESET 480 421 TENVITYCHYFRGINESRACLMDPKAQPHVNHLPPPTVNSLMLTNPEGREKESET 480	
Db	481 IIGTDEDVPGEVPPVSKSLOGTSFENKIFLNWKBEPLPENGITTOYEVSYSIRSFDPAVPVA 540 481 IIGTDEDVPGEVPPVSKSLOGTSFENKIFLNWKBEPLPENGITTOYEVSYSIRSFDPAVPVA 540	
Qy	541 GPOTVTSNTKNSTHVFMHLHPGTYOFFIRASTVKGPFATAINTTNISAPSLSLDDYEG 600 541 GPOTVTSNLWNSTHVFMLHHPGTYOFFIRASTVKGPFATAINTTNISAPSLSLDPYEE 600	
Db	Qy 601 VDASINETATTITVLRPAQKGAPSAYQIVVLEQHPTKREAGAMECYQPVTVQNA 660 601 VDASINETATTITVLRPAQKGAPSAYQIVVLEQHPTKREAGAMECYQPVTVQNA 660	
Db	Qy 661 LSGGAFYYFAELPPCNLPEPAPFTYGDNRITYKGFFNPPLAPRKGNNIYFORMSSYKEET 720 661 LSGGAFYYFAELPPCNLPEPAPFTYGDNRITYKGFFNPPLAPRKGNNIYFORMSSYKEET 720	
Qy	721 KTQCYBIAATKAATTAPEPEVIPDPAQTDRVVKIASAGLVEILLVVVTKSKLA 780 721 KTQCYTRIAATQAATTAPEPEVIPDPAKOTDRVVKIASAGLVEILLVVVTKSKLA 780	
Db	Qy 781 KKRKDAMGNTQEMTMVNAMDRSYADQSTLHAEDLSLTFMDQHNSPRLENPDPLYPTA 840 781 KKRKDAMGNTQEMTMVNAMDRSYADQSTLHAEDLSLTFMDQHNSPRLENPDPLYPTA 840	
Db	Qy 841 VLDENHSATAESRLLDVPRLCEGTEPSYOTGOLPAIRAVDLQHINLMKTSDSYGFK 900 841 VLDENHSATAESRLLDVPRLCEGTEPSYOTGOLPAIRAVDLQHINLMKTSDSYGFK 900	
Db	Qy 841 VLDENHSATAESRLLDVPRLCEGTEPSYOTGOLPAIRAVDLQHINLMKTSDSYGFK 900 841 VLDENHSATAESRLLDVPRLCEGTEPSYOTGOLPAIRAVDLQHINLMKTSDSYGFK 900	
Qy	901 EYESFEFGQSASMVAKCQONRANBYGNCIAYDHSVPLQVENDPSSDXINYANYIDI 960 901 EYESFEFGQSASMVAKCQONRANBYGNCIAYDHSVPLQVENDPSSDXINYANYIDI 960	
Db	Qy 961 WLYRQYQRSHYIATQGPVHETVDFRNWQBOQACIYWTNLBVGRVYCKYKWPDD 1020 961 WLYRQYQRSHYIATQGPVHETVDFRNWQBOQACIYWTNLBVGRVYCKYKWPDD 1020	
Db	Qy 1021 TEVYCFPKUTCVEMEPPLAETVVRTFLERRGYNIREVKOFHFTGPDPDHGVYPHATGILLS 1080 1021 TEVYCFPKUTCVEMEPPLAETVVRTFLERRGYNIREVKOFHFTGPDPDHGVYPHATGILLS 1080	
Db	Qy 1081 FIRRYKLSNPPSAQPTVWVCSAGAGRTGCYIVIDIMDMAEREGVTDIYNCYKALPSRRI 1140 1081 FIRRYKLSNPPSAQPTVWVCSAGAGRTGCYIVIDIMDMAEREGVTDIYNCYKALPSRRI 1140	
Db	Qy 1141 NMVQTEEQYFPIHDALEACLGCTETAPICEFKAAVFDMRIDSQNSHILKDEFQTLNS 1200 1141 NMVQTEEQYFPIHDALEACLGCTETAPICEFKAAVFDMRIDSQNSHILKDEFQTLNS 1200	
Db	Qy 1141 NMVQTEEQYFPIHDPFLASLGCEPAPIYVCERKAAVFDMRIDSQNSHILKDEFQTLNS 1200 1141 NMVQTEEQYFPIHDPFLASLGCEPAPIYVCERKAAVFDMRIDSQNSHILKDEFQTLNS 1200	
Db	Qy 1201 VTPRLOQEDCSIACLPRNHDKNRFMDMLPPDRCLPLPLITDGESSNYINAALMDSYRQPA 1260 1201 VTPRLOQEDCSIACLPRNHDKNRFMDMLPPDRCLPLPLITDGESSNYINAALMDSYRQPA 1260	
Db	Qy 1201 VTPRLOQEDCSIACLPRNHDKNRFMDMLPPDRCLPLPLITDGESSNYINAALMDSYRQPA 1260 1201 VTPRLOQEDCSIACLPRNHDKNRFMDMLPPDRCLPLPLITDGESSNYINAALMDSYRQPA 1260	
Qy	1261 AFIVTQYPLPNTVWYDFWMLYDGGTSIVMINEVDLSQGCPQYWPREGMLRYGPIQEVCM 1320 1261 AFIVTQYPLPNTVWYDFWMLYDGGTSIVMINEVDLSQGCPQYWPREGMLRYGPIQEVCM 1320	
Db	Qy 1321 SCSMDODVNRIFRICNLTRPQEGYLMVQOYLGIAHSEREVPGSKRSFLKLILQEKWQ 1380 1321 SCSMDODVNRIFRICNLTRPQEGYLMVQOYLGIAHSEREVPGSKRSFLKLILQEKWQ 1380	
Db	Qy 1381 EECEREGRTIHCLNGGRSGMFCAIGIVEMVRQNVYDFHAYTKLRSKPNVNEAP 1440 1381 EECEREGRTIHCLNGGRSGMFCAIGIVEMVRQNVYDFHAYTKLRSKPNVNEAP 1440	
Db	Qy 1441 EQYRCYDYLEXLS 1457 1441 EHRYFCYDPLDYLEXLS 1457	
Db	421 TENVITYCHYFRGINESRACLMDPKAQPHVNHLPPPTVNSLMLTNPEGREKESET 480 421 TENVITYCHYFRGINESRACLMDPKAQPHVNHLPPPTVNSLMLTNPEGREKESET 480	
Qy	421 TENVITYCHYFRGINESRACLMDPKAQPHVNHLPPPTVNSLMLTNPEGREKESET 480 421 TENVITYCHYFRGINESRACLMDPKAQPHVNHLPPPTVNSLMLTNPEGREKESET 480	RESULT 3 AARS332 ID AAR61632 standard; Protein; 1439 AA.

XX	AAR63632;		Qy	1 MD-VAAAALPAFAVALWLLYPWPILLGSAALGOFSGAGCTFDGGPAGDYHDLYDDPBWVH 59
AC			Db	1 MDTRAAALPAFAVALWLLSPWILLGSAACGSAACGTFDGGPAGDYHDLYDDPBWVH 60
XX	DT 21-OCT-2004 (revised)		Qy	60 SAQEPHYLPPBMPQGSYMMYDSSNDPGEKARLOLPMTKENDTICIDFSYLSOKGLNP 119
DT	25-MAR-2003 (revised)		Db	61 SAQEPHYLPPBMPQGSYMMYDSSNDPGEKARLOLPMTKENDTICIDFSYLSOKGLNP 120
DT	26-OCT-1995 (first entry)			
DE	Human receptor-type protein tyrosine phosphatase (RPTP) kappa.			
XX	Receptor-type protein tyrosine phosphatase protein; cellular signal;			
KW	RPTPase-kappa; RPTPase.			
XX	Homo sapiens.			
OS	Unidentified.			
XX	Key	Location/Qualifiers	Qy	120 GTINLVRVNGKPLANPINNUTGETCDMIRPFLAESTFPMNEYVIVIFEAEVSGGRSGYI 179
FT	Domain	/label = Ig-like domain	Db	121 GTINLVRVNGKPLANPINNUTGETCDMIRPFLAESTFPMNEYVIVIFEAEVSGGRSGYI 180
FT	Domain	755..774		
FT	Label	= alpha helical transmembrane domain		
XX	PN WO9421161-A1.		Qy	180 ADDQVLSYPCDISPHFRLGQDVENVAGAGNATCQCIATORDAVINKLWLRQRNEDIPV 239
PN	207..277		Db	181 ADDQVLSYPCDISPHFRLGQDVENVAGAGNATCQCIATORDAVINKLWLRQRNEDIPV 240
PD	27-OCT-1994.		Qy	240 AQTKINHREPAASFRQLQEVYTKTDODLYRCVTSQSERGSVSNFAOLIVREPRPAPQL 299
XX	PR 20-APR-1994:	94WO-US004377.	Db	241 AQTKINHREPAASFRQLQEVYTKTDODLYRCVTSQSERGSVSNFAOLIVREPRPAPQL 300
PF	21-APR-1993;	93US-00049384.	Qy	300 LGVGPTXYLJQLNANSIIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLWHLDDPTEYR 359
XX	PR 01-JUL-1993;	93US-00087244.	Db	301 LGVGPTYLJLJQLNANSIIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLWHLDDPTEYR 360
PA	(UYN-) UNIV NEW YORK MEDICAL CENT.		Qy	360 IRVLTTRPGGGTGPGLPPLITRCAEPMPRTPTKLIKARIQARIAVDMESLGYNITRC 419
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.		Db	361 IRVLTTRPGGGTGPGLPPLITRCAEPMPRTPTKLIKARIQARIAVDMESLGYNITRC 420
XX	PI Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;		Qy	420 HTFNNTICHTYHRGNESRADCLMDPKAPQHQVNHLPPTNVSKMLTNPEGKESE 479
XX	DR WPI: 1994-341769/42.		Db	421 HTFNNTICHTYHRGNESRADCLMDPKAPQHQVNHLPPTNVSKMLTNPEGKESE 480
XX	DR N-PSDB; AA072913.		Qy	480 TLIQTEDVGPVPPVSKLQGTSPEKFLINWKEPLEPNGLITQVEYSSIRSFPDPAVPV 539
XX	PT Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)		Db	481 TLIQTEDVGPVPPVSKLQGTSPEKFLINWKEPLEPNGLITQVEYSSIRSFPDPAVPV 540
PT	protein and DNA - useful to identify cpas; which bind to RPTP-k and		Qy	540 AGPPQTVSNLWNSTHVFMLHPGTYQFPIRASVXKGFBPATANVNTNISAPSLPDYE 599
PT	modulate enzymatic activity. Also inhibition of type II RPTP homo:philic binding (Eng).		Db	541 AGPPQTVSNLWNSTHVFMLHPGTYQFPIRASVXKGFBPATANVNTNISAPSLPDYE 600
XX	PS	Claim 4 : Fig 15; 144pp; English.	Qy	600 GVDASINEATTITVLRLPAQAKGAPISAYQIVVWQLHPHTRKAGAMECYQVPTVYQN 659
XX	CC	The novel receptor-type protein tyrosine phosphatase protein or glycoprotein is termed RPTP kappa (also known as RPTP-kappa). Human breast cancer cell line SK-BR-3 was examined by PCR using primers correspond to conserved sequences within the PRP catalytic domains shared by all identified PRases. Several known PRases were revealed together with some novel members of the PRPase family. One of the novel sequences, designated MCP7 (Mammary carcinoma-derived PRPase clone 7) was highly represented in all 121 clones examined. The MCP7 PCR fragment was used to screen a SK-BR-3 cDNA library. The results are AA072913 and its deduced AA sequence AAR63632. The AA sequence displays the structural organization of a type II transmembrane PRPase. The N-terminal hydrophobic stretch of 20-26 AsS is typical of signals peptides. A second region consisting of hydrophobic residues (see FT) is predicted to be a single alpha-helical transmembrane domain. It is followed by a short region of mainly basic residues characteristic of a transfer stop sequence. The amino-terminal portion of the putative extracellular domain contains a sequence motif, a so-called MAM domain, spanning a region of about 170 residues. This motif is followed by one possible Ig-like domain (see FT). (Updated on 25-MAR-2003 to correct PN field.)	Db	601 GVDASINEATTITVLRLPAQAKGAPISAYQIVVWQLHPHTRKAGAMECYQVPTVYQN 660
CC	CC	CC	Qy	660 ALSGCAPPYPAELPGNLPEPAPPTVGDNRTYKGFWNPPLAPRKGYNTYFOAMSSVEKE 719
CC	CC	CC	Db	661 AMGGCAPPYPAELPGNLPEPAPPTVGDNRTYKGFWNPPLAPRKGYNTYFOAMSSVEKE 720
CC	CC	CC	Qy	720 TKTQCYRIATAKKAAEEPEVLPDPKQTDPRVKIGISAGLVLFLLLVIVIKSKL 779
CC	CC	CC	Db	721 TKTQCYRIATAKKAAEEPEVLPDPKQTDPRVKIGISAGLVLFLLLVIVIKSKL 779
CC	CC	CC	Qy	840 AVLDENHSATAESSRLLDPVRYLCETESTPQTGQLHPAIRVADLQLQHINLMKTSDSYGF 899
CC	CC	CC	Db	832 --- ENHSATAESSRLLDPVRYLCETESTPQTGQLHPAIRVADLQLQHINLMKTSDSYGF 887
CC	CC	CC	Qy	900 KEEKEYEFFEGOSASDVAKEDQNRKRNQGNIYADHSRVLQPYEDDPSSDYTNANYID 959
CC	CC	CC	Db	888 KEEKEYEFFEGOSASDVAKEDQNRKRNQGNIYADHSRVLQPYEDDPSSDYTNANYID 946
CC	CC	CC	Qy	960 IWLYRDGYQRFSHYIATGQPVHETYDFWRMWQWOSACIYMTLVEVGRVKCYKWPD 1019
CC	CC	CC	Db	947 ----DGYQRFSHYIATGQPVHETYDFWRMWQWOSACIYMTLVEVGRVKCYKWPD 1001
XX	SQ	Revised record issued on 21-OCT-2004 : Correction to feature table key Sequence 1439 AA;	Qy	1002 DTEVYGDKEYTVCVENMEPLAEVVRPTTLERRGYNEREVKOFHTCPWDHGVPYHATGLL 1079
Query Match	97.1%	Score 7586; DB 2; Length 1439;	Db	1002 DTEVYGDKEYTVCVENMEPLAEVVRPTTLERRGYNEREVKOFHTCPWDHGVPYHATGLL 1061
Best Local Similarity	97.5%	Pred. No. 0; Mismatches 12; Gaps 4;	Qy	1080 SFIRYVKLNSNPPSAGP1VWHCSAGAGRGCYIVIDIMLDWAEREGVYDIYNCVAKLRSRR 1139

1062 SFIRRKVLNPPSAGPIVHCSAGARTGYIVIDIMLMAERSGVDDYNTVKALRSR 1121
Db 1140 INMVQTEEVYTFIDHAILEACLGTAIPICEKAYFMDIRIDSQTNSHLKDBFQTIN 1199
Qy 1142 INMVQTEEVYTFIDHAILEACLGTAIPICEKAYFMDIRIDSQTNSHLKDBFQTIN 1181
Db 1200 SVTPRLQAECDSTIACLPRHDKNRFMDMIPDRCLPFLITDGESSIONYNAALMDSYRQP 1259
Qy 1182 SVTPRLQAECDSTIACLPRHDKNRFMDMIPDRCLPFLITDGESSIONYNAALMDSYRQP 1241
Db 1260 AAPIVTVQPLPNTYDFWMLYYDYGCTSIVMLNEVDLSQCPQIWPEBMLRGPIQVE 1319
Qy 1262 AAPIVTVQPLPNTYDFWMLYYDYGCTSIVMLNEVDLSQCPQIWPEBMLRGPIQVEC 1301
Db 1320 MSCSNDCDVNTRIFRICNTRPQEYLMQQFOTLGWAHREVPFGSKRSFLKLQVKNW 1379
Qy 1322 MSCSMDCDVNTRIFRICNTRPQEYLMQQFOTLGWAHREVPFGSKRSFLKLQVKNW 1361
Db 1362 QEECEEGERTIIHCLNGGSRSGMCAIGIVVENVKRVQNYDVFHAVKTLRNSKPNNYEA 1439
Qy 1440 PEQYRFQCYDALEYLESS 1457
Db 1422 PEQYRFQCYDALEYLESS 1439

RESULT 4
ADJ68478 standard; protein; 1439 AA.
XX ADJ68478
AC ADJ68478;
XX 06-MAY-2004 (first entry)
XX Human heat mitochondrial protein as a therapeutic target SeqID284.
XX mitochondrial, human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy; ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; rootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cycostatic.
XX Homo sapiens.
XX WO2003037768-A2.
XX 23-OCT-2003.
PD 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0339987P.
PR 20-SEP-2002; 2002US-0412418P.
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGB RES.
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for
treating diseases associated with altered mitochondrial function,
comprises detecting a modified polypeptide in a sample and correlating
with the disease.

XX TKTOQVRATKAATEEPEVIPDPAKOTDRVKTAGISAGILYFILLLYVIVYVKKSKL 779
PS 721 TKTOQVRATKAATEEPEVIPDPAKOTDRVKTAGISAGILYFILLLYVIVYVKKSKL 779

CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, rootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cycostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX Sequence 1439 AA;
SQ Query Match 97.1%; Score 7582; DB 7; Length 1439;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1430; Conservative 13; Mismatches 5; Indels 20; Gaps 4;
Matches 1430; Conservative 13; Mismatches 5; Indels 20; Gaps 4;
Qy 1 MD-VAAAALPAFAVWLLYPWPWLLGALGQSAGGCTPDDGPQADYHDLYDDPFEMVHY 59
Db 1 MDTAAALPAFAVWLLSPWPWLLGSAQGQSAGGCTPDDGPQADYHDLYDDPFEMVHY 60
Qy 60 SAQEPHYLPPEMPGSSYMWVDSANHDPGEKARQLQPTMKBDNTCHIDFSYLLYSQKGILNP 119
Db 61 SAQEPHYLPPEMPGSSYMWVDSANHDPGEKARQLQPTMKBDNTCHIDFSYLLYSQKGILNP 120
Db 120 GTLNILVRYNKQGPANPIWNVTGFGRDWLRAELAVSTFWPNYEQVIFAEVSGGRSGYI 179
Db 121 GTLNILVRYNKQGPANPIWNVTGFGRDWLRAELAVSSFWPNYEQVIFAEVSGGRSGYI 180
Qy 180 AIDDQVLSYPCDKSPHFLRGLGDYEVNAQNATFOCIATGRDAYVKNLWLQRNRNGEDIPV 239
Db 181 AIDDQVLSYPCDKSPHFLRGLGDYEVNAQNATFOCIATGRDAYVKNLWLQRNRNGEDIPV 240
Qy 240 AQTKNINHRRPAASFRQLQEVTKTDQDLIRCVCVTSERGSCSVNFNPAQLIVREPPIAPPQL 299
Db 241 AQTKNINHRRPAASFRQLQEVTKTDQDLIRCVCVTSERGSCSVNFNPAQLIVREPPIAPPQL 300
Qy 300 LGYGPYLLIQLNANSIIGDGPITLEKEYVRMTSGSWTETHAVNAPTYKLWHLDPDTYE 359
Db 301 LGYGPYLLIQLNANSIIGDGPITLEKEYVRMTSGSWTETHAVNAPTYKLWHLDPDTYE 360
Qy 360 IRVLLTRPGEGGTGLPGPPLITRTKACBPMRTPPTKIAEIQARRIAYDWESLGYNITRC 419
Db 361 IRVLLTRPGEGGTGLPGPPLITRTKACBPMRTPPTKIAEIQARRIAYDWESLGYNITRC 420
Qy 420 HTPNVTICHYPHGNESPADCDDMDPQAPQHVNHLPPYTNTSLKMLLTNPBKRKESE 479
Db 421 HTPNVTICHYPHGNESPADCDDMDPQAPQHVNHLPPYTNTSLKMLTNPGRKESE 480
Qy 480 TIIQDDEDVPGPVVKSLQGTSPEKIKFLWKERPLEPGNLTQEVSSSIRSFDPAVY 539
Db 481 TIIQDDEDVPGPVVKSLQGTSPEKIKFLWKERPLEPGNLTQEVSSSIRSFDPAVY 540
Qy 540 AGPPQTVSNLWNSTHHPMHLHPOTTYOFFIRASTVKGFGPATAINVTINISAPSPLDYE 599
Db 541 AGPPQTVSNLWNSTHHPMHLHPOTTYOFFIRASTVKGFGPATAINVTINISAPLDPDE 600
Qy 600 GVDASLNETATTIVLLPAQAKGAPISAYQIVVQLUPHTRKREAGAMECYQVPTVQN 659
Db 601 GVDASLNETATTIVLLPAQAKGAPISAYQIVVQLUPHTRKREAGAMECYQVPTVQN 660
Qy 660 ALSGCAGPYFAAELPGNLPPEAPPFTVGDNRTYKGFWNPLAPKQGNTYFOAMSVEKE 719
Db 661 AMSGCAFPAAELPGNLPPEAPPFTVGDNRTYGFWNPPLAPKQGNTYFOAMSVEKE 720
Qy 720 TKTOQVRATKAATEEPEVIPDPAKOTDRVKTAGISAGILYFILLLYVIVYVKKSKL 779
Db 721 TKTOQVRATKAATEEPEVIPDPAKOTDRVKTAGISAGILYFILLLYVIVYVKKSKL 779

Qy	780	AKKRKDAMGNTRQEMTHVNAMDRTSYADQSTLHAEDPLSLTFMDOINFSPLNDPLVPT	839	XX	Hah HJ,	Kil MC,	Yang Y,	Byun GH;
Db	780	AKKRKDAMGNTRQEMTHVNAMDRTSYADQSTLHAEDPLSLTFMDOINFSPRY-----	831	XX	WPI : 1999-335582/28.			
Qy	840	AVLDENHSAEASSRLLDPRYLCEGTEPSYQTGOLHPATRAVDLQHINLMKTSDSYGF	899	XX	DR : N-PSDB; AAZ08339.			
Db	832	---ENHATASESSRLLDPRYLCEGTEPSYQTGOLHPATRAVDLQHINLMKTSDSYGF	887	XX	Human Protein phosphatase, base sequence thereof and amino acid sequence thereof.			
Qy	900	KEBYESPFGOSAWDVAKKDNRAKRNLYIADYDHSRVLQVPPDSSDYINANYID	959	XX	PS Disclosure; Fig 1a-d; 14pp; Korean.			
Db	888	KEBYESPFGSASWDAKKDNRAKRNLYIADHSSRVLQVPPDSSDYINANYI-	946	XX	CC The present sequence represents human protein phosphatase k (HPTPK).			
Qy	960	IWLRYDGYQRPHSYIATQGPVTHETYDFWMNWQEOSACIWMNTNLVEGRVKCYKWPD	1019	XX	SQ Sequence 1440 AA;			
Db	947	----DCYQRPHSYIATQGPVTHETYDFWMNWQEOSACIWMNTNLVEGRVKCYKWPD	1001	XX	Query Match 96.9%; Score 7567.5;	DB 2;	Length 1440;	
Qy	1020	DTEVYCGDFKVTCVEMEPLAEYVVRTFELERGYNETREVKOFHETCGWPDHGVPHATGLI	1079	XX	Best Local Similarity 97.0%; Pred. No. 0;			
Db	1002	DTEVYCGDFKVTCVEMEPLAEYVVRTFELERGYNETREVKOFHETCGWPDHGVPHATGLI	1061	XX	Matches 1414; Conservative 16; Mismatches 9; Indels 19; Gaps 3;			
Qy	1080	SPIRRYKLSNPSAGPPIVHCSAGAAGRTPGCVIVIDMLDMAEREGVTDINCVKALRSRR	1139	XX	QY 1 MD-VAAAALPAFAVNLWLYMPWPLUGSALGQFSAGGCTFDGPGACDYZHQDLDDPEWVH 59			
Db	1062	SPIRRYKLSNPSAGPPIVHCSAGAAGRTPGCVIVIDMLDMAEREGVTDINCVKALRSRR	1121	XX	Db 1 MDTAAAAPAFVALLLSSPWPLLESAQQGFSAGGCTFDGPGACDYZHQDLDDPEWVH 60			
Qy	1140	INMVQTEEQYIFHDIALEAACIGETAIPIVCFKAAYFDMRIDSTQNSHLKDEQTLN	1199	XX	QY 60 SAQEYPHLPPPEMPOQGSYMMVYDVSNNPGEKARLQLQPTMKENDTHCDFSYLSSQKGKLN P 119			
Db	1122	INMVQTEEQYIFHDIALEAACIGETAIPIVCFKAAYFDMRIDSTQNSHLKDEQTLN	1181	XX	Db 61 SAQEYPHLPPPEMPOQGSYMMVYDVSSEDIDPGEKARLQLQPTMKENDTHCDFSYLSSQKGKLN P 120			
Qy	1200	SVTPRLOAEDCSIACIPLRNHDKNREMDMLPPDRCLPFLITDGESSIONYNAALMDSYRQP	1259	XX	QY 120 GTLNLLVRVNRKGPLANPIWWNTGFTGRDMLRAELAVSTFPNEYQVIFEAEVSGRSGYI 179			
Db	1182	SVTPRLOAEDCSIACIPLRNHDKNREMDMLPPDRCLPFLITDGESSIONYNAALMDSYRQP	1241	XX	Db 121 GTLNLLVRVNRKGPLANPIWWNTGFTGRDMLRAELAVSTFPNEYQVIFEAEVSGRSGYI 180			
Qy	1260	AAPITTOQYPLENTVKDFWRLYDGTSIVMLNEVDLSQGPQYWPBEGMLRYGPQVEC	1319	XX	QY 180 AIDDIOVLSYPCDKSPHFLRLQDVENAGONATFOCIATGRDVAHNKLMLQRNGEDIPV 239			
Db	1242	AAFITVQYPLNTVKDFWRLYDGTSIVMLNEVDLSQGPQYWPBEGMLRYGPQVEC	1301	XX	Db 181 ADDQVLSPCDKSPLSHFLRQDVENAGONATFOCIATGRDVAHNKLMLQRNGEDIPV 240			
Qy	1320	MSCSMDCDVIINRIFRICNLTRFQEGYIMVOFOYLGMWSHREVPGSKRSFLKLILQVEKW	1379	XX	QY 240 AQTKNINHRRFAASFRQLEYVTKTDDOLYRCVTOQSRSGCVSNFAQLVIREPRPRAPPQL 299			
Db	1302	MSCSMDCDVIINRIFRICNLTRFQEGYIMVOFOYLGMWSHREVPGSKRSFLKLILQVEKW	1361	XX	Db 241 AQTKNINHRRFAASFRQLEYVTKTDDOLYRCVTOQSRSGCVSNFQLVIREPRPRAPPQL 300			
Qy	1380	QEECEEGEGRTLIHCINGGRSGMFCAIGIIVEMVKRQNYYDVFHAKTLRNKPNNMVEA	1439	XX	QY 300 LGVGPyLLQLQNLANSIIGDGPILIKEVYRMTSSSWTEHAVNPYTKLWHLDPTTEYE 359			
Db	1362	QEECEEGEGRTLIHCINGGRSGMFCAIGIIVEMVKRQNYYDVFHAKTLRNKPNNMVEA	1421	XX	Db 301 LGVGPyLLQLQNLANSIIGDGPILIKEVYRMTSSSWTEHAVNPYTKLWHLDPTTEYE 360			
Qy	1440	PEQYRFCCYDVALEYLESS	1457	XX	QY 360 IRVLITRPGEGGTGLPGPPLTRICAEPLRPTKTLKIAEQARRIAVDWESLGYNITRC 419			
Db	1422	PEQYRFCCYDVALEYLESS	1439	XX	Db 361 IRVLITRPGEGGTGLPGPPLTRICAEPLRPTKTLKIAEQARRIAVDWESLGYNITRC 420			
RESULT 5								
Qy	AY29591	AY29591 standard; protein; 1440 AA.		QY 420 HTENYTICHYFRGHNESRADCLDMDPKAPOHVNHLPPTVNSLKMILTNPEGRKSEEE 479				
ID	AY29591			Db 421 HSFNTTICHYFRGHNESRADCLDMDPKAPOHVNHLPPTVNSLKMILTNPEGRKSEEE 480				
XX	AY29591;			QY 480 TIQTEDDVCPVPKSLOGTSPEKIKFLWKPELPGNLTTOYEVSYSSRSFDPAVPV 539				
AC	AY29591;			Db 481 TIQTEDDVCPVPKSLOGTSPEKIKFLWKPELPGNLTTOYEVSYSSRSFDPAVPV 540				
XX	14-OCT-1999	(First entry)		QY 540 AGPPQIVSNLWNSTHVFMELHPGTTQFFTRASTVKGFPATAVNTTNISAPSPLDYE 599				
DB				Db 541 AGPPQIVSNLWNSTHVFMELHPGTTQFFTRASTVKGFPATAVNTTNISAPSPLDYE 600				
XX				QY 600 GVDASLINEATTITVLLRPAOKGAPISAYQIVVEQOLHPHRTKREAGAMECYQPVPTYON 659				
DB				Db 601 GVDASLINEATTITVLLRPAOKGAPISAYQIVVEQELHPHRTKREAGAMECYQPVPTYON 660				
XX				QY 660 ALSGGAPYPAEELPGNLPAPPTVGDNRTYKGFWNPPLAPRGCYNTIIFOAMSSYVEK 719				
PN	KR98026246-A.			Db 661 AMSGGAPYFACTPGLPAPPTVGDNRTYQCFWNPPLAPRGCYNTIIFOAMSSYVEK 720				
XX	15-JUL-1998.			QY 720 TKTQCYTRIATKAEEPEPVIPDPAKOTDRVVKAGISAGILVFLILLVVIVIYKSKL 779				
PR	08-OCT-1996;	96KR-00044614.		Db 721 TKTQCYTRIATKAEEPEPVIPDPAKOTDRVVKAGISAGILVFLILLVVIVIYKSKL 780				
XX	(KOAD) KOREA ADV INST SCI & TECHNOLOGY.			QY 780 AKKRKDAMGNTRQEMTHVNAMDRTSYADQSTLHAEDPLSLTFMDOINFSPLNDPLVPT 839				

Db	781. AKCRKDAMNTQEMTHVNAMDTSYADQSTLHABDPLSITFMDQHNFSPRY-----	832	XX	Cowert LM, Freier SM;
Qy	840 AVLDENHSTAESSRLLDPRYLDRGTEPQYOTQQLHPIAVRDLQHINLMKTSDSYGF-----	899	PI	
Db	833 ---ENHSATAESSRLLDPRYLDRGTEPQYOTQQLHPIAVRDLQHINLMKTSDSYGF-----	888	XX	WPI; 2004-033493/08.
Db	900 KEEYBSFFGQSASWDVAKKDQNAAKRNRYGNITIAYDHSEVILQEDSSDSDYTNANTID	959	DR	N-PSDB; ADI23748.
Qy	889 KEEYESFFGQSASWDVAKKDQNAAKRNRYGNITIAYDHSEVILQEDSSDSDYTNANTY-	947	XX	New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding PTPRK, useful for preparing a composition for treating diabetes, inflammation or hyperproliferative disorder, e.g., cancer.
Db	960 IWLRYDGYCORPHSYATOGSPVHETTYDFWFRMVMQEQAACIVMTNLVEGRVCKYKMPD	1019	XX	Example 13; SEQ ID NO 4; 150pp; English.
Db	948 ---DGXRPHSYATOGSPVHETTYDFWFRMVMQEQAACIVMTNLVEGRVCKYKMPD	1002	XX	The present invention describes an antisense oligonucleotide (I), having a sequence comprising 8-80 base pairs, targeted to a nucleic acid encoding protein tyrosine phosphatase receptor type K (PTPRK), that specifically hybridises with the nucleic acid encoding PTPRK and inhibits expression of PTPRK. Also described: (1) a composition comprising the compound and a carrier or diluent; (2) a method of inhibiting the expression of PTPRK in cells or tissues; (3) a method of treating an animal having or suspected of having a disease or condition associated with PTPRK; and (4) a method for screening for an antisense compound. (I) has cytostatic, antiinflammatory and antibiotic activities, and can be used in antisense gene therapy. The antisense oligonucleotide (I) can be used for preparing a composition for treating diabetes, inflammation or hyperproliferative disorder, e.g., cancer. The present sequence represents human PTPRK, which is used in an example from the present invention. The human PTPRK gene is located on chromosome 6, more specifically to 6q22.-23.1.
Qy	1020 DTEVYGDPRVTTCVMEPLEBEVYVPTPLERRGNEBIRETKQFHFTGMWPHGVYHATCL	1079	CC	Sequence 1440 AA:
Db	1003 DTEVYGDPRVTTCVMEPLABYVVRFTFLERRGNEBIRETKQFHFTGMWPHGVYHATCL	1062	CC	Query Match 96.9%; Score 7567.5; DB 8; Length 1440;
Qy	1080 SFIRRVLKLNPSSAGPIVWHCSAGAGRGTCCYIVDILMAERGVDDLYNCYKALRSR	1139	CC	Best Local Similarity 97.0%; Prod. No. 0; Mismatches 3;
Db	1063 SFIRRVLKLNPSSAGPIVWHCSAGAGRGTCCYIVDILMAERGVDDLYNCYKALRSR	1122	CC	Matches 1414; Conservative 16; Indels 19; Gaps 3;
Qy	1140 INWQTEROYIFTHDAILEAFLCGETAIVCEPKAYFMRIDSQTNSHLKDEFTQIN	1199	Qy	1 MD-VAAALPAFVALLWLYPPWPLIGSAQGFSAGCTPFDGPGACDHYQDLYDDFETWV 59
Db	1123 INWQTEROYIFTHDAILEAFLCGETAIVCEPKAYFMRIDSQTNSHLKDEFTQIN	1182	Db	1 MDITTAAGAVPAFVALLWLYPPWPLIGSAQGFSAGCTPFDGPGACDHYQDLYDDFETWV 60
Qy	1200 SUTPLLOADCDCSIACLPRHDKORFMDMLPPDRCLPFLITIDGESSNNYNAALMDSTQP	1259	Qy	60 SAQEPHYPILPEMPOGSYMWVDSNHDPGEKARIQLPMTKENDTHCIDSYLLSQKGILNP 119
Db	1183 SVTPLLOADCDCSIACLPRHDKORFMDMLPPDRCLPFLITIDGESSNNYNAALMDSTQP	1242	Db	61 SAQEPHYPILPEMPOGSYMWVDSNDHPGEKARIQLPMTKENDTHCIDSYLLSQKGILNP 120
Qy	1266 AAFIVTQYDPLNPTYKDFWFLVYDYGCTSIVMLNEVDLSGCCPOYWPEBGLRYGPIQYC	1319	Qy	120 GTLNILVVRVNGKGPIANP1WNYTGFTGRDWLRAIAVSTFWPNEXQYFEEAVSGRSGYI 179
Db	1243 AAFIVTQYDPLNPTYKDFWFLVYDYGCTSIVMLNEVDLSGCCPOYWPEBGLRYGPIQYC	1302	Db	121 GTLNILVVRVNGKGPIANP1WNYTGFTGRDWLRAIAVSTFWPNYQVTFIAEVSGRSGYI 180
Qy	1320 MSCSMDCDVNRIFRICNLTROPGYLMQFOYLGWASHREVEGSKRSFLKLQVEKW	1379	Qy	180 ADDIQVLSYPCDKSPHFLRGLDVEVNGQNTAQCIATGRDAVHNKLWQRNGEDTV 239
Db	1303 MSCSMDCDVNRIFRICNTRQPGYLMQFOYLGWASHREVEGSKRSFLKLQVEKW	1362	Db	181 ADDIQVLSYPCDKSPHFLRGLDVEVNGQNTAQCIATGRDAVHNKLWQRNGEDTV 240
Qy	1380 QEECEEGERTIIHCLNGGRSGMFCAIGIVVEMVKRQNVDFHAKVTLRISKPNVYEA	1439	Qy	240 AQTKNINRRFAASFRLOQETKTQDLYRCVTOSERGSCVNSAQLTREPPAPQL 299
Db	1363 QEECEEGERTIIHCLNGGRSGMFCAIGIVVEMVKRQNVDFHAKVTLRNSKPNVYEA	1422	Db	241 AQTKNINRRFAASFRLOQETKTQDLYRCVTOSERGSCVNSPQLTREPPAPQL 300
Qy	1440 PEQYRFCCYDALEYLESS 1457		Qy	300 LGVGPTTYLIQMANISIGDGPILKEYVRMTSGSNTEHTAIVAPTYKUWHDPTDEYE 359
Db	1423 PEQYRFCCYDALEYLESS 1440		Db	301 LGVGPTTYLIQMANISIGDGPILKEYVRMTSGSNTEHTAIVAPTYKUWHDPTDEYE 359
RESULT 6			Qy	360 IRVLLTRPSEGGLPGLPPLITRKACPMRPTKTLKAEIQARRIAYDWESLGYNITRC 419
AD123886			XX	361 IRVLLTRPSEGGLPGLPPLITRKACPMRPTKTLKAEIQARRIAYDWESLGYNITRC 420
ID123886	standard: protein; 1440 AA.		XX	420 HTFNVITYHYFGHNESSADCLMDPKAQHVNLPKLEPLNGLITQTYEVSYSIRSFPAYV 539
XX	22-APR-2004 (first entry)		XX	421 HSFNVITYHYFGHNESSADCLMDPKAQHVNLPKLEPLNGLITQTYEVSYSIRSFPAYV 540
XX	Human PTPRK protein SEQ ID NO:4.		Qy	480 TIIQTDENVPGPVKVSLOGTSFKNKFLUNWKPEPLEPNGLITQTYEVSYSIRSFPAYV 539
XX	antisense oligonucleotide; human		Db	481 TIIQTDENVPGPVKVSLOGTSFKNKFLUNWKPEPLEPNGLITQTYEVSYSIRSFPAYV 540
KW	protein tyrosine phosphatase receptor type K; PTPRK; cytostatic;		PA	540 AGPQQTWSNLWNSTHIVPMHLHGTQYFPIRASTVGEGPATAINVTNISAPSPLPDYB 599
KW	antiinflammatory; antiabetic; antisense gene therapy; diabetes;			
KW	inflammation; hyperproliferative disorder; cancer; chromosome 6.			
OS Homo sapiens.				
PW02004005312-A1.				
XX				
DT 22-APR-2004				
XX				
DE Human PTPRK protein SEQ ID NO:4.				
XX				
AC AD123886;				
XX				
DT 15-JAN-2004.				
XX				
DE Human PTPRK protein SEQ ID NO:4.				
XX				
PR 03-JUL-2002; 2002US-00189429.				
XX				
(ISIS-) ISIS PHARM INC.				

Db	541 AGPPQTIVSNLNSTHHVFMHILHPGTTYQFFIRASTVKFGFDATAINVNTNISAPTLPDYE 600	DB XX Murine receptor-type protein tyrosine phosphatase protein (RPTP- kappa).
Qy	600 GUDASINEATTITIVLRAQAKGARISAYQIVVEQLHPHRTKREAGAMCQYQVPTYQN 659	KW Receptor-type protein tyrosine phosphatase protein; cellular signal;
Db	601 GVDASLINEATTITIVLRAQAKGAPTSAYQIVVEELHPHRTKREAGAMCQYQVPTYQN 660	KW RPTPase-kappa; enzyme.
Qy	660 ALSGGARYYFAEELPPENLPEPAFPVGDNRTYQFWNPPLAIPRCKYNIFQAMTSVEKE 719	XX OS Mus musculus.
Db	661 AMSGGAYYFACRTPPONLPEPAFPVGDNRTYQFWNPPLAIPRCKYNIFQAMTSVEKE 720	OS Unidentified.
Db	720 TKTQCVRIATAKAATEPEVIDPAKOTDRVVKIAGISAGLVFTLLLIVIVIVKKSKL 779	XX Key Location/Qualifiers
Qy	721 TKTQCVRIATAKAATEPEVIDPAKOTDRVVKIAGISAGLVFTLLLIVIVLIVKKSKL 780	1. .25 Peptide /label= signal
Db	780 AKKRKDAMGNTQEMTHMMNAMDRAADQSTLHAEPPLSLFPMQDNFSPRLPNPLVPT 839	FT Region 210. .270 FT /label= Ig-like repeat
Qy	781 AKKRKDAMGNTQEMTHMMNAMDRAADQSTLHAEPPLSLFPMQDNFSPRY----- 832	FT Domain 703. .724 FT /label = Transmembrane
Db	840 AVLDEHNHSATAECSRLLDVPRYLCEGTBSPYQGQHPAIRDQLQHINMKTSDSYGF 899	FT Domain 877. .1108 FT /label = PTpase 1
Qy	833 ---ENIATASSRLLDVPRYLCEGTBSPYQGQHPAIRDQLQHINMKTSDSYGF 888	FT Domain 1168. .1404 FT /label = PTpase 2
Db	900 KEYESEPFEGOSASWYDAKKDNRKAKRGNNTIAIDHRSRVLQVYEDPSSDYINANYYID 959	XX PN WO9424161-A1.
Qy	889 KEYESEPFEGOSASWYDAKKDNRKAKRGNNTIAIDHRSRVLQVYEDPSSDYINANYYI- 947	XX XX PD 27-OCT-1994.
Db	960 IWLRYDKQYQRPSHYIATQGPVHETVDFWRMWTQEQSACTIATVNIVLVEGRVKCYKWPD 1019	XX PF 20-APR-1994;
Qy	948 -----DGYQRPYSHYIATQGPVHETVDFWRMWTQEQSACTIATVNIVLVEGRVKCYKWPD 1002	XX PR 21-APR-1993; PR 01-JUL-1993;
Db	1020 DTEVYGDPKTVTCVEMBLAETVVRTFLTERRYNEIREVKOPHTGWPDHGVPHATGLL 1079	XX PA (UNNY-) UNIV NEW YORK MEDICAL CENT. (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Qy	1003 DTEVYGDPKTVTCVEMBLAETVVRTFLTERRYNEIREVKOPHTGWPDHGVPHATGLL 1062	XX PI Schlaessinger J, Sad JM, Ullrich A, Vogel W, Fuchs M;
Db	1080 SFTIRRVKLSNPPSAGPIVVHCSAGAGRTGYCIVIDMLDMAEREQYDITYNCVRALRR 1139	XX DR WPI; 1994-341769/42.
Qy	1063 SFTIRRVKLSNPPSAGPIVVHCSAGAGRTGYCIVIDMLDMAEREQYDITYNCVRALRR 1122	XX PT Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)
Db	1140 INMVQTEQQYIPTHDATLEACUCGETAPIVCEFKAAIDMRIDSQTNSSHLKDEFOQIN 1199	XX PT protein and DNA - useful to identify ccds, which bind to RPTP-k and modulate enzymatic activity. Also inhibition of type II RPTP homo:philic binding (Eng).
Qy	1123 INMVQTEQQYIPTHDATLEACUCGETAPIVCEFKAAIDMRIDSQTNSSHLKDEFOQIN 1182	XX PT Claim 2; Fig 3; 144pp; English.
Db	1200 SVPRLQEDS1TACLRPHNDKRNFRMNLPPDRCLPPLITDGESSNYINALMDSYRQP 1259	XX CC NB: It appears that one line, comprising 50AA is missing from Figure 3 (cf. APP63633). The novel receptor-type protein tyrosine phosphatase protein or glycoprotein is termed RPTP kappa (also known as Rptase-kappa). The first approx. 170AA of RPTP kappa show similarity (26% overall identity) to a region in the Xenopus cell surface protein A5 with features of Ig-like domains. There are four putative fibronectin type III like repeats (residues 296-681). The tandem repeat of two PTPase homologues is typical for most RPTPases. A feature of RPTP kappa is the extended distance between its transmembrane domain and the start of the first phosphatase homology domain. (Updated on 25-MAR-2003 to correct PN field.)
Qy	1183 SVPRLQEDS1TACLRPHNDKRNFRMNLPPDRCLPPLITDGESSNYINALMDSYRQP 1242	CC Sequence 1407 AA:
Db	1260 AAFIVTOYPLPNVTKDPRFLVYDGCTSIVMLNEVDLSQGCFQYWPBEGMRYGPQVEC 1319	CC Query Match 94.9%; Score 7412; DB 2; Length 1407;
Qy	1243 AAFIVTOYPLPNVTKDPRFLVYDGCTSIVMLNEVDLSQGCFQYWPBEGMRYGPQVEC 1302	CC Best Local Similarity 95.6%; Pred. No. 0;
Db	1320 MSCSMIDCQVINRFLRICNTRQEGQMLVQOFOYLGNSHREVPGSKRFLKLQVKEW 1379	CC Matches 1393; Conservative 5; Mismatches 9; Indels 50; Gaps 1;
Qy	1303 MSCSMIDCQVINRFLRICNTRQEGQMLVQOFOYLGNSHREVPGSKRFLKLQVKEW 1362	CC
Db	1380 QEECEEGGRTHIHLNGGRSNSMFCAGIGVVMVRKHNQVVDVFHAVTRLNSKPNVA 1439	CC
Db	1363 QEECEEGGRTHIHLNGGRSNSMFCAGIGVVMVRKHNQVVDVFHAVTRLNSKPNVA 1422	CC
Qy	1440 PEQYRFCDYALEYLESS 1457	CC
Db	1423 PEQYRFCDYALEYLESS 1440	CC
RESULT 7		
XX	AAR63631 standard; protein; 1407 AA.	Qy 1 MDVAAALPAVALWLYPWPLLGALQFAGGTFDDGPGACDHYQDLDFPENTHVS 60
XX	AAR63631	Db 1 MDVAAALPAVALWLYPWPLLGALQFAGGTFDDGPGACDHYQDLDFPENTHVS 60
AC	AAR63631;	Qy 61 AQEPhYLPPMFQGSYMWVDSNNHIDGEKARLQLPTMKENDTHCIDESYLLYSQKGLNPG 120
XX		Db 61 AQEPhYLPPMFQGSYMWVDSNNHIDGEKARLQLPTMKENDTHCIDESYLLYSQKGLNPG 120
DT	21-OCT-2004 (revised)	Qy 121 TLNLYRVNKQGPPLANPIWNNTGFTGRDWLRAELAVSTFWPNEYQVIFEAEGGRSGSYIA 180
DT	25-MAR-2003 (revised)	
DT	08-JUN-1995 (first entry)	
XX		

Db	121 TLNILVRVYNGPLANPIWVNTGFTGRDWTTRAELAVSTFWPENEYQVIFAEVSGGRSGYIA 180	Qy	181 IIDIQVLSPCDKSPHFLRGLDVEVNAGGNATFOCIANGRDVAHNKWLQRNRNGDIFPA 240	Db	181 IIDIQVLSPCDKSPHFLRGLDVEVNAGGNATFOCIANGRDVAHNKWLQRNRNGDIFPA 240	Db	1211 AFIVTQYPLPNTYKDFWRLVYDYGCTSIVMLNEVDLSOGCPQYWPEEGMLRYGPIQVBCM 1320
Db	181 IIDIQVLSPCDKSPHFLRGLDVEVNAGGNATFOCIANGRDVAHNKWLQRNRNGDIFPA 240	Qy	241 QTKNINHRHFAASFRQLQEVTKTDPDLYRCCTQSERGSVSNPAOLIVREPPTIAPPOL 300	Db	1321 SCSMDCDVINVIRFCNCNTRPQEGLYMVOQFQYLGASHREVGSKRSFLKLQVERWQ 1380	Qy	1321 SCSMDCDVINVIRFCNCNTRPQEGLYMVOQFQYLGASHREVGSKRSFLKLQVERWQ 1380
Db	241 QTKNINHRHFAASFRQLQEVTKTDPDLYRCCTQSERGSVSNPAOLIVREPPTIAPPOL 300	Db	1271 SCSMDCDVINVIRFCNCNTRPQEGLYMVOQFQYLGASHREVGSKRSFLKLQVERWQ 1330	Qy	1381 EECBEGERTITHCLGGGRSGNFCAGIVVENVKRQNVDVFHAVKTLRNSKPNMVEAP 1440	Qy	1381 EECBEGERTITHCLGGGRSGNFCAGIVVENVKRQNVDVFHAVKTLRNSKPNMVEAP 1440
Qy	301 GVGPTYLJLQLNANSIIIGGPILLKEYRVTMRTSGSWTETHAVNAPTYKLWHDLDPTDEYEI 360	Db	301 GVGPTYLJLQLNANSIIIGGPILLKEYRVTMRTSGSWTETHAVNAPTYKLWHDLDPTDEYEI 360	Db	1331 EECBEGERTITHCLGGGRSGNFCAGIVVENVKRQNVDVFHAVKTLRNSKPNMVEAP 1390	Qy	1441 EQYRFCDVALEYLESS 1457
Qy	361 RVLTRPGEGGTGLGPPIITRKYKCAEPRTPTKTLKAEIQARRIADWESLGYNITRCH 420	Db	361 RVLTRPGEGGTGLGPPIITRKYKCAEPRTPTKTLKAEIQARRIADWESLGYNITRCH 420	Db	1391 EQYRFCDVALEYLESS 1407	Qy	1391 EQYRFCDVALEYLESS 1407
Qy	421 TENVVTCIHYFRGHINESRADCLCDMDPKAPQHVYNVNLHPPTVNSLKMILTNPGRKESEET 480	Db	421 TENVVTCIHYFRGHINESRADCLCDMDPKAPQHVYNVNLHPPTVNSLKMILTNPGRKESEET 480	Db	450 ID AAM79159 standard; protein; 1452 AA.	Db	450 ID AAM79159 standard; protein; 1452 AA.
Qy	481 IIQTDDEVPGPVPKVSLQCTSEFNKILWKPLEPENGITQEVSYSSIRSDFPAYVA 540	Db	451 -----SPEHKIFLWKPLEPENGITQEVSYSSIRSDFPAYVA 490	Db	491 GPOTVSNINWSTHVFMLHPGTTYQFIRASTVKGPPATAINVNNTNISAPSILPDVEG 600	Db	491 GPOTVSNINWSTHVFMLHPGTTYQFIRASTVKGPPATAINVNNTNISAPSILPDVEG 550
Qy	541 GPPOTVSNINWSTHVFMLHPGTTYQFIRASTVKGPPATAINVNNTNISAPSILPDVEG 600	Db	541 GPPOTVSNINWSTHVFMLHPGTTYQFIRASTVKGPPATAINVNNTNISAPSILPDVEG 600	Db	551 VDASLNETATTITVLLRPAQKAPISAQYQIVVEQLPHRTKREAGAMECYQVPVTVONA 660	Db	551 VDASLNETATTITVLLRPAQKAPISAQYQIVVEQLPHRTKREAGAMECYQVPVTVONA 610
Qy	661 LSGGAPYYFAAELPPGNLFEPAFPPTVGDNRTYKGFMNPPLAQPKGNYNFOAMSSEYKET 720	Db	661 LSGGAPYYFAAELPPGNLFEPAFPPTVGDNRTYKGFMNPPLAQPKGNYNFOAMSSEYKET 670	Db	671 KTQCVRARIKAAATEEPEWIPDPAKQTDRVVKTAGISAGILVPLLLVIVVTKKSKLA 780	Db	671 KTQCVRARIKAAATEEPEWIPDPAKQTDRVVKTAGISAGILVPLLLVIVVTKKSKLA 730
Qy	721 KCRKDAMGNTRQENTHMYNDRSYADOSTLHAEDPLSLTMQHNFNSPRLPNDPLVFTA 840	Db	721 KCRKDAMGNTRQENTHMYNDRSYADOSTLHAEDPLSLTMQHNFNSPRLPNDPLVFTA 840	Db	731 KCRKDAMGNTRQENTHMYNDRSYADOSTLHAEDPLSLTMQHNFNSPRLPNDPLVFTA 790	Db	731 KCRKDAMGNTRQENTHMYNDRSYADOSTLHAEDPLSLTMQHNFNSPRLPNDPLVFTA 790
Qy	781 VLDENHSATAEESRLLDYRYLCEGTESPQYQTFQHLPAIRVALLOHINLMKTSDSYGFK 900	Db	781 VLDENHSATAEESRLLDYRYLCEGTESPQYQTFQHLPAIRVALLOHINLMKTSDSYGFK 900	Db	791 VLDENHSATAEESRLLDYRYLCEGTESPQYQTFQHLPAIRVALLOHINLMKTSDSYGFK 850	Db	791 VLDENHSATAEESRLLDYRYLCEGTESPQYQTFQHLPAIRVALLOHINLMKTSDSYGFK 850
Qy	901 BEYESFPECQASWIDVAKFDQNAKRNQYNIAYDHRSVYILOQVEDDPSDYNANVYD 960	Db	901 BEYESFPECQASWIDVAKFDQNAKRNQYNIAYDHRSVYILOQVEDDPSDYNANVYD 910	Db	951 BEYESFPECQASWIDVAKFDQNAKRNQYNIAYDHRSVYILOQVEDDPSDYNANVYD 910	Db	951 WLYRDGYOPSHYIATQGVHETYDFWMMWOBOSACTVMTNLVEGRVICKYKWFDD 1020
Qy	951 WLYRDGYOPSHYIATQGVHETYDFWMMWOBOSACTVMTNLVEGRVICKYKWFDD 1020	Db	951 WLYRDGYOPSHYIATQGVHETYDFWMMWOBOSACTVMTNLVEGRVICKYKWFDD 970	Db	911 WLYRDGYOPSHYIATQGVHETYDFWMMWOBOSACTVMTNLVEGRVICKYKWFDD 970	Db	1021 TEYVGDFKTVMEPLAERYVVRPTPTLBRGYNEIREYKQFHFTGWPDHGVYPHTGILS 1080
Qy	1021 TEYVGDFKTVMEPLAERYVVRPTPTLBRGYNEIREYKQFHFTGWPDHGVYPHTGILS 1080	Db	971 TEYVGDFKTVMEPLAERYVVRPTPTLBRGYNEIREYKQFHFTGWPDHGVYPHTGILS 1030	Db	1081 FIREVKLSNPPSAGPIVVCAGAGRITGCVYDILMNAERGQVVDLYNCYKALRSRI 1140	Db	1031 FIREVKLSNPPSAGPIVVCAGAGRITGCVYDILMNAERGQVVDLYNCYKALRSRI 1090
Qy	1141 NMVQTEEOYTFHDAILEACLGCTAIPCEKAYFMDIRIDSQTNSHLDKFDTQINS 1200	Db	1091 NMVQTEEQIFHDAILEACLGCTAIPCEKAYFMDIRIDSQTNSHLDKFDTQINS 1150	Qy	1141 NMVQTEEOYTFHDAILEACLGCTAIPCEKAYFMDIRIDSQTNSHLDKFDTQINS 1200	Db	1091 NMVQTEEQIFHDAILEACLGCTAIPCEKAYFMDIRIDSQTNSHLDKFDTQINS 1150
Qy	1201 VTPRLOAECSIACLPRNHDKNRPMDFLUDPRDCLPFLITIDGESSNNYNAALMDSYROA 1260	Db	1151 VTPRLOAECSIACLPRNHDKNRPMDFLUDPRDCLPFLITIDGESSNNYNAALMDSYROA 1210	Qy	1201 VTPRLOAECSIACLPRNHDKNRPMDFLUDPRDCLPFLITIDGESSNNYNAALMDSYROA 1260	Db	1151 VTPRLOAECSIACLPRNHDKNRPMDFLUDPRDCLPFLITIDGESSNNYNAALMDSYROA 1210

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52881), 2111 CC (AAK52821) and 3666 (AAM0020) are omitted as the relevant pages from the CC sequence listing were missing at the time of publication.

XX SQ Sequence 1452 AA:

Query	Score 61.8%; Length 1452;	Db	907 FFEGGOSAPNDSAKKDENRMKNRYGNIIAYDHSRVALQTLIEDDTNSDYINGNYI-----D 960
Best Local Similarity	61.5%; Pred. No. 0;	Qy	966 GYQRSHYIATQGPHETTYDWFNMNWOEASACIWMNTNLVEGRVKCYKXWPDTENYG 1025
Matches 892; Conservative 210; Mismatches 320; Indels 29; Gaps 9;		Db	961 GHRRPHHYIATQGPMEITYDWFNMWHENTASIMTMNTNLVEGRVKCCKXWPDTDEIYK 1020
Db	22 LIGSALQFSGAGCTTDDGPGACDTHQDLYDFDENTHVAQEPHYLPPMPQGSTMVNDS 81	Qy	1026 DFKVTCVEMPLAEVVRIFTLERYGYNE TREVKPHFTGWPDHGVPYHATGLLSPIRV 1085
Db	14 LLLTAAGETPSGGCLDEPVSTCGTQSSEQGDFENNEQVNTLTKPTSDPWNPGSEPMVNA 73	Db	1021 DIRVLLIEFLAETVIRFAVERGQHETREIRPHFCWPDIQSYPAITGLLFVRQV 1080
Qy	82 SNHDPGEKARIQLOPTMKENDTHCIDPSYLISQSGKINPGLTINILVRVNGPPLANJWNT 141	Qy	1086 KLSNPPSAGPIVVRSAGAGRTGCYIVIDIMLDMAEREGYDVIYCKALSRRIANMVQT 1145
Db	74 SGRPEGORAHILLPOLKENDTHCIDPHYFVSSKSNSPGLNUNVYKVNGPGLGNPWINIS 133	Db	1081 KSKSPPSAGAVHSSAGAGRTGCYIVIDIMLDMAEREGYDVIYCKRERSRRNMVQT 1140
Qy	142 GFTGROWLRAELAVSTFWNPNEYQVIFEAEVSGGRSGYIAADDIOVLSYPCDKSPHPFLRG 201	Qy	1146 BEQYIPIHDALLEACLGEGTAIPVCEFKAYAFDMTRIDSOQNTHLKEFOTLNSTVTPRL 1205
Db	134 GDTTRTWNRRAEAISTFWNPYQVIFEAEVSGGRSGYIAADDIOVLSYPCDKSPHPFLRG 192	Db	1141 BEQYVPTHDALEACLGDTSPVAQRSVLYYDMDNKLDPOTNSQIKEERTLNNVTPTL 1200
Qy	202 DVEVNACQNAQATFOCIATGRDAHVNKWLQRRNGEDIPVAAQTKNINHRFAASFRQLQEVTK 261	Qy	1206 QAEDSIACLPRNHDKNRFDMLPDRCLPPLITDGESSIONYINALMDSYKROPAFIVT 1265
Db	193 NVEVNACQAFATFOCSAIGRTVAGDRLWLQGDVDRAPLKETKVTSRREFLASENVNTTK 252	Db	1201 RVEPDSSIALPRNHTKRCMDILPDRCLPPLITDGESSIONYINALMDSYKOPAFIVT 1260
Qy	262 TDQDLVRCTQSERGSVGSNPAQLTIREPPIAPPQLGPGTVLILQMANSLIGDGP 321	Qy	1266 QYPLPNTVKDFWRLLYDYGCTSIVMLNEVDLSQGCPQYWWBEGMLRYGPIQEVMSCSM 1325
Db	253 RDAGKYROMIRTEGGGINSYNAELVYKEPPVPIAPPQLASGATILWQNANSINGDGP 312	Db	1261 QHPLPNTVKDFWRLLYDHTCTSVWLNNDVPAQLCQYWWBENGVRHGPQVEFTSADL 1320
Qy	322 IILKEYVRMTGSWTTETHA(NAPTYKLWHLDPDTBEYIYVLTREGEGETGLGPBPPLT 381	Qy	1326 CDVNBIPFRICNLTRPQEGVLMVQEQXGLMASHEVPGSKRSFELKLILQVEKMQEECE 1385
Db	313 IVAREVYCTASGSWNRQPVDTSTYKGHDLPDTBEYIYVLTREGEGETGLGPBPPLT 372	Db	1321 EDIISRFIYNAARPDQGYTRMVPQFQLGPMPTDVPSKRSFRLQYDVKWPEYEYNG 1380
Qy	382 RTKCAEPMRTPTKTLKIAEIQARRIAYDWESLGYNIRCHTENVTICYHFRGHNESRAD- 440	Qy	1386 GEGRLIHUNGGSMSGMCAIGIVTEMVKQNVVDFHVAKTLNSKPNVVAEADQYRF 1445
Db	373 RTKCADPMRGPKRPLEVVEKSRQITIRWEPEFSYNTRCHSYNLTVHCYQVGGQEQVRE 432	Db	1381 GEGRTVHCLNGGGSGTCAISIVCEMLPHQRTDVHVAKTLNPKPNVVDLQYKF 1440
Qy	441 -CLDDMDKRAQPVVNHLPPTYNVSRLMILTPERGRKESBTIQTBDVPGPPVPSLOG 499	Qy	1446 CYDVALEYLES 1456
Db	433 VSWDTENSHPQHTITNLSPTYNVSVLKILMNPGRKESQELIVQDIDLPAPVPTESIQG 492	Db	1441 CYEVALEYLN 1451

RESULT 9

ABR56629	ID ABR56629 standard; protein; 1452 AA.
XX	XX ABR56629;
XX	XX DT 09-JUL-2003 (first entry)
XX	XX DE Human cancer related protein SEQ ID NO:286.
XX	XX DB
XX	XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
XX	XX OS Homo sapiens.
XX	XX PN WO2003025138-A2.
XX	XX PD 27-MAR-2003.
XX	XX PF 17-SEP-2002; 2002WO-US029560.
XX	XX PR 17-SEP-2001; 2001US-0323469P.
XX	XX PR 20-SEP-2001; 2001US-0323487P.
PR	PR 13-NOV-2001; 2001US-0350666P.
PR	PR 08-FEB-2002; 2002US-0355145P.
PR	PR 08-FEB-2002; 2002US-0355157P.
PR	PR 12-APR-2002; 2002US-0372246P.
XX	XX XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX	XX PI Afar D, Aziz N, Gish KC, Hevezzi PA, Mack DH, Wilson KE;
XX	XX PI Zlotnick A;
DR	XX WPI; 2003-354600/33.

R N-PSDB: ACC72776

X New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating those diseases.

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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC7261 to AC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR5521 to ABP58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screenings, particularly for identifying agents for treating these pathologies.

Sequence 1452 AA:

Query Match 61.6%; Score 4812.5; DB 6; Length 1452
 Best Local Similarity 61.4%; Pred. NO; 0;
 Matches 891; Conservative 209; Mismatches 322; Indels 29;

RW protein tyrosine phosphatase receptor type mu; PTPRM; cytosolic;
 KW antidiabetic; gene therapy; expression pattern;
 KW hyperproliferative disorder; cancer; metabolic disorder; diabetes;
 KW infection; inflammation; tumour formation; human.
 XX
 OS Homo sapiens.
 OS Unidentified.
 PN US2004014699-A1.
 XX
 PD 22-JAN-2004.
 XX
 PF 18-JUL-2002; 2002US-00200293.
 XX
 PR 18-JUL-2002; 2002US-00200293.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 Cowser LM, Dobie KW,
 XX
 WPI; 2004-121596/12.
 DR N-PSDB; ADI80645.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT protein tyrosine phosphatase receptor type mu, useful for treating cancer
 PT or diabetes or modulating expression of protein tyrosine phosphatase
 PT receptor type mu.
 XX
 PS Example 13; Page 33-38; 56pp; English.
 XX
 CC This invention relates to a novel compound with an oligonucleotide 8-80
 CC nucleotides in length targeted to a nucleic acid molecule encoding
 CC protein tyrosine phosphatase receptor type mu (PTPRM) which specifically
 CC hybridises with the nucleic acid molecule encoding PTPRM and inhibits the
 CC expression of PTPRM or specifically hybridises with at least 8-nucleotide
 CC portion of a preferred target region on a nucleic acid molecule encoding
 CC PTPRM. The invention may be useful for the production of compositions
 CC with a cytostatic or antidiabetic activity. In addition, the disclosed
 CC sequences may be useful for gene therapy. The compound, particularly the
 CC antisense oligonucleotide is useful in modulating the function of nucleic
 CC acid molecules encoding PTPRM. The antisense compound can also be used as
 CC research tools and diagnostics. It can also be used as tools in
 CC differential and/or combinatorial analyses to elucidate expression
 CC patterns of a portion or the entire complement of genes expressed within
 CC cells and tissues. The compound can also be used for treating diseases or
 CC conditions associated with PTPRM, preferably hyperproliferative disorder,
 CC for example cancer or metabolic disorders, for example diabetes. The
 CC compound can also be used as prophylaxis, for example to prevent or delay
 CC infection, inflammation or tumour formation. The present sequence is that
 CC of the human protein tyrosine phosphatase receptor type mu (PTPRM) which
 CC is related to the invention.
 XX
 Sequence 1452 AA;

Query Match 61.6%; Score 4812.5; DB 8; Length 1452;
 Best Local Similarity 61.4%; Pred. No. 0;
 Matches 891; Consistency 209; Mismatches 322; Indels 29; Gaps 9;

Qy 22 LIGSALGOFSGAGCTFDGGACDTHDLYDDFEMVHSAQEPHYLPPMPOGSXMYVD 81
 Db 14 LLLTAAGTTFSGGCLFDPPYSTCGYSOEQGDDENNEDQNTLTKPTSDPMMPSGLMLVNA 73

Qy 82 SNHDPEKARLQLOPTMKENDTCIDFSYLISOKGKLNPTNLNLYVNGKPLANP 141
 Db 74 SCRPEGQAHLLLPQLKENDTHCIDFTYFVSSSKSNSPGLANYYVKNCNGPLGNPWNIS 133

Qy 142 GPTGRDWRIAELAVSTFWPNENQVIFENEVSGRSGYIAIDIOQSYCDKSPHFLRG 201
 Db 134 GPTGRDWRIAELAVSTFWPNENQVIFENEVSGRSGYIAIDIOQSYCDKSPHFLRG 192

Qy 202 DVEVNAGGONATFOCIATGRDAVHNKLWYQRNGDEDIPVAOTKNINHRFAASFRLOEVT 261
 Db 193 NVEVNAGGOFATFOCIATGRDAVHNKLWQGIDVRDAPLKEIKVTSRRFIASFNVNTK 252

Qy 262 TDQDLYRCYTOSESGSGVSNFAOLIIVREPRPTAPPQQLGVGPTYLLIOLNANSITGDGP 321
 Db 253 RDAGYKRCMIRTEGGVGSYNAELVVKKEPVPIAPQLASVGATLWQINANSITGDGP 312

Qy 322 IILKEVEYMTSGSWTEHAVNAPTYKLWHLDPDTPEYEIRVLLTRPGEGTGTLPGPPLIT 381
 Db 313 IVARAEYCTAGSMNDRQEVDTSYKIGHDPEPEYEISVLLTRPGEGTGTGPSPALRT 372

Qy 382 RTKCAEPMPPTPKLIAETQARRIAWDWESLGNTNTRCHTFNVTCTYHYPRGHNESTRAD- 440
 Db 373 RTKCAADPMRGPRKLEVEVKSROITIRWEBFGNTNTRCHSYNLTWHYCQVGGQQBVREE 432

Qy 441 - CLMDPDKPAOHVNHLPYPTVNSLKMILTNPEGRKESEETIQTODEDVPGPVPTKSLOG 499

Db 433 VSWDPTNSHQHTTINLSPPTNVSQYKLLNPNPEGKESQQLIVQDDEDLGAVPBPESIQ 492

Qy 500 TSFENKIFLWKPEPLEPNGLITQYEVSSSIRSRSPTAINTVNTNISAPLPDYEGVDAELNETATTITLRLPA 619

Db 493 STFEKIFLQWREPQTYGVTLTETITYKAVSSFPPEIDLSNOSGRVSKLGNETHFLFFG 552

Qy 560 LHPGTYQFFTRASTVKGRSPATAINTVNTNISAPLPDYEGVDAELNETATTITLRLPA 619

Db 553 LYPTTYSFTIRASTAKGFCGPATNQFTKISASMPAYE-LETPLNQTDNTVTMPLKPA 611

Qy 620 QAKGAPIASAOIVVOLPHPTKRAAGEMCYQVPTVONALSGGAPYPAEELPPGNLP 679

Db 612 HSRGGAPSVYQIWVEBERPTKKTIELLCYPVINFQASLINSQYAAEFFPADSLQ 671

Qy 680 EPAPPTVGDNRTYKGFWNPPLAPRKGNYIXYQANSSVEKETKTQCVRIATKAATEEEPEV 739

Db 672 AAQPPTGDNRTYNGWNTLPLPYSYRIFTQQAARGETKIDCVQVATKGAAPPKP-- 729

Qy 740 IPDPAKQTDRVVKLAGISAGILVFLVLLVIVVKKSCLAKRKIDAMGNTRQENTHMVN 799

Db 730 VPEPEQTDHTVVKLAGIVAGLFLVWLNKVKRKLAKRKETMSSTROENTMVN 789

Qy 800 AMDRSYADQSTLHARDPLSLTEMDOHNSPRLNDP-----LYPTAVL-DENH 846

Db 790 SMDK3AEGQNCDE--AFSEMDTHNLNGRSVSSSFTMKINTLSTSVEVNSYPPDETH 846

Qy 847 SATAESSRLLDVPRY LCEGTEBSPYQTGOTGOLHPAIRVADLQHINLMKTSDSYGFKEBEYES 905

Db 847 TMASTDSSLYQSHTYKCREPADVPYQTGOLHPAIRVADLQHINQMKCAEGYGFKEBEYES 906

Qy 906 FFEQGQASWDAKKQDNRAKRNQGNIAYDHSRVLQFQVEDDPSDYYINANYIDWLYRD 965

Db 907 FFEQGQAPWDSSAKDQDENRMNQYGNIIAYDHSRVLQFQEDTNSVINGNYI-----D 960

Qy 966 GYQRPSHYIATQGPYTHETVDFWRMWWQEQSACIYMTNLYVEGRVYKCYWPDDTBEVYG 1025

Db 961 GYHRPHYIATQGPQETIDFWRMWHENTASIMVNLVEGRVYKCKYWPDDTEIYK 1020

Qy 1026 DFKVTCVEMEPLAEXYVVRTFTLERGYNEIREVKQDFHGTGMDHGPYHATGLLSPFIRR 1085

Db 1021 DIKVTLIETELLAEVTRPAVEKGVHEIRFHGTGMDHGPYHATGLLGPFRQV 1080

Qy 1086 KLSNPISAGPVVHCSAGAGTGTGYVVDLMDMAREGVUDIYNCVKAISRRNMVOT 1145

Db 1081 KSKSPSSAGPLVHCSAGAGRTGFVTDMSYRQPAAFIVT 1140

Qy 1146 BEQYIIFHDALEACLGCTGETAIYPCBECFKAAFYFDMIRIDSQTNSHUKDEFOTLNSTMTPRL 1205

Db 1141 BEQYVFHDALEACLGDTSPASQVRSLYDMNKLDPQINSSQIKEEFTLNWYPTPL 1200

Qy 1206 QAEDCSTACIPLRNHDKNRFMMLPDRCLPFLITIDGESSIONYINAALMDSYRQPAAFIVT 1265

Db 1201 RVEDCSTALLPRNHEKRNCDILPDRCLPFLITIDGESSIONYINAALMDSYRQPAAFIVT 1260

Qy 1266 QYPLNPTVKDFTWRLYDGCTSIVMENEVDSLQGCPQYWPREGMLRYXPQIOVECMSCSM 1325

Db 1261 QHPLNPTVKDFTWRLYDGCTSIVMENEVDSLQGCPQYWPREGMLRYXPQIOVECMSCSM 1320

Qy	13226 CDVINRIFRICCNLTPQEGLYIMVOOFQYLWASHREVPSSKRSFLKLILQVEKWKQEECBB	1385	xx	Sequence 1452 AA;
Db	13221 EDISRIFRIVNAAPQDGTRMVOOFQLGPMIRDTpVSKRSFLKLILQVDKHKQEEYNG	1380	xx	Query Match 61.3%; Score: 479.5; DB 7; Length 1452;
Qy	1386 GEGRTIITHCLNGGRSGMFGAIGITVEMYKRONTYDVEHAKTTLRNKSNMVEAPEQYRF	1445	xx	Best Local Similarity 61.1%; Pred. No. 0;
Db	1381 GEGPTVHACLNGGRSGTFCASITCIVEMLRHQTVDVEHAKTTLRNKSNMVDLUDQZKF	1440	xx	Matches 88%; Conservative 211; Mis matches 324; Indels 29; Gaps 9;
Qy	1446 CYDVALEYLES 1456		Qy	22 LGSAIGQFSAGGCTEDDGPAGACTDLYDDFEMWVHSAQEPHYLPPPEMQGSYMWVDS 81
Db	1441 CYEVALEYLNS 1451		Db	14 LLI.PAGETSGGCIFDEPYSTCXSQSEGDDFWEQNTLTkpSDPMPGSGMLVNAA 73
RESULt 11			Qy	82 SNHDEGEKARLQLQPTMKENDTHCDFSLLYSOKGLNPGTNLILVRVNGPLANFIWNT 141
ADJ68277			Db	74 SGRDEGORAHILLPOLKENNDTHCDFSLLYSOKGLNPGTNLILVRVNGPLANFIWNT 133
ID ADJ68277 standard; protein; 1452 AA.			Qy	142 GFTCRDWRNLAELAYSTSFWNNEYQVFEAEVSGGRSGYTAIDDIQVLSYCDKSPLFLRG 201
XX			Db	134 GDPPTRNWALAASTFWFNFYQVFEV-ITSGHQGYLADEVKLGHCTRTHFLRLIQ 192
AC ADJ68277;			Qy	202 DVEYNAGQNAATFOCIATGRDAVHNKLWLQRNGEDIPV/AQTKNINHRRFAASFRQEVTK 261
XX			Db	193 NVEVAGQAFATFOCAIGRTVAGDRWLQGIDYRDAPIKEIKTSRRRIASFNVNNTK 252
DE Human heat-mitochondrial protein as a therapeutic target SeqID83.			Qy	262 TDQDLYRCVTVQSERGGSVNFAQLIVREPRPPIAPOLLGVGPTLLFOLNANSIGDGP 321
XX			Db	253 RDAGKRYCMIRTEGGVGISNYAELVKPVPVAPIAPOLASVGTATLWIQLNANSINGDGP 312
KW mitochondrial; human; screening assay; diabetes mellitus;			Qy	322 IILKEVEYRMTSGWETHEAVNACTYKLWHLDPTYEYRVLILTRPGEGCTGLPQPPLT 381
KW Huntington's disease; osteoarthritis;			Db	313 IVARBEVEYCTASGSWNRDQEVDSYTKIGHDPTYEYSVLLTRPGEGCTGSPEPALRT 372
KW Leber's hereditary optic neuropathy; LHON;			Qy	382 RTKCEPMPRTPKTLKIAELOQARRIAWDWESLGYGNITRCHTENTTCYHYFRGHNESRAD- 440
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;			Db	373 RTKCDAPMRGPRKLEVEVYTSRQITIRWEPPFGTNVTRCHSYNLTIVYCQVGGQEVREE 432
KW myoclonic epilepsy; ragged red fibre syndrome; MERRF; cancer;			Qy	441 -CLDDMPKAPQHVNWHLPYTYNLSKMLILTNPGRKESBETIQTDEDVPGPVPKSLOG 499
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;			Db	433 VSWDTENSHPQHTITNLSPYTNTSYVKLILMNPGRKESQELIVQTDEDLPGAVPESIQ 492
KW osteopathic; ophthalmological; cytosstatic.			Qy	500 TSFINKIFLNWKPEPNPITQEVSSIRSDFPAVPGPQTVSNLWNSTHVFVMH 559
XX			Db	493 STFEEKFLQWRPPTQYGVITLWETYKAVSSSPDPEIDLSNQSGRVSQKGNETHFLFFG 552
PN WO2003037768-A2.			Qy	560 LHPGTTYQPFIRASTVKGFGPATAINVTNNISAPSPLDYEGVDAISNTPATTITVLLRP 619
XX			Db	553 LYPTTYSPIRASTAKGFGPATTNQFTKISAPSMPAYE-LETPLNQTDNTVTVMLKPA 611
PD 23-OCT-2003.			Qy	620 QAKPAPISAYQIVVBLQHPRHTKREGAMECYQVPTVONALSGGAPYFAAELPPGNLP 679
XX			Db	612 HSRGAPVSYQIVVBEERRTKTEILKCYPVPHFONASLNSQYFAAEPADSLO 671
PF 04-APR-2003; 2003WO-US010870.			Qy	680 EPAFPYGDNRTYKGFMNPLAPKQGNTYFOAMS SVEREKETKOCVRATKAATTEEPEV 739
XX			Db	672 AAQFTIGDNKTYQWNTPLPPLPKSYRYYQASRANGEETKIDCQVATKGATPKP-- 729
PR 12-APR-2002; 2002US-0373843P.			Qy	740 IPDKAQDTRDVKTAGISGIGILVPLLLLWIVTKSKLAKERKDAQNTQEMTHMTN 799
PR 17-JUN-2002; 2002US-038987P.			Db	730 VPEPBDKOTDHTVKIAGVLAGILLFVUFLGIVLWMMKKRKLAKERKETMSSTROQTMVYN 789
PR 20-SEP-2002; 2002US-0412418P.			Qy	800 AMDRSYADOSTLHAEDPLSLTFMDQHNFSPRLPNDP-----LVPTAVL-DENH 846
XX			Db	790 SMDKSYAEQGTNCDB--AFSEMDTHNLNGRSVSSFTMKTNTLSTSVPNSYYPDETH 846
(MITO-) MITOKOR.			Qy	847 SATABSSRLDVPRY-LCEGTESTPSYQTGOLHPAIRVALQHNLMKTSDSYGFKEYES 905
(BUCK-) BUCK INST AGB RES.			Db	847 TMA2DTSSVYQSHTYKKGREPADVEYQTGOLHPAIRVALQHNLMKTSDSYGFKEYES 906
PA			Qy	906 FFEQSASHDVAKDQNRAKNRYCNIAYDHSRVILQPYEDDSSDYIMANYIDIWLYRD 965
PA (BUCK-) BUCK INST AGB RES.			Db	907 FFEQSASPDASAKEDENRMKQYCNIIYDHSRVTQLQTEGDTNSDYINGNYI ----D 960
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;			Qy	966 GYOSPHYIATOGVHETTYDWFWMWWQFQSACTIVMVNLVECRVKCYKWPDDTEVYVG 1025
PI Warnock DE;			XX	mitochondrial protein of the invention.
XX			PS 1; SEQ ID NO 83; 180pp; English.	
XX			CC This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy, ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nociceptive, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytosstatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.	

Db	961	GYHRPNIYIATOGPMOETTYDEFWRMWHENTASIMVTNLYEVGRVCKYWPDDETEYK	1020	DR	WPI; 2001-476283/51.
Qy	1026	DEKUTCUBMEDPLAEVYTRTFBLERRGYNBIREVKQHTGFDHGYPYHATGLLSFIRV	1085	XX	Nucleic acids encoding polypeptides with cytokine-like activities, useful
Db	1021	DIKVLTJETELLAEVYTRTFBLERRGYNBIREVKQHTGFDHGYPYHATGLLSFIRV	1080	PT	in diagnosis and gene therapy.
Qy	1086	KLSNPPIAGAPIVHCSSAGAAGRGCYLVTDIMLDAREGVVDIYNCVKAERSRRINMQT	1145	XX	Claim 20; Page 437-438; 6221pp; English.
Db	1081	KSNSPPAGPBLVHCSAGAAGRGCYLVTDIMLDAREGVVDIYNCVKAERSRRINMQT	1140	XX	The invention relates to polynucleotides (AAK51456-AAK53435) and the
Qy	1146	EQQYIFIHADALEBACGETAIPVCEFKAYFDMIRISQTINSHLKEFOTLNSTVPRL	1205	CC	encoded polypeptides (AM78343-AM80302) that exhibit activity eliciting to
Db	1141	EEQYVFIFHADALEBACGDTSPASOVRSLYDMDNRKDPQTINSSQKEEFTLNNVTPL	1200	CC	cytokine, cell proliferation or cell differentiation or which may induce
Qy	1206	QAEDECSTACLPBNHDKNPBMMLPPBCLPLPLITGEESNYINALMDSYRPAFIVT	1265	CC	production of other cytokines in other cell populations. The
Db	1201	RVEDCSTALLPNHEKNRMDLIPDPCRLPLPLITGEESNYINALMDSYRPAFIVT	1260	CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
Qy	1266	QYPLPLNTYKDFKFLVLDYGCSTIYMANEVDSLQGCPQWPEBGMLRYGTOVECMSCSM	1325	CC	peptide therapy. The polypeptides have various cytokine-like activities,
Db	1261	QHPPLPNTYKDFKFLVLDYGCSTIYMANEVDSLQGCPQWPEBGMLRYGTOVECMSCSM	1320	CC	e.g., stem cell growth factor activity, haemopoiesis regulating
Qy	1326	CDVINRIFRICNLTRPOGGYLWQOFQYLGASHREVPGSKRSFLKLLOVEKWOECEE	1385	CC	activity, tissue growth factor activity, immunomodulatory activity and
Db	1321	EDISRFRITNAARPQDHMRVQQRFLGPMYRDPVSRSALLRQDVKWOEYNG	1380	CC	activity/inhibit activity and may be useful in the diagnosis and/or
Qy	1386	GGRTTIIHCLNGGRSSMCAGISIVEMKQIVNWDYHATAKTLRNSKRMVNEAEQYRF	1445	CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
Db	1381	GGGPTVTHCLNGGRSSMCAGISIVEMKQIVNWDYHATAKTLRNSKRMVNEAEQYRF	1440	CC	inflammation. Note: Records for SEQ ID NO 2110 (AAK5281), 2111
Qy	1446	CYDVALEYLSE 1456		CC	(AAK5282) and 3666 (AM80020) are omitted as the relevant pages from the
Db	1441	CYEVABLYNS 1451		CC	sequence listing were missing at the time of publication
Qy				XX	Sequence 1455 AA;
SQ				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
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				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
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				XX	Best Local Similarity 61.0%; Pred. No. 0;
				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
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				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
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				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
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				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
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				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
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				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
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				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
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				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
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				XX	Sequence 1455 AA;
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				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4; Length 1455;
				XX	Best Local Similarity 61.0%; Pred. No. 0;
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				XX	Matches 887; Conservative 210; Mis-matches 326; Indels 30; Gaps 10;
				XX	Sequence 1455 AA;
				XX	Query Match 61.2%; Score 4783; DB 4

Qy	211 ATFOCIATGRDAVNKLWLRNNGEDIIPVAQTQINHRFRFAASFRLOETVTKTDDOLYRCV 270	Db	1310 TTPDFWGLVYDYGCTIVMLNQLQNSAWPCLQWPEPRQRQYLMVEFMSGTADEDI 1369
Db	251 ASFQCMAGRAEARFLLQRQSGLVPAVGVRHLSHRRPLATPLAASRAEQLYRCV 310	Qy	1329 INRIFRICNITRPOEGYLWVQQFOYLGWASHREYGSRSFLKLILQVZKWKQEEEEEGEG 1388
Qy	271 TOSERSGSVS-NFAOLIVRVERPPTAPPOLLGVGPTYLILQLQNLANSIIICPDGPILIKEVY 329	Db	1370 VARVFRVNQNTSRLOGHLLVRHFQLRWSAYRDPSDKAFKLHLAARGDWQ--AESGDG 1427
Db	311 SOAPGRGTSILNFABFMVKCEPPTAPPQULRAGPTYLILQLQNLANSIIICPDGPILIKEVY 370	Qy	1389 RTI1HCLNGGRGSMCAGTGYVVMKRONVVDYFHAVKTLRNSKPNMVEAPEYRFYCVD 1448
Qy	330 RMTGSSWTEHTAVNAPTYKLWHLDDDTETEYBIRVLTLTRPGGCTGLPGPLIITPKCAEDM 389	Db	1428 RTIVCLNGGRGSMFCATVLEMIRCHNLVDVFFAAXTLRNKPNNMVEPMQTHFCYD 1487
Db	371 RMARGPWAEYHAVSQTYKLWHLDDDTETEYBISVLLTRPGGCTGRGPPLISRTKCAEDM 430	Qy	1449 VALEYLE 1455
Qy	390 RTPKTLKIAETQARRIAVADWESLGNNTIRCHTFNTVTCHYFRG--HNNSRADCLMDDX 447	Db	1488 VALEYLE 1494
Db	431 RAKPGIAFAETQARQLTQBLPQBLGYNVTRCHTFNTVLCYHNTIRECVYKTEQ 490		
Qy	448 APOHVNVNHLHPPYTNTVSLKMLITNPGRKSEETIITQDDEDPGPVVPVRSQGTSFENKF 507		RESULT 15
Db	491 VSRYTMKNLNPYRNRVHVRVLTNPGRKEKIVETQTDDEPVSGIAAESLTFTPLEDMMP 550	Db	AAW41361 standard; protein; 1436 AA.
Qy	508 LNWKPEPLPENGITTOYEVSYSSTIRSFDPAVPVAGBPOTYSNLWNSTHAYFMHLHPGTTQ 567	Db	XX
Db	551 LKWERPQEPLNGLITYEISSTQSISSSDPAPVNPGERRTSKLNRNETHYFSNLHHPGTTYL 610	Qy	XX
Qy	568 FPIRASTVKGFPATAINTTNTNAPSLLPYEGDASLNATATTIVLRLPAQKGAPS 627	Db	XX
Db	611 FSVARTGCGFQGAALTEITNISAPSF-DYADMSPSPLGESENTIVLRLPAQKGAPS 669	Qy	XX
Qy	628 AYQIVVEQ-L-PHRTKREAGAMECYQVPTTYQNALSGGAPYFFAAELPPGNLPEPAPFTV 686	Db	KW
Db	670 VIQVIVEEGSRRRLRREPQGDCEPVPVLFPEAALRGVDFGAEELASSLPPAMPFFRV 729	Qy	KW
Qy	687 GDNPRTYKGFTNQNPPLAPRKGNINYFOAMSVKEETKTOCVRIAKTAATEPEEVIPDPAKQ 746	Db	KW
Db	730 GDNKTYRGFTNQNPPLERPKAVLYFQAAQSHLKGETRLNCIRARAAKESKRPL-EVSQR 788	Qy	Misc-difference 158
Qy	747 TDRVVKIAGISA-GILVFIILLVIVVIVKSK-----LACKRKDAMGNTAQ 792	Db	FT
Db	789 SEENGCLIGCAGGLAVLILLGAIIVRKGRDHAYASYYSPKPVNMTK---ATVNYRQ 844	Qy	/label= unknown /note= "encoded by TWT"
Qy	793 EMTHMVNAIDRSYADQSTLHAEDPLSLTMDQHNFSPRLNDPLVPTAVLDENHSATAES 852	Db	FT
Db	845 EKTHMSAIVRSFTDQSTLQEDERGLSMDTHGYSTR-----GDQRGGVTIA 893	Qy	Misc-difference 340
Qy	853 SRLI-DVPRVLCGETESPOTGOLHPAIRYADLQHNLMKTSDSYGPKEYESFEGCS 911	Db	FT
Db	894 SSLLGGSSPRPGRGKGSPTHTGOLHPAVRYADLQHNLQKMTAEGYGPKEYESFEG-- 951	Qy	/label= unknown /note= "encoded by CAR"
Qy	912 ASWDVAKDONRAKNRGNTIAYDHSRVLQDPSDSDYINANVYDLYRDGYQRS 971	Db	FT
Db	952 -WDATEKKCDKVKGSRQEMPMPAYDHRVHLHPMLGDPNDADYINANVYDTRINREGYHSN 1009	Qy	Misc-difference 1208
Qy	972 HYIATQGPYTHEETYDFWRMWVQEoSACIYMTNVLVEGVKCYKWPDPDTEVYDFKVTC 1031	Db	FT
Db	1010 HFIAUTQGPXPEMVDFWRMWWQEHSIMIITKLVBSGVVKCSRYWPEISDTGDIKML 1069	Qy	/label= unknown /note= "encoded by YGC"
Qy	1032 VEMPLAETVYVTRTFLERGYNEREVKQHFTGMPDHGYPIATGGLSPIRVYKLSNP 1091	Db	XX
Db	1070 VKTEFLAETVYVTRTFALERYSASRHEVRQHFHTAWPEHGYPYHATGLLAFIRRVKA-TPP 1129	Qy	W09744458-A1.
Qy	1092 SAGPFTVHCSAGAGRTGCTIVIDMMAEREGVUDYCNVCKAURSRRIINVQTEEQYTF 1151	Db	XX
Db	1130 DAGPVIHCSAGTGTGCTIVDMLMACEGQVUDTNCVKTLCSRNNMIEQEYQTF 1189	Qy	27-NOV-1997.
Qy	1152 IHDATLEACLGCTEAIPVCEFKAAYFDMRIDSQTSNSSLKDEFQTLNSVTPRLOAEDOS 1211	Db	XX
Db	1190 IHDATLEACLGCTEAIPVCEFKAAYFDMRIDSQTSNSSLKDEFQTLNSVTPRLOAEDOS 1249	Qy	97WO-US009056.
Qy	1212 IACIPRNHDKNRNFNDMLPDRCLPLITDGESSNYINALMDSYRQPAPFITYQVPLN 1271	Db	22-MAY-1997;
Qy	1250 IALLPRNRDQNSMDVLPDRCLPLFSLGDSNNYINALTDSYTRSAFIFTLHPLQS 1309	Qy	PR 24-MAY-1996;
Qy	1272 TVRDFWRLYDYGCTSIVMLNEVDSLQG--CPOYWPEBGMRLYGPQVCMCSMDCIDV 1328	Db	XX
Qy		CC	Claim 6; Fig 1; 118pp; English.
Qy		CC	This sequence represents the mouse receptor protein tyrosine phosphatase (PTP) 1ambda polypeptide of the invention. PTP 1ambda is: (i) mainly expressed in adult mammalian brain, lung and kidney; (ii) not expressed in adult liver; and (iii) can dephosphorylate phosphorylated tyrosine (pT) residues. The DNA sequence is used to express recombinant PTP 1ambda, and also as a source of probes for screening DNA libraries. PTP 1ambda is used to isolate the receptor's cognate ligand (potentially useful for treating paralytic diseases), and for preventing metastatic spread. PTP 1ambda is also used as a molecular marker for particular

CC tissues, as a reagent in an assay for identifying PTP (ant)agonists, and
 CC as a molecular weight marker in protein gels. The Ab is used in
 CC diagnosis, tissue-typing and purification of PTP Lambda, also it may
 CC crosslink the receptor, resulting in its upregulation. PTP Lambda is a
 CC mediator of cell adhesion and may be involved in development of
 CC epithelial and neuronal structures (neuronal pathfinding)

xx Sequence 1436 AA;

Query Match Score 58.4%; Score 4575; DB 2; Length 1436;

Best Local Similarity 59.8%; Pred. No. 0;

Matches 858; Conservative 209; Mismatches 332; Indels 36; Gaps 12;

Qy	32 AGGCTFDDGPG---ACDYHQDLYDDFEWVHSAQECPHYPPEMPMPOGSYMMYDSSNHDPGEE 88	925 KNRYENNTIAYDHSRVLQILQPVYEDDPSPDYINANYDIWLVRDGYQPSHYIATOGVHETV 984
Db	24 AAGCTTFFEADSDPVPCPESFSQAYDDFWEQRIHPGTRTPDLPHGAYLMVNASOPTPGQ 83	906 GGRQDPVSAYDRHVKLHPMLADPDADTSANYI----DGYHRSNNHFATQSKPPEMI 959
Qy	89 KARLQLPTMKENDTHC1DFSYLILSYOKGLNPQTNLILYRINKGPLANPIIWAVTGFGRDW 148	985 YDFWMWYKWEQSACTVMVTNLVEYGRVKCYKWPDDTEVYGGDFKWTCVEMEPPLAEYXVRT 1044
Db	84 RAHIIFQTLSENDTHCQFSTFLYSRDGHSPETLGYVYRNGGLGSAVNMMTGSHGRQW 143	960 YDFWMWVWQOCASITMILKLVLRVKGCSRYWPDSMDYGDIKATLVKBFTLAEXVVRT 1019
Qy	149 LRAELAVSTFWNENEYQVTFEAEVSGCRSGYTAIDDIQVLSPYCDKSPHFIRLGDVENVAG 208	1045 FTLEBRGYNBIREKVQFHFGWPMQDGPVPHATGLSEFIRVKLNSNPPSAGPIVYVCSAGA 1104
Db	144 HOELAVSTFWNEEXQVLFIALEALSPDHKGTYGLDDILFSLFSCPKAACPHFSFLGIDDVENVAG 203	1020 FALERGYSARHEVRQFHFTAWPERGVYHTATGLAFTIRVKASTPPDAGPVIHCSAGT 1079
Qy	209 QNATFOCATGERDAVINKLWLQRNGEDIPVQTKNINHRFAASPLRQEVTKTDDLYR 268	1105 GRTGCVIVIDIMLDMAEREGVVDYNCVKAVERSREINMVQTEEQNIFHDAILELCGEE 1164
Db	204 QNASFQMAAGAAEAHHFFLORQSGCVLVPAGVRHSRERELATEPLASGRSBEDLYR 263	1080 GRTGCVIVDMLDIAECBQVWDYNCVKTLCSPRNVMQTEEQYIFHDAILELCGEE 1139
Qy	269 CTVQSERGSVSNPAQIIVRSPRPIAPOLLGVGPTYLQLQANANSIIGDGPILKEVE 328	1165 TAIPVCEFKAYFDMDRIDSOQNTHSSNLSYRQAFAFIVTOXPRLQAEPCSIAICLPRNHDKNRF 1224
Db	264 CVSQAPRGAVGSVNAELVKEEPTPLAPOLLRAGPYTLQLQNTNSIIGDGPIVRKIE 323	1140 TTIPNEFRATYREMIRDQSNSQLREFQTNISVTPPLDVETCSIALLPRNEDKNSR 1199
Qy	329 YRMARGPWAEVHVNLYTKLWLHDPTDEYEYRVLJTRGEGTGTGPGPLPLTRTCAP 388	1225 MDMLUDPDRCLPFLITIDGESSNSYINANLMDSYRQAFAFIVTOXPRLQAEPCSIAICLPRNHDKNRF 1284
Db	324 YRMARGPWAEVHVNLYTKLWLHDPTDEYEYSVLLTRPGDGTGRPGPLLSRTYCAEP 383	1200 MDVLPUPDRXLPLFLISSDGDPNNYINANLTDTSYTRAFAFIVTLHPQSTTDFWRVLYDYG 1259
Qy	389 MRTPTKLUKIAEIOARRTADVWSIGNTNITRCHTFNTVTCYHFRG---HNESRADCLMDP 446	1285 CTSIVMLNEVDSLQG---CPQYWPPBGMARYGPTQVECMCSMDDCVDINRIFRICNLTRP 1341
Db	384 TRAPKGIAFAEQARQTLQWPLGLGNVTRCHTAYSLCYTGLQHNSHNOTIRECVTRMER 443	1260 CTSIVMLNQINQNSAWPCLQYWPPBGMARYGPTQVECMCSMDDCVDINRIFRICNLTRP 1319
Qy	447 KAPQHVUNHLPPTVNSLKMILTNPGEKRESSETILOTDEDVPGPVPVKSLOGTSFENKI 506	1342 QEGYLMVQQFOYLGPASHREVPGSKRSFLKLQVEKWOEECEBEGRTIHCINGGGRS 1401
Db	444 GASRYTIKLNLFERNTHVRLLTNPGEKREKEGBFTQFDEDVPGG3IAAESLTFTPLDEMI 503	1320 QEGHLLVURHQFLRISAYRDTDPSKAFHLILABDKWQ--AESGGRTVHCLNGGGRS 1377
Qy	507 FUNKEPEIPLPGLTTOVEVSYSSIRSDDPAEVAGPPTQTVSNLWNSTHVMNHLHFTY 566	1402 GMFCAGIVVBMVKQNVNDVFEHAVKTLRNSKPNVVAEAPOQYRFYCDALEYLES 1456
Db	504 FLKWEPEOEPGLTQIYEISQSIESSDPATVNPGRTRTISKLNRTYHVSNLHFTY 563	1378 GTFPCACATVLEMIRCHSLVDFFAKTLRNYKPVNMTDQYHFCYDVALEYLEA 1432
Search completed: June 1, 2005, 13:49:19 Job time : 156.411 secs		

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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:44:18 ; Search time 133.324 Seconds
(without alignments)

Title: US-09-887-669-1
7809

Perfect score: Sequence: 1 MDVAAAALPAFVALNLYPW.....EAPEQYRFYCVDALLELESS 1457

Scoring table: BLASTM62 Gapext 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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 /cn2_6_ptodata/1/pubbaa/PCTU_PUBCOMB.pep:
 2: /cn2_6_ptodata/1/pubbaa/US16_NEW_PUB.pep:
 3: /cn2_6_ptodata/1/pubbaa/US16_NEW_PUB.pep:
 4: /cn2_6_ptodata/1/pubbaa/US07_NEW_PUB.pep:
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 20: /cn2_6_ptodata/1/pubbaa/US60_PUBCOMB.pep:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	7809	100.0	1457	9	US-09-887-669-1	Sequence 1, Appli
2	7582	97.1	1439	16	US-10-408-765A-284	Sequence 2, Appli
3	7571	97.0	1439	9	US-09-887-669-2	Sequence 8, Appli
4	4843	5.5	62.0	1452	9	US-09-887-669-8
5	4789	5.5	61.3	1452	16	US-10-408-765A-83
6	4591	58.8	1436	14	US-10-205-219-15	Sequence 15, Appli
7	4577	58.6	1499	15	US-10-296-115-1283	Sequence 1283, Ap
8	4552	58.3	1444	15	US-10-058-270A-98	Sequence 98, Appli
9	4542.5	58.2	1463	14	US-10-176-847-22	Sequence 24, Appli
10	4542.5	58.2	1463	14	US-10-205-823-343	Sequence 343, Appli
11	4359	55.8	1442	16	US-10-408-765A-805	Sequence 805, Appli
12	4325	55.4	1430	13	US-10-087-993-34	Sequence 34, Appli
13	2471.5	31.6	623	15	US-10-296-115-1190	Sequence 1190, Ap

ALIGNMENTS

RESULT 1
US-09-887-669-1
Sequence 1, Application US/09877669
Publication No. US20020082397A1
GENERAL INFORMATION:
 ; APPLICANT: SCHLEISINGER, JOSEPH
 ; APPLICANT: SAP, JAN M.
 ; APPLICANT: ULLRICH, AXEL
 ; APPLICANT: VOGEL, WOLFGANG
 ; APPLICANT: FUCHS, MIRIAM
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
 ; FILE REFERENCE: 038602/1246
 ; CURRENT APPLICATION NUMBER: US/09/887-669
 ; CURRENT FILING DATE: 2001-10-10
 ; PRIORITY APPLICATION NUMBER: 09/234, 883
 ; PRIORITY FILING DATE: 1999-01-21
 ; PRIORITY APPLICATION NUMBER: 08/087, 244
 ; PRIORITY FILING DATE: 1993-07-01
 ; PRIORITY APPLICATION NUMBER: 08/049, 384
 ; PRIORITY FILING DATE: 1993-04-21
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1457
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-887-669-1
 Query Match 100.0%; Score 7809; DB 9; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0;
 Gaps 0;
 Qy 1 MDVAAAALPAFVALWLLYPWPLIGSALGSAGCTTDFDGPAGCDYHQLYDDFWVIVS 60
 Db 1 MDVAAAALPAFVALWLLYPWPLIGSALGSAGCTTDFDGPAGCDYHQLYDDFWVHS 60

Qy	61	AQEPHYLPPMEQGSYMWVDSNNHDPCEKARLQLPTMKENDTHCIDSFLYLYSQKGLNPG	120		Db	1141	NMVQTEEQYIIFIHQDILEAQLCGETAIPVCFKAAYFDMIRIDSQTNSHLKDEFQTLNS	1200
Db	61	AQEPHYLPPMEQGSWVDSNNHDPCEKARLQLPTMKENDTHCIDSFLYLYSQKGLNPG	120		Qy	1201	VTPRLOAEDCSIACIOPRNHDIGNRFNDMLPPDRCLPLITDGESSIONYINALMDYRQPA	1260
Qy	121	TLNILYRKNGPPLANPIWNTGFTGRDWLRAELAVSTFWPNPEYQVIFEAEVSGGRSGYIA	180		Db	1201	VTPRLOAEDCSIACIOPRNHDIGNRFNDMLPPDRCLPLITDGESSIONYINALMDYRQPA	1260
Db	121	TLNILYRKNGPPLANPIWNTGFTGRDWLRAELAVSTFWPNPEYQVIFEAEVSGGRSGYIA	180		Qy	1261	AFIVTOYPLPNTVKDFKFWRLLVYDGGTSIVMLNEVLSOCGPQYWEFGMLRYGPQVECM	1320
Qy	181	IDDIQVSYPCDKSPHFLRGPLIVWAGQNTFOCATGRDAVNLKLWQRNGEDIPIVA	240		Db	1261	AFIVTOYPLVPLNTVKDFKFWRLLVYDGGTSIVMLNEVLSOCGPQYWEFGMLRYGPQVECM	1320
Db	181	IDDIQVSYPCDKSPHFLRGPLIVWAGQNTFOCATGRDAVNLKLWQRNGEDIPIVA	240		Qy	1321	SCSMCDVIRIPIRCNLTRPOEGLMVQFOYLGAWSHREVPGSKRSFLKLILQYBKWQ	1380
Qy	241	QTKNINERFRFAASFRLOBTKTIDOLYLRCYTOSERGSVSNFAQLIVREPRPIAPPQJL	300		Db	1321	SCSMCDVIRIPIRCNLTRPOEGLMVQFOYLGAWSHREVPGSKRSFLKLILQYBKWQ	1380
Db	241	QTKNINERFRFAASFRLOBTKTIDOLYLRCYTOSERGSVSNFAQLIVREPRPIAPPQJL	300		Qy	1381	EBCBEGEGRITIHCLNGGRSGMFCAGIVVEMYRQNVDVFHAVKTLRNSKPNNVEAP	1440
Qy	301	GVGPTYLIQLNANSIIGDGPTLKEVYRMITSGSTETHAVNAPTYKLWHDPTDEYEI	360		Db	1381	EBCBEGEGRITIHCLNGGRSGMFCAGIVVEMYRQNVDVFHAVKTLRNSKPNNVEAP	1440
Db	301	GVGPTYLIQLNANSIIGDGPTLKEVYRMITSGSTETHAVNAPTYKLWHDPTDEYEI	360		Qy	1441	EQYRFCDYVALEYLSS	1457
Qy	361	RVLLTRIGEGGTGLPGPLIPTKCAPMRPTKLIKAEQARRIAVWDWESLGYNITRCH	420		Db	1441	EQYRFCDYVALEYLSS	1457
Db	361	RVLLTRIGEGGTGLPGPLIPTKCAPMRPTKLIKAEQARRIAVWDWESLGYNITRCH	420					
Qy	421	TENVTCICHYFRGHNESRADCLMDPKAPQHVNHLPPTNVSLSKMLTNPBEGRKESET	480	RESULT 2				
Db	421	TENVTCICHYFRGHNESRADCLMDPKAPQHVNHLPPTNVSLSKMLTNPBEGRKESET	480	US-10-408-765A-284				
				Sequence 284, Application US/10408765A				
				Publication No. US20040101874A1				
				GENERAL INFORMATION:				
				APPLICANT: Ghosh, Sounitra S.				
				FAHY, Boin D.				
				Zhang, Bing				
				APPLICANT: Gibson, Bradford W.				
				APPLICANT: Taylor, Steven W.				
				APPLICANT: Glenn, Gary M.				
				APPLICANT: Warnock, Dale E.				
				TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION				
				FILE REFERENCE: 660088.465				
				CURRENT APPLICATION NUMBER: US/10/408,765A				
				CURRENT FILING DATE: 2003-04-04				
				NUMBER OF SEQ ID NOS: 2077				
				SOFTWARE: FastSEQ for Windows Version 4.0				
				SEQ ID NO 284				
				LENGTH: 1439				
				TYPE: PRT				
				ORGANISM: Homo sapiens				
				US-10-408-765A-284				
Qy	661	LSGGAPYFAAELPPGNLPEPAPFTYQDNRTYKGFWNPPLAPRKGYNYIQAMSSYKEI	720	Query Match	97.1%	Score 7582;	DB 16;	Length 1439;
Qy	661	LSGGAPYFAAELPPGNLPEPAPFTYQDNRTYKGFWNPPLAPRKGYNYIQAMSSYKEI	720	Best Local Similarity	97.4%	Pred. No. 0;		
Db	721	KTOCVRATKAAATEEEPVIPAKTQDRVKIAGSAGILVFLILLVIVVKRSKLA	780	Matches 1420;	Conservative	Mismatches 5;	Indels 20;	Gaps 4;
Qy	721	KTOCVRATKAAATEEEPVIPAKTQDRVKIAGSAGILVFLILLVIVVKRSKLA	780	Qy	1	MD-VAAAALDAFVALMLYPPNPLIGSAGQSAGGCTFDGDPGACDYHODLYDDFWHVH	59	
Db	721	KTOCVRATKAAATEEEPVIPAKTQDRVKIAGSAGILVFLILLVIVVKRSKLA	780	Db	1	MDTTAAALPAFPVALLLSPPLIGSAGQSAGGCTFDGDPGACDYHODLYDDFWHVH	60	
Qy	781	KGRDANGNTROEMTHNMAMDRSYAQSTLHAEDPLSLTMQHNFSPRLNDPLVYTA	840	Qy	60	SAQBPYLLPPMPQGYSYMDVSNDPGEKARLQLPTMKENDTHCDFSTLILYSGKGLNP	119	
Db	781	KGRDANGNTROEMTHNMAMDRSYAQSTLHAEDPLSLTMQHNFSPRLNDPLVYTA	840	Db	61	SAQBPYLLPPMPQGYSYMDVSNDPGEKARLQLPTMKENDTHCDFSTLILYSGKGLNP	120	
Qy	841	VLDENHSATAESSRLLVYPRYLCGETESPYQGQLHPAIRYADLLOHINLMTSDSYGF	900	Qy	120	GTLNLLVRYNKGPLANPIWNTGFTGRDWLRAELAVSTFWPNEXYQVTFEAEVSGRSGYI	179	
Db	841	VLDENHSATAESSRLLVYPRYLCGETESPYQGQLHPAIRYADLLOHINLMTSDSYGF	900	Db	121	GTLNLLVRYNKGPLANPIWNTGFTGRDWLRAELAVSTFWPNEXYQVTFEAEVSGRSGYI	180	
Qy	901	EEYESFFEGOSASWDYAKDQNRKAKYGN1TAYDHSRILVQVEDPSSDYNANYIDI	960	Qy	180	ADDIQYLSPYCDKSPHFLRGDVYENAGONATEQCIATGRDAVHNKLWLORRNGEDIPV	239	
Db	901	EEYESFFEGOSASWDYAKDQNRKAKYGN1TAYDHSRILVQVEDPSSDYNANYIDI	960	Db	181	ADDIQYLSPYCDKSPHFLRGDVYENAGONATEQCIATGRDAVHNKLWLORRNGEDIPV	240	
Qy	961	WLYRDGYCRPSHYIATQCPVHETVYDPMRFTLERRGYNEIREVKOFHFTGWPDHGVPYHATGLS	1020	Qy	240	AGTQTNINRRPAASFLQEVTKDQLYRCVTSQSGSYNSNAQIVLREPRPIAPPOL	299	
Db	961	WLYRDGYCRPSHYIATQCPVHETVYDPMRFTLERRGYNEIREVKOFHFTGWPDHGVPYHATGLS	1020	Db	241	AGTQTNINRRPAASFLQEVTKDQLYRCVTSQSGSYNSNAQIVLREPRPIAPPOL	300	
Qy	1021	TEVYGDFTVTCYMEPLAEYVYRTFTLERRGYNEIREVKOFHFTGWPDHGVPYHATGLS	1080	Qy				
Db	1021	TEVYGDFTVTCYMEPLAEYVYRTFTLERRGYNEIREVKOFHFTGWPDHGVPYHATGLS	1080	Db				
Qy	1081	FIRRVKISNPPSAGPITYCHSAGAGTCYVTDIMDMAEFGNDIYNCYKALPSRI	1140	Qy				
Db	1081	FIRRVKISNPPSAGPITYCHSAGAGTCYVTDIMDMAEFGNDIYNCYKALPSRI	1140	Db				
Qy	1141	NMVQTEEQYIIFIHQDILEAQLCGETAIPVCFKAAYFDMIRIDSQTNSHLKDEFQTLNS	1200	Qy				

QY	3001	LGVGPYLLQLNANSIIGDOPILIKEKEVTRMTSSWTHAIVNAPTYKLWHDDBTEY	359	Db	13.62	QECEEGEGERTIICLNGGSRSGMCAIGIVVEMKRQNTVYDVFFAVKTLRNKSNMVEA	1419
QY	301	LGVGPYLLQLNANSIIGDPIILKEVTRMTSSWTHAIVNAPTYKLWHDDBTE	360	Qy	14.40	PEQTRFCYDVALEYLESS	1457
QY	360	IIRVLTRPGEGTGLPGPLIITRCKAEPMRTPKTLKIAIBIQARIAVWESLGYNITRC	419	Db	14.22	PEQTRFCYDVALEYLESS	1439
QY	361	IIRVLTRPGEGTGLPGPLIITRCKAEPRTPTKLIQARIAVWESLGYNITRC	420				
QY	420	HTFNYTICXHYFRGHNESRADCLMDPKAQHVNHLPPYTNSLKMILTNPEGRKESSE	479		RESULT 3		
QY	421	HTFNYTICXHYFRGHNESRADCLMDPKAQHVNHLPPYTNSLKMILTNPEGRKESSE	480		US -09-887-669-2	Sequence 2, Application US/09887669	
QY	480	TIIQDDEDPGPVPKSLQSTSFKIPLINKEPLEPGNGITQYEVSKSISRSIDPAVY	539			; Publication No. US20020082397A1	
QY	481	TIIQDDEDPGPVPKSLQSTSFKIPLINKEPLDNGNITQYBISYSSISRSIDPAVY	540			; GENERAL INFORMATION:	
QY	540	AGPPOTVSUNWNSTHVFMLHPGTTYQFFTRASTVKGSPATAINVNTNISAPSLPDY	599			; APPLICANT: SCHLESINGER, JOSEPH	
QY	541	AGPPOTVSUNWNSTHVFMLHPGTTYQFFIRASTVKGSPATAINVNTNISAPSLPDY	600			; APPLICANT: SAP, JAN M.	
QY	600	GVDASLNEATTITVLLRPAQAKCAPISAQYIVVEOLHPRTKREAGAMECYQVPVTYON	659			; APPLICANT: ULLRICH, AXEL	
QY	601	GVDASLNEATTITVLLRPAQAKCAPISAQYIVVEOLHPRTKREAGAMECYQVPVTYON	660			; APPLICANT: VOGEL, WOLFGANG	
QY	660	ALSGGAPYFAAEI.PPGNL.PEPAPPTVGDRTYQGFNNPLAPKGKYNYFOAMSSVEK	719			; APPLICANT: EUCHS, MIRIAM	
QY	661	AMSGGAPYFAAEI.PPGNL.PEPAPPTVGDRTYQGFNNPLAPKGKYNYFOAMSSVE	720			; TITLE OF INVENTION: NOVEL RECEPTOR - TYPE PHOSPHOTYROSINE PHOSPHATASE - KAPPA	
QY	720	TKTQCVRIATAAAEPEPYIDPAKOTDRVKLAGISAGILVILLVIVIVTKKSL	779			; CURRENT APPLICATION NUMBER: US/09/887,669	
QY	721	TKTQCVRIATK-AATEPEPYIDPAKOTDRVKLAGISAGILVILLVILVKKSL	779			; CURRENT FILING DATE: 2004-10-10	
QY	780	AKCRKDAMGNTROQENTHNMADRSYADOSTLHAEDPLSLTMDFNFSRPLPNPDLVPT	839			; PRIORITY DATE: 1999-01-21	
QY	780	AKCRKDAMGNTROQENTHNMADRSYADOSTLHAEDPLSITMDFOHNFSPRY-----	831			; PRIOR APPLICATION NUMBER: 08/087,244	
QY	840	AVLDENHSAATAESSRLDPRYLCGETTESPYQTQLHPAIRVALLOQHNLMTSDSYOF	899			; PRIOR FILING DATE: 1993-07-01	
QY	832	---ENHSATAESSRLDPRYLCGETTESPYQTQLHPAIRVALLOQHNLMTSDSYOF	887			; PRIOR APPLICATION NUMBER: 08/049,384	
QY	900	KEEYESFFEQQSASWDACKDQNBAKNRGNITAYDHSHVILQPVEDDSSDYINANTID	959			; PRIOR FILING DATE: 1993-04-21	
QY	888	KETYESFFEQQSASWDACKDQNRAKNRGNIIAYDHSHVILQPVEDDSSDYINANTII-	946			; SOFTWARE: PatentIn Ver. 2.1	
QY	960	IWIYRDGYQRPSHYTATCGPYHETTYDDEFWRMVWQEOSSACIVMNTNLVYEVGRVCCYKWD	1019			; SEQ ID: NO 2	
QY	947	----DGXRPSHYTATCGPYHETTYDDEFWRMINQEOSSACIVMNTNLVYEVGRVCCYKWD	1001			; LENGTH: 1439	
QY	1020	DTEVYGDPRYTCVMEPLAEYVVRTFTLBERGNEIREKTFHFTGWPHGVPYHATGL	1079			; TYPE: PRT	
QY	1002	DTEVYGDFTKVTCVMEPLAEYVVRTFTLBERGNEIREKTFHFTGWPHGVPYHATGL	1061			; ORGANISM: Homo sapiens	
QY	1080	SPIRRVKLNPSNPPSAGPVIYHCSAGGRGTCYIVDMLMAERGVVDIYNCYKALRSRR	1139			US -09-887-669-2	
QY	1062	SFIRVKLNPSNPPSAGPVIYHCSAGGRGTCYIVDMLMAERGVVDIYNCYKALRSRR	1121				
QY	1140	INMYTQEQQYIFIHDAILEACLGCTTAIPVCEFKAYAFDMRIDSQTNSSHLDKDEFQTLN	1199				
QY	1122	INMYTQEQQYIFIHDAILEACLGCTTAIPVCEFKAYAFDMRIDSQTNSSHLDKDEFQTLN	1181				
QY	1200	SUTPLQAECISACLPRTFDKRPMDMPPDRCLPFLITDGESSIONYNAALMDSYROP	1259				
QY	1182	SUTPLQAECISACLPRTFDKRNFMPLPPDRCLPFLITDGESSIONYNAALMDSYCP	1241				
QY	1260	AAFITVQYLPLNTYDYGCTSTVMLNEVDLSQCPQYWPBEGMLRYGPIOYC	1319				
QY	1242	AAFITVQYLPLNTYDYGCTSTVMLNEVDLSQCPQYWPBEGMLRYGPIOYC	1301				
QY	1320	MSCSMDCDVTINRIFRICNLTROQEGYLMQFOYLGASHREVPGSKTSFLKLJLQVEKW	1379				
QY	1302	MSCSMDCDVTINRIFRICNLTROQEGYLMQFOYLGASHREVPGSKTSFLKLJLQVEKW	1361				
QY	1380	QECEEGEGERTIICLNGGSRSGMCAIGIVVEMKRQNVTVDFAVKTLRNKSNMVEA	1439				

TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE - KAPPA													
APPLICANT: SCHLESSINGER, JOSEPH													
APPLICANT: SAP, JAN M.													
APPLICANT: ULRICH, AXEL													
APPLICANT: VOGEL, WOLFGANG													
APPLICANT: FUCHS, MIRIAM													
FILE REFERENCE: 038602/1-246													
CURRENT APPLICATION NUMBER: US/09/887,669													
CURRENT FILING DATE: 2001-10-10													
PRIOR APPLICATION NUMBER: 09/234,883													
PRIOR FILING DATE: 1999-01-21													
PRIOR APPLICATION NUMBER: 08/087,244													
PRIOR FILING DATE: 1993-07-01													
PRIOR APPLICATION NUMBER: 08/049,384													
PRIOR FILING DATE: 1993-04-21													
NUMBER OF SEQ ID NOS: 13													
SOFTWARE: PatentIn Ver. 2.1													
SEQ ID NO: 8													
LENGTH: 1452													
TYPE: PRT													
ORGANISM: Homo sapiens													
US-09-887-669-8													
Query Match Score 4843.5; DB 9; Length 1452;													
Best Local Similarity 61.9%; Pred. No. 0;													
Matches 206; Mismatches 318; Indels 29; Gaps													
Query 22 LIGSALCQFSAGGCTFDGPACDYDLYNDFENWVHSQAQEPHYLPEMPQGSMVVDS 81													
Db 14 LLLTAGETFGCLDEPYSTGYQSEGDDPMMPSGLMLVNVA 73													
Query 82 SNHDPGEKARQLQPTMKENDTHCIDSYSLYSQKGHNPGTILNLYRVNKKGPLANPWNVT 14													
Db 74 SGRPEGRAHULLPOLKENDTHCIDSYPLDHVFSKNSPPGULLNVYVKNPNQGPWNIVS 13													
Query 142 GFTGROWLRAETA VSTWPNPYQVTPAEEVGGSYTAIDQVLSYPDCDKSPHFLRG 20													
Db 134 GDPTRTWNRAELAISTFWPNYQVIFEV -ITSGHQGLAIDEVKVLGHPCTRPHFRIQ 19													
Query 202 DVBNAGQNAQTFOCIATGRDAVHKNUWLQRNGEDIPVACTKNINHRRAFAASFRQLQEVTK 26													
Db 193 NVEVNAQQFATFQCSAIGRTYAGDRWLGIDVRDAPLKEIKVTSRRIASFNVNNTK 25													
Query 262 TDQDLRYCUTOSBEGGSVSNPAQIIVREPRPIAPPQQLGCVPTYLIOQANANSICDGDP 32													
Db 253 RDAGKYRCMIRTEGGGINSNTYAEVLYKEPPVPIAPPOLASTGATYLWQIOLNANSINGDGP 31													
Query 322 IILKEVYRMISGSWTHAATNAPTKLWHLDPTTYEIRVLTTRPEGGTLGPGLPLIT 38													
Db 313 IVAREVEYCTASGSWNRDQPVDTSTKIGHLDPTDEYISVLTTRPEGGTSSPGPLRLT 37													
Query 362 RTKAEPMRPTKTKIAEIQARRIADWESLGYNITRCHTFNTVTCHYFRGNESRAD- 44													
Db 373 RTKACADEMRGPRIKLEVEVKSRQITIRWEPQYNNTRCHSYNLTVYCYQVQGQEYQVREE 43													
Query 441 -CLDMDPKAOPHVNLHPPTYNVSLKMLTNPGEKSEETIIQTEDDVPGVPVPSLOG 49													
Db 433 VSWDTENSHPQHTITNLSPTYNSVSKLIMNPGRKESQELTVQTDDELPGAVPTESTQG 49													
Query 500 TSFENK1FLNKYKEPLENGTITQOYEYSSRSFDPAYVPGCPQTYSNLNTSHYFMH 55													
Db 553 LYPTGTYSFTRIASTAKGFGPPATNQETKTISAPSMPAYE -LETPLNQTDNTVTLKPA 61													
Query 620 QAKGAPISAYQIVVEQDQPHTRKREAMECYQVPTYONALS GGAPYFAELPPGNLP 67													
Db 612 QSRGAPSVYQVILNQVVEERPRTKTIBLKCPVPIHQNALSQQYFAAREPADSLQ 67													
RESULT 4													
; Sequence 8, Application US/09887669													
; CENPBL, TUNFORMATION, NO. US2002008239781													
; Publication, Sequence 8, Application US/09887669													
; FILE REFERENCE: 038602/1-246													
; CURRENT APPLICATION NUMBER: US/09/887,669													
; CURRENT FILING DATE: 2001-10-10													
; PRIOR APPLICATION NUMBER: 09/234,883													
; PRIOR FILING DATE: 1999-01-21													
; PRIOR APPLICATION NUMBER: 08/087,244													
; PRIOR FILING DATE: 1993-07-01													
; PRIOR APPLICATION NUMBER: 08/049,384													
; PRIOR FILING DATE: 1993-04-21													
; NUMBER OF SEQ ID NOS: 13													
; SOFTWARE: PatentIn Ver. 2.1													
; SEQ ID NO: 8													
; LENGTH: 1452													
; TYPE: PRT													
; ORGANISM: Homo sapiens													
; US-09-887-669-8													
Query Match Score 4843.5; DB 9; Length 1452;													
Best Local Similarity 61.9%; Pred. No. 0;													
Matches 206; Mismatches 318; Indels 29; Gaps													
Query 22 LIGSALCQFSAGGCTFDGPACDYDLYNDFENWVHSQAQEPHYLPEMPQGSMVVDS 81													
Db 14 LLLTAGETFGCLDEPYSTGYQSEGDDPMMPSGLMLVNVA 73													
Query 82 SNHDPGEKARQLQPTMKENDTHCIDSYSLYSQKGHNPGTILNLYRVNKKGPLANPWNVT 14													
Db 74 SGRPEGRAHULLPOLKENDTHCIDSYPLDHVFSKNSPPGULLNVYVKNPNQGPWNIVS 13													
Query 142 GFTGROWLRAETA VSTWPNPYQVTPAEEVGGSYTAIDQVLSYPDCDKSPHFLRG 20													
Db 134 GDPTRTWNRAELAISTFWPNYQVIFEV -ITSGHQGLAIDEVKVLGHPCTRPHFRIQ 19													
Query 202 DVBNAGQNAQTFOCIATGRDAVHKNUWLQRNGEDIPVACTKNINHRRAFAASFRQLQEVTK 26													
Db 193 NVEVNAQQFATFQCSAIGRTYAGDRWLGIDVRDAPLKEIKVTSRRIASFNVNNTK 25													
Query 262 TDQDLRYCUTOSBEGGSVSNPAQIIVREPRPIAPPQQLGCVPTYLIOQANANSICDGDP 32													
Db 253 RDAGKYRCMIRTEGGGINSNTYAEVLYKEPPVPIAPPOLASTGATYLWQIOLNANSINGDGP 31													
Query 322 IILKEVYRMISGSWTHAATNAPTKLWHLDPTTYEIRVLTTRPEGGTLGPGLPLIT 38													
Db 313 IVAREVEYCTASGSWNRDQPVDTSTKIGHLDPTDEYISVLTTRPEGGTSSPGPLRLT 37													
Query 362 RTKAEPMRPTKTKIAEIQARRIADWESLGYNITRCHTFNTVTCHYFRGNESRAD- 44													
Db 373 RTKACADEMRGPRIKLEVEVKSRQITIRWEPQYNNTRCHSYNLTVYCYQVQGQEYQVREE 43													
Query 441 -CLDMDPKAOPHVNLHPPTYNVSLKMLTNPGEKSEETIIQTEDDVPGVPVPSLOG 49													
Db 433 VSWDTENSHPQHTITNLSPTYNSVSKLIMNPGRKESQELTVQTDDELPGAVPTESTQG 49													
Query 500 TSFENK1FLNKYKEPLENGTITQOYEYSSRSFDPAYVPGCPQTYSNLNTSHYFMH 55													
Db 553 LYPTGTYSFTRIASTAKGFGPPATNQETKTISAPSMPAYE -LETPLNQTDNTVTLKPA 61													
Query 620 QAKGAPISAYQIVVEQDQPHTRKREAMECYQVPTYONALS GGAPYFAELPPGNLP 67													
Db 612 QSRGAPSVYQVILNQVVEERPRTKTIBLKCPVPIHQNALSQQYFAAREPADSLQ 67													
RESULT 4													
; Sequence 8, Application US/09887669													
; CENPBL, TUNFORMATION, NO. US2002008239781													
; Publication, Sequence 8, Application US/09887669													
; FILE REFERENCE: 038602/1-246													
; CURRENT APPLICATION NUMBER: US/09/887,669													
; CURRENT FILING DATE: 2001-10-10													
; PRIOR APPLICATION NUMBER: 09/234,883													
; PRIOR FILING DATE: 1999-01-21													
; PRIOR APPLICATION NUMBER: 08/087,244													
; PRIOR FILING DATE: 1993-07-01													
; PRIOR APPLICATION NUMBER: 08/049,384													
; PRIOR FILING DATE: 1993-04-21													
; NUMBER OF SEQ ID NOS: 13													
; SOFTWARE: PatentIn Ver. 2.1													
; SEQ ID NO: 8													
; LENGTH: 1452													
; TYPE: PRT													
; ORGANISM: Homo sapiens													
; US-09-887-669-8													
; RESULT 4													
; Sequence 8, Application US/09887669													
; CENPBL, TUNFORMATION, NO. US2002008239781													
; Publication, Sequence 8, Application US/09887669													
; FILE REFERENCE: 038602/1-246													
; CURRENT APPLICATION NUMBER: US/09/887,669													
; CURRENT FILING DATE: 2001-10-10													
; PRIOR APPLICATION NUMBER: 09/234,883													
; PRIOR FILING DATE: 1999-01-21													
; PRIOR APPLICATION NUMBER: 08/087,244													
; PRIOR FILING DATE: 1993-07-01													
; PRIOR APPLICATION NUMBER: 08/049,384													

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 63
 LENGTH: 1452
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-048-765A-83

Query Match 61.3%; Score: 4789.5; DB 16; Length 1452;
 Best Local Similarity 61.1%; Pred. No. 0;
 Matches 887; Conservative 211; Mi matches 324; Indels 29; Gaps 9;

QY 847 SATESSRLIDPVRY-LCEGTESPYQTGQLHPAIRDVLQHINIMKTSDSYGPKKEEYES 905
 QY 847 TMASDTISSVQSHTYKKGREPADVPTQGQLHPAIRDVLQHINIMKTSDSYGPKKEEYES 906
 QY 906 FFEQGSASPDYAKEDQNRAKRNRYGNLIAKDHSRVLQPEDDPSDYKANYDIWLRD 965
 Db 907 FFEQGSASPDYAKEDQNRAKRNRYGNLIAKDHSRVLQPEDDPSDYKANYDIWLRD 966
 QY 966 GYQRFSHYATQGPVHETYDIFWRMWMQBGACIIVMTNLVEGRVKCYKWPDDTEYGG 1025
 Db 961 GYHRNHYATQGPVHETYDIFWRMWHENTASIINVNLVEGRVKCKYWPDDTEYK 1020
 QY 1026 DFKVTCVMEPLAEYVVRFTLERRGYNBIREVKQFHFTGWPDHGVYPYATGLLSFIRY 1085
 Db 1021 DIKVLTIELTLLAEXYVTFRAVERGKIIIREIQFHFTGWPDHGVYPYATGLGFVRQV 1080
 QY 1086 KLSNPPSAGPIVTHCSAGAGRGTGCVIVIDIMDMAEREVSDVYNCVKALRSRRNMYQT 1145
 Db 1081 KSKSPPSAGPIVTHCSAGAGRGTGCVIVIDIMDMAEREVSDVYNCVKALRSRRNMYQT 1140
 QY 1146 EEQYTFPHDAILEAGLCGETAIPCFKAAYFDMTRIDESQNTSSHLDDEFQTLNSVTPL 1205
 Db 1141 EQYQVFPHDAILEAGLCGDTSPVQSRVSLYDANKLDDQTNSSQIKEFRTLNMVTPL 1200
 QY 1206 QAEDCSIACLPRNHDKRNFMDDLPDPDCFLPLITIDGESSNYINAALMDSYROPAAFIT 1265
 Db 1201 RVEDCSIAALLPRNEHKRNCDILPDPDCFLPLITIDGESSNYINAALMDSYKQPSAFIT 1260
 QY 1266 QYPELNTWDWFRLYDIGCTSIUMLNEYDLSQCPCQTYLQWVQKQPSAFIT 1325
 Db 1261 QHPLPNTVCKDFWRLLVLDYHTCSVVMNLNDPAOLCPQYKENGPHRGFIQYEFVSALE 1320
 QY 1326 CDVINRNPSCCNLTRPOQEYLYMVOOQYLGWASHREVPGSKRSPLKLTLQVERKQEECB 1385
 Do 1321 EDIISRRIFYNAARPQDGTYRMQOFQJGWPMYRDTPSKRSPLKLTLQVDKWQEBTNG 1380
 QY 1386 GEGRTLIKCLNGGSRGMFCAGIGIVVEMYKRONTYDVFHAVKTLRNNSKENNMVAPEQYRF 1445
 Db 1381 GEGPTrVHCLNGGSRGTCASIVCMEMLRHQRTVDVFHAVKTLRNNSKENMVDLLDQTKF 1440
 QY 1446 CYDVALEYLES 1456
 Db 1441 CYEVALEYLNS 1451

RESULT 5
 US-10-408-765A-83
 Sequence: 83, Application US/10/0408765A
 Publication No. US20040101874A1
 GENERAL INFORMATION:
 i APPLICANT: Ghost, Soumitra S.
 i APPLICANT: Faly, Boin D.
 i APPLICANT: Zhang, Bing
 i APPLICANT: Gibson, Bradford W.
 i APPLICANT: Taylor, Steven W.
 i APPLICANT: Gleisn, Gary M.
 i APPLICANT: Warnock, Dale E.
 i TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 i TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 i FILE REFERENCE: 66088-465
 i CURRENT APPLICATION NUMBER: US/10/408,765A
 i CURRENT FILING DATE: 2003-04-04
 i NUMBER OF SEQ ID NOS: 3077

QY 600 EPAPPTVGDNRTYKGFNNPPLAPRKGNYYFQAMSVEKETKTOQVRIATKAATEEPV 739
 Db 672 AAQFTIGDNKTYGYNTPLPYKSYRIYQQASRANGEKITLDCVQVATKGAATPKP - 729

QY 740 IPDPAKQDPRVVKIAGISAGILVILLLUVIVVTKSCLAKERKETMSSTQEMTMVN 799
 Db 730 VPEPEKQDHTVKGIAVAGILLFVIFGUVVLMKCRKLAERKETMSSTQEMTMVN 789

QY 800 ANDRSYADQSTLRAEDPLSLTMQDNHFSPLENDP-----LVPTAYL-DNH 846
 Db 790 SMDRSYAQGTTNCDE--AFSFDHDNNGRSVSSFTMKINTLSTSVPNSYPDFETH 846

QY 847 SATESSRLDVRY-LCEGTESPYQTQGQLPAIRDLOHINLMKTSDSYGFKEYES 905
 Db 847 TMASTDSSVQSHSTYKKGREPADVPTQGQLPAIRDLOHINLMKTSDSYGFKEYES 906

QY 906 FPEQGSASMDVAKKDQIAKRNRYGNLAYDHSRVRTLQVVEDPSSDYNANYDIWLRD 965

907	FFGEGOSAIPWDSSAKDDEMRKORYGNLTAYDHISRVRLQTEGDTNSDINGNYI-----D	960
Db		
Qy		
966	GYORPSHYIATQGPVHETVDFWRMWTQEQSACIMVNTLVVEGRVKCYKWPDDTEVG	1025
Db		
Qy		
961	GYHRPNHYIATQGPMTETIYFWRMWHENTASIMVNTLVVEGRVKCYKWPDDTEVK	1020
Db		
Qy		
1026	DFKVTCVMEPLAAYVTRFTLERRGEYIREVKQFHFTGWPDHGVYPYHATGLSFIRV	1085
Db		
Qy		
1021	DIKVTLIBETELAAYVTRTFAVEKGHEIREIRQHFTGWPDHGVYPYHATGLGFVRV	1080
Db		
Qy		
1086	KLSNPPSGAIPVWCHCSAGAGRTGCVLYTDIMDMAEREGVYDINYCYKALESRRINMVOT	1145
Db		
Qy		
1081	KSKSPPAGAIPVWCHCSAGAGRTGCFIVIDIMDMAEREGVYDINYCVERJRSRRAVMVQT	1140
Db		
Qy		
1146	EEQYIIFHDALBACLGETAIPVCERKAAYFDMDTRISQTNSSHILKEDEPTLNSTVTRL	1205
Db		
Qy		
1141	EEQYVFETHDALBACLGDTSPVQSRSLYDMNKLDPTQNSSQIKEFRTLNMMVTPL	1200
Db		
Qy		
1206	QAECDSTAICLPENHDKRNFMDMLPPDRCLPFLITIDESSYINAALMDSYROPAFITV	1265
Db		
Qy		
1201	RVEDCSTALLPANEKRCMDLPPDRCLPFLITIDESSYINAALMDSYKQPSAFITV	1260
Db		
Qy		
1266	QYPLNPTVKDFWKRYDYYGCGTSSVMMNEVDSLQSOGCPQWPEEGMLRYGPIQVECMSCMD	1325
Db		
Qy		
1261	QHPLNPTVKDFWKRLVLDYHCTSVVMINDVPAQLCPOQWPGNGVIRHGPQYEFVSADLE	1320
Db		
Qy		
1326	CDVINRIFRICNLTRPQDGMLVQOFYLGWASHREVPGSRFSFLKLQVWKQWECEE	1385
Db		
Qy		
1321	EDIIISRFIRINAARPQDGHRMVQQFOLGWMYRDTPVRSRSLALLRQDVKNQEEYNG	1380
Db		
Qy		
1386	GEGRITIHLCLNGGRSGMFCAGIYVEMVKRONVVDVFHAVKTLRNKSNPMVNEAPEQYRF	1445
Db		
Qy		
1381	GEGPTVHCLNGGRGSFTCAISIVCMRLHORTYDVFHAVKTLRNKNNVDDLUQYKF	1440
Db		
Qy		
1446	CYDVALLEYLES 1456	
Db		
Qy		
1441	CYEVALLEYLNS 1451	
Db		
RESULT 6		
US-10-205-219-15		
	Sequence 15, Application US-10-205219	
	Publication No. US20030138802A1	
	GENERAL INFORMATION:	
	APPLICANT: Warner-Lambert Company	
	APPLICANT: Lee, Kevin	
	APPLICANT: Dixon, Alastair	
	APPLICANT: Brookbank, Robert	
	TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain	
	CURRENT APPLICATION NUMBER: US-10/205,219	
	PRIOR APPLICATION NUMBER: GB 0118354.0	
	PRIOR FILING DATE: 2001-07-27	
	NUMBER OF SEQ ID NOS: 197	
	SOFTWARE: Patent In Ver. 2.1	
	SEQ ID NO: 15	
	LENGTH: 1436	
	TYPE: PRT	
	ORGANISM: Rattus norvegicus	
	FEATURE: Receptor protein tyrosine phosphatase-1-lambda	
	OTHER INFORMATION: Receptor protein tyrosine phosphatase-1-lambda	
	US-10-205-219-15	
	Query Match Score: 4591; DB: 14; Length: 1436;	
	Best Local Similarity: 59.9%; Pred. No. 0;	
	Matches: 859; Conservative: 210; Mismatches: 330; Gaps: 12;	
Qy		
32	AGGCTFDGPG---ACDYHQDLYDDFEVNVHSAQEPEPHLPPPEMPOGSSYMDVSSNHDPGE	88
Db		
Qy		
32	AGGCTFDGPGP-SQASQATQDFQEVRIHPGTRTPEDLPHGMLMMNASQHTPGQ	83
Db		
Qy		
1045	FTLERGYNREKVKQFHFTGWPDHGYPYHATGLSPIRKYKLSPNPSSAGPVVHCSAGA	110
Db		
Qy		
1020	FALEERRYSAHHRVQFHFTAWPHGPYHATGLAFTTRVKAStPDAGPVIHCSAGT	107
Qy		
1105	GRTGTYVIDMMDAERGVUDIYNCVKALSRNRMVQEBOYIFIHDALEACLGEB	116
Db		
1080	GRTGTYVIDMMDAECGVVYDVKLCSRNMQIEQYIFIHDALEACLGEC	113
Qy		
1165	TAIPVCCEKAAYFMDMIRDSOTNSHLKDEFOTLNSVTPRLODCSIACLPRNHDKNRF	122

Db	1140	TTPVNEFRATYREMIRDPSQNSNQSLREFQTLSVTPLDVCECSIALPPRNDRKRS	1199	Qy	448	APOHVNVHLPPPTVNSLKMILTNPEGRKESEETIITQTPBDVPGPVVKSLQGTSFENKIF	507
Qy	1225	MDDMLPDRCLPFLITIDGESESSNYNAALDSYRPAFFTTOQPLPNTVTDKFWRLLVDIG	1284	Db	491	VSRITMKNLPPRNTLPPRNTVHVRVLTNPRTSRLAEESAAESTTTPLEDMTF	550
Db	1200	MDVLPPDRCLPFLISGDPPNYYNAALDSYRPAFFTTLPLQSTPDPFWLVDIG	1259	Qy	508	LWKWPEPLNGLITQYEVSYSIRSFDPAVVAQSPOTYSNLWNSTHYVMHLLHGTTVQ	567
Qy	1285	CTSTMNLNEYDLSQG--CPOYWPEGMRLRGPLQVECMSCSMCDVNMTRICNLTP	1341	Db	551	LWKWPEPLNGLITQYEVSYSIRSFDPAVVAQSPRTTSKLRLNETVTHVSNLHGTTVYL	610
Db	1260	CTSMNLQNOSNAPLQWPSBPGQDQYGLMVEFSGTANEDLVRVFRVQNSSL	1319	Qy	568	FPIASTVKGFPATIAINTNNISAPSLEDYEGVDAISNBATTITVLRPAQAKGAPIS	627
Qy	1342	QEGYLMMVQFOYLGASHREVPGSKRSFSLKLQLQUEKMQECEGEGRPTIHCNGGFS	1401	Db	611	FSPRARTRGFGQALTEITNNISAPSFDYADMPSPLGESSENTITVLRPAQGRGAPIS	669
Db	1320	QEGYLIVRHEQFLRNSAYRTDPSKNAEYDKWQ-AESEGDRTVHCLNGGFS	1377	Qy	628	AYQIVVEQQLH-PHTKREAGAMECYQPVPTVQNALSGGAPYFAELPGCNLPPEPAFTV	686
Qy	1402	GMFCAIGIVVEMVRQRNNVDFHAYTKLNSKPNVNEAEPYRCYDVALEYLES	1456	Db	670	VIQVIVBEEQGSRRLRRBPEGQDCPVPLFEANALRGLYDVFGEAELAASSLPEAMPFTV	729
Db	1378	GTPCACATVLEMIRCHSLUDVFAAKTLYNKPNMVETMDQYHFCYDVALEYEA	1432	Qy	687	GDNRTYKGFWNPPLAPLRKGYNIXYFOAMSSVEKETKTKTCVYRIATAEPEVIPDPAQ	746
Qy	1402	GMFCAIGIVVEMVRQRNNVDFHAYTKLNSKPNVNEAEPYRCYDVALEYLES	1456	Db	730	GDNKTYTRGFWNPPLERKAYLIVYFOAAASHLKGETRLNCIRIARKACKESKRPL-EVSQR	788
Qy	744	TDRVVKIAGISA-GILVFILLVLLVTVVYKSKS-----LAKKRDAMGNTFQ	792	Qy	747	TDRVVKIAGISA-GILVFILLVLLVTVVYKSKS-----LAKKRDAMGNTFQ	792
Db	789	SEEINGILGICAGGAVLILLGAIIVIIRKGDHAYSYYPKPVNMTK-----ATVNTRQ	844	Db	789	SEEINGILGICAGGAVLILLGAIIVIIRKGDHAYSYYPKPVNMTK-----ATVNTRQ	844
Qy	793	EMTHINNAMDRSYADQSTLHAEDPLSLTMQDNINFSPRLPNDLPLVPTAVLDENHSATAS	852	Db	845	EKTAMMSAVDRSFQDQSTLQEDERLGLSPLMDTNGYSTR-----GDQRSGGVTEA	893
Qy	853	SRLL-DVPRYLCESTESPYQTGQLHPAIRVADLQHINIMKTSDSYGFKEYESBSFEGQS	911	Db	894	SSLUGSPRPGKGSPTVHTGQLHPAVRDLQHINOMKTAEGYGFQKEYSFEGE--	951
Db	912	ASWDVAKKDQNRAKRYGNMIAHDHSRVLQVPEDDPSSDYINANYYD1IWLYRDGYQRPS	971	Qy	912	ASWDVAKKDQNRAKRYGNMIAHDHSRVLQVPEDDPSSDYINANYYD1IWLYRDGYQRPS	971
Db	952	-NDATKKDKVKGSRQEPMPAYDHRVYKLHPMLGDNADYDINANYYD1IRNREGYHRSN	1009	Db	952	-NDATKKDKVKGSRQEPMPAYDHRVYKLHPMLGDNADYDINANYYD1IRNREGYHRSN	1009
Qy	972	HYIATQGPVHETYDFWRMVWQEOACITVMTNIEVERGVCKYKWPDDTEVYGDFTVTC	1031	Qy	972	HYIATQGPVHETYDFWRMVWQEOACITVMTNIEVERGVCKYKWPDDTEVYGDFTVTC	1031
Db	1010	HFIATQGPKPMEYDFWRMVWQEHICSSIWITKUVEGRVKCSRYWPEUSDTYGDIKIML	1069	Db	1010	HFIATQGPKPMEYDFWRMVWQEHICSSIWITKUVEGRVKCSRYWPEUSDTYGDIKIML	1069
Qy	1032	VEMPLAELYVVRTPTLERRGYNETREVKOFHFGWPDHGCVPHATGLLSFIRRYVLSNPP	1091	Qy	1032	VEMPLAELYVVRTPTLERRGYNETREVKOFHFGWPDHGCVPHATGLLSFIRRYVLSNPP	1091
Db	1070	VKTEELAETVVRTPALERRGYSARHEVROFHFATWPERGCVPHATGLAFIRYKASTPP	1129	Db	1070	VKTEELAETVVRTPALERRGYSARHEVROFHFATWPERGCVPHATGLAFIRYKASTPP	1129
Qy	1092	SAGIVVHSAGAGRGCYVIVIDLMNAERGVYD1NCVKALSRRIINVQTEEQYIF	1151	Qy	1092	SAGIVVHSAGAGRGCYVIVIDLMNAERGVYD1NCVKALSRRIINVQTEEQYIF	1151
Db	1130	DAGPVIHCSAGTGTGCVYILDVMDMAECGVDTINCVKTLCSRRVNMTCITEQYIF	1189	Db	1130	DAGPVIHCSAGTGTGCVYILDVMDMAECGVDTINCVKTLCSRRVNMTCITEQYIF	1189
Qy	1152	IHDIALEACLGCTAAPECFKAAYFDMTRDTSOTNSHLDKDFQTLNSVTPRIQAEDCS	1211	Qy	1152	IHDIALEACLGCTAAPECFKAAYFDMTRDTSOTNSHLDKDFQTLNSVTPRIQAEDCS	1211
Db	1190	IHDIALEACLGCTTIPSEFKATYKEMTRDTSOSSNOLREETQTLNSVTPPDEECS	1249	Db	1190	IHDIALEACLGCTTIPSEFKATYKEMTRDTSOSSNOLREETQTLNSVTPPDEECS	1249
Qy	1212	IACIPRNHDKNRFMDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAPIVITYQPLPN	1271	Qy	1212	IACIPRNHDKNRFMDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAPIVITYQPLPN	1271
Db	1250	IALIPRNHDKNRSMVLPEDRCLPFLISTDGDENNYINAALTDTSYTRSAAFIVTLHPLQS	1309	Db	1250	IALIPRNHDKNRSMVLPEDRCLPFLISTDGDENNYINAALTDTSYTRSAAFIVTLHPLQS	1309
Qy	1272	TVKDFWRLVYDYGCTSIYLNVEVDSLQG---CPQWPERGMLRYGPIQEVCMSCSDCDV	1328	Qy	1272	TVKDFWRLVYDYGCTSIYLNVEVDSLQG---CPQWPERGMLRYGPIQEVCMSCSDCDV	1328
Db	1310	TTPPDWGLVYDYGCTSIYLNQLNQNSNAWPCQLYWPEPGRQQYGLMEVEFMGTADEL	1369	Db	1310	TTPPDWGLVYDYGCTSIYLNQLNQNSNAWPCQLYWPEPGRQQYGLMEVEFMGTADEL	1369
Qy	1329	INRIFRICNLTRPOEGYLMVQFOYLGWASHREVPGSKRSFLKLILQVEKWORECCEGEG	1388	Qy	1329	INRIFRICNLTRPOEGYLMVQFOYLGWASHREVPGSKRSFLKLILQVEKWORECCEGEG	1388
Db	1370	VARYFRVONISRLQEGHLLVRHFQLRMSAYRDPDSKAFLHLLAEGRKQW-AESGDG	1427	Db	1370	VARYFRVONISRLQEGHLLVRHFQLRMSAYRDPDSKAFLHLLAEGRKQW-AESGDG	1427
Qy	1389	RTIHCJLNGGGRSGMFCAGIVVMMKRONVYDVFHAVTLRNSKPNMVAPEQYRFCDY	1448	Qy	1389	RTIHCJLNGGGRSGMFCAGIVVMMKRONVYDVFHAVTLRNSKPNMVAPEQYRFCDY	1448
Db	1428	RTIVHCLNGGGRGCTFCATVLEMRCHNLVDVFFAQTLRNYKPNMVBETMQHFCYD	1487	Db	1428	RTIVHCLNGGGRGCTFCATVLEMRCHNLVDVFFAQTLRNYKPNMVBETMQHFCYD	1487
Qy	1449	VALEYLE 1455		Qy	1449	VALEYLE 1455	
Db	1488	VALEYLE 1494		Db	1488	VALEYLE 1494	

RESULT 8

US-10-058-270A-98
Sequence 98, Application US/10058270A
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
APPLICANT: Afar, Daniel
APPLICANT: Bio-Technology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and FILE REFERENCE: 018501-005210US
CURRENT APPLICATION NUMBER: US/10/058,270A
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 60/263,965
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: US 60/265,928
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US 09/829,472
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 60/282,598
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 60/288,590
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,443
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 98
LENGTH: 1444
TYPE: PRT
ORGANISM: Homo sapiens
US-10-058-270A-98

Query 542 PPOTVSNLWNSTTHVFMHLHPGTTYOFFIRASTVKGFPATAINVTNISAPSLLPDYEGV 601
Db 538 QRICKPKLRNETHHIFVGlyPGTYSFTIKASTANGFGPVTRATKISAPSMBYD-T 596
Query 602 DASLMETATTITLILRPAQKAGPASAYQIVVEQHLPHTKREAGAMECYQPVYQNAL 661
Db 597 DTPUNETDTTIVMUKPAQSRGAPSvYQLVVKERLQSRRAOITECFSVPSYRNAs 656
Query 662 SGGAPPYFAELPPNLPBAPFTGDNRATYKGFWNPPLA PRKGVNITYFOAMSSVKBETK 721
Db 657 SLDSHYFAELKPANLPVPTQPFITGDNKTYNGTNPPLSPLKSSTIYFQALSKANGETK 716
Query 722 TQCVRATKAATEPEVTDPAKQTDRVVKTAGISAGLIVFLILLWVIVVKK----- 776
Db 717 INCVERLATGASTONNTV-EPEKQDNTVX-KMAGTAGLIMFIITLGVLTRKRRNAY 775
Query 777 -----SKLAKKRKDAMGNTRQEMTHVNMADSDYASADOSTLHAEDPLSLTEMDOHNFs 828
Db 776 SYSYVLSQRKLAKRKETQSGAORENGPASA-DEPPTKLSASRNDGEFSSSOOVNGFT 834
Query 829 PRLPDPDVYPTAVLBDBNSATAESSRLLDVPRYLCGTSBSPYQTQLPHPAIRVALQHI 888
Db 835 DGSRGELSQPLTII-QTH-----PYRTCDPVEMSYSPRQFQLAIRVALQHI 881
Query 889 NLMKTSDSYKPEKEYESFFPGQASWDVAKDQNRAKNRGNIITAYDHSLRVTLQPOVEDDP 948
Db 882 TQMKGQGYGKKEEALPQGTAWDTADEDENBNKRNRGNI-SYDHSLRVTLVLDGDP 941
Query 949 SSDYINANYIDIWLYRDGTORPSHVIATQGPVHETVYDFRMWQEOASACIVMTNLVEY 1008
Db 942 HSDYINANYI-----DGZERPRHIVTATQGPMOETVYDFWMQINQDENSASIVMTNLVEY 995
Query 1009 GRVKCYKWPDDTEYGDPKVTCVNEPLAEYVFTBLERGNTINEREVQFHFGWPD 1068
Db 996 GRVKCYKWPDDTEYGDVTRGDIKVLTIEPLAEYVFTBLERLFLHTSWPD 1055
Query 1069 HGVPYTHATGILSFIRRVLSNPPSAQPVYHCASAGRTGCVIVDILMDMAERGSVDI 1128
Db 1056 HGVPYATGIGFVQVKFVINPPEAGPVYHCASAGRTGFFIAIDTMDMAENEVVDI 1115
Query 1129 YNCVIALRSRINMMQTEQYQFHDIALEACLGETAIPCEPKAAFDMIRIDSQTONs 1188
Db 1116 FNCVRLRAQDNVLTQTEEQYVFTBLAEACLGNTAIPCEFRSLYYNSRLDQTNs 1175
Query 1189 SHLKDFOTINSVTPRLQAEDCSIALPRHDFNEMDPDRCLPFLITIDGESNSYI 1248
Db 1176 SQKDEFQTLNIVTPRVPEDSIGLPRHDKNSMDVLPDRCLPFLISVGDGESNSYI 1235
Query 1249 NAALMDSYROPAAFIVTQYPLPNTYKDFWRLVYDGCSTSIVMLNEYDLSQGPQKWPPEEG 1308
Db 1236 NAALMDSHKOPAFAVVTFQHPDENTADFWRIVFDNCSSVWLNENDTAQICMQTFPEKT 1295
Query 1309 MLRYGPTQVECMSMCDVNRIFRICNLTRPOEGYLMYQOFQVILGWASHREVPGSKRS 1368
Db 1296 SGCYGPQVERVSADIDETHIRFRICNNARPDGYRIYOLQYIGWPAYRDTPPSKRS 1355
Query 1369 FLKLJLQEVKQECBEGERTIINCINGGRSGMCAIGIVVEMYKRONVUDFHAKT 1428
Db 1356 LKVKVRLERKQBOYDGRCTVHNGGRSGFCACISVCMEIQQQNITIDVHFHVKT 1415
Query 1429 LRNSKPNMVVAPEQRCYDVALEYLIES 1456
Db 1416 LRNNKSNMVTELQKVFIVEALEYLSS 1443

RESULT 9

US-10-176-847-22
; Sequence 22, Application US/10176847
; Publication No. US2003068656A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

Query 422 FNVTCIHYFRGHNESRADCLDMDPKAQHQVNVNLPPVTVNSLMLNPERKESBTI 481
Db 420 YNITVQYHVV-FNQOQYBAEVITQTSYHPTGLERPMTRPLRLLSNPERMEEEL 477
Query 482 IOTDEDEVGPVTKSLOCTSSENKIFLNUKWEPLPNTITOYEVSSYSSRFDPAVFVAG 541
Db 478 VQTEEDVFGAVPLES1QGGPFEEK1QMKPPNETNGVITYBINKAVGSLDPSADLSS 537

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
 TITLE OF INVENTION: AND OVARIAN CANCER
 FILE REFERENCE: MRI -039
 CURRENT FILING DATE: US/10/17/6,847
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 22
 LENGTH: 1463
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-176 847-22

Query Match 58.2%; Score 4542.5; DB 14; Length 1463;
 Best Local Similarity 56.7%; Pred. No. 0;
 Matches 843; Conservative 242; Mismatches 341; Indels 61; Gaps 11;

Qy 3 VAAALPAVALWILLYPPWPLIGSALGQFSGGGCTPDDGPGACDYHQDL-YDDFFEWVAVSA 61
 Db 4 LAALALSLLRLQL---PPIPGARAQASAPGGCSDEHYTSNNGCYSVVALGTNGFTWEQINT 59

Qy 62 QEPHFLPPENPOGSTWMVDSNHIDEGAKARLQLPMTKENDTHCIDSYLVLSORGNLNPT 121
 Db 60 TEKPMLDQAVPTGSTMVNSGRASQSKAHILLPTLKENDTHCIDSYLVLSORGNLNPT 119

Qy 122 LNLYRVNKGPLANPIWNTYTGFTGRDWLRQBLAELAVSTFWPEYQVIFAEVSGGRSGYIAI 181
 Db 120 LNYYVKVNGGQPQGNVWNVNGVUTBGWVAELAISTFWPHFYQVTFESVSLKGHPGYIAV 179

Qy 182 DDIQVLSYPDKSPDHPLRQLDVEINAGQNTFOCIATGRDAVANKLWLRNNGDIPVQA 241
 Db 180 DEVRLAHPCKRAFKPLRQLQNVNGQNTFOCAGKWSQHDKLWLQWNGRDTALMV 239

Qy 242 TKNNINHRARRASAFRLQEVTKTQDLYRCTTQSBERGSVYVNAQTLVPEYER 301
 Db 244 TRVONHRRASATVSYADTAQRSVSKYRCTRSQDGSVYNAELIVKEPTPAPPBLA 299

Qy 302 VGPYLLQCOLNANSITGDGPYLKEVEYRMTSGSWTEHAVNAPTYKWLHLDPPTEYER 361
 Db 300 VGATYLWIKPENANSITGDSPYLKEVEYRMTSGSWTEHAVNAPTYKWLHLDPPTEYER 359

Qy 362 VLLTRPGEGSTGLPOPPLTRTKCAEPMRTPKTUKIAEQLARRIADWESLGYNITRC 421
 Db 360 VLLTRPGEGSTGPGAPLTTRKCADPVGPNVIEVDIARQTLQNEPFGAVTRCHS 419

Qy 422 FNVTCYHTFRGHNSRADLQMDMKAPDFVNHLPPTYNVLNMRMLTPEGRKESSEETI 481
 Db 420 YNLTYQYQTV--FNUQQYRAEEVQTSSHTRGLRPFTIRLILLSSPEGMESETI 477

Qy 482 IQTDEDVPSPVPKSLOQTSFENKIFLNKEPLEPGNLTTOYEVSYSSTSRSFDPAVYAG 541
 Db 478 VQTEBDVPGAVPLESIQGPFEEKLYIQKPNPNTNGVITLYEINYKAVGSLDESADLS 537

Qy 542 PPOTYSNLNSTHAYMHPMHPGTYQFFRASTYKFGDATAINVTINISAPSPLPDYECV 601
 Db 538 ORGKWFKLNETHILFVGLYPTYSFTIKASTKGFPVTRIASPSMPEYD-T 596

Qy 602 DASINLETATIVLRLPQAKGAPSAYQVBEOLHPPHTKREAGAMECTQVPTYQNL 661
 Db 597 DTPLNEDTTTVMKPAOSRGAPSVTQUVKBRQLQSRRAADIIEFSVPSVSYRNAS 656

Qy 662 SGGAPYYFAELPPGNNLPPEPAPFTVGDNRRTYKGFWNPPLAPEKGYNYIYQAMSSVKEKTK 721
 Db 657 SLDSLHYFAELKPNLPYQFTVGDNNTKYNGWNPPSPLKSYSITVQSLKANGETK 716

Qy 722 TQCVRIATA-----AATEBEVILEDPAKOTDRVYKAGISAGILV 762
 Db 717 INCYRLATKAPMGSAQVTPGTPLCLITGASTQNSNTV-EPEKODNTKMGVIAGLIM 775

Qy 763 FIIILGVNLTIKRRNAYSYSYLSQRKLAKKRETQSGAQREMPVASA-DKPTTKUS 809
 Db 776 FIIILGVNLTIKRRNAYSYSYLSQRKLAKKRETQSGAQREMPVASA-DKPTTKUS 834

RESULT 10
 US-10-205-823-343 ; Sequence 343, Application US/10205823
 ; Publication No. US20030108963A1
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Endge, Wilson O.
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Gorbatcheva, Bella
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Kanatkar, Shubhangi
 ; APPLICANT: Worsley, Angela M.
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Anderson, Dustin
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; THERAPY OF PROSTATE CANCER
 ; FILE REFERENCE: MRI-044
 ; CURRENT APPLICATION NUMBER: US/10/205,823
 ; CURRENT FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/1307,982
 ; PRIOR FILING DATE: 2001-07-25
 ; PRIOR APPLICATION NUMBER: 60/314,356
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/325,020
 ; PRIOR FILING DATE: 2001-09-25

34 GCTFDDGPG---ACDYHODLDDPEWVHVSQAQEPHYLPPMPMPOGSYMDSSNNHDPGKKA 90
 33 GCTFEEGSDPAVPCEYSQQYDDQWDPS-----PADLPHESYLMNTSHARGRA 85
 Qy 91 RLQLQPTMKENDTHCTIDESYLISQOKGLNPGTINILVRVNKGPLANPIKVVTFGTGRDMLR 150
 Db 86 HVIQFSLSENDTHCVCQFSFLYSLRDGHSGTGLTYVVRNGGLGSAVNMGTSHGRQHQ 145
 Qy 151 AELAVSTFWNPNEYQVIFPELEVSRSRSGYAIDDIQVLQSPCDKSPPHFLRLGDVEVNAQCN 210
 Db 146 AELAVSTFWNPNEYQVLFEEALISPQRGTMQGLDDCILSYSPCAKAFPHSFRSGDVEVNAQCN 205
 Qy 211 ATFOCIATGRDAVENKLWLRQRNGEDIPAAQTKNINHREFAASPRLOQEVTKTQDLYRCV 270
 Db 206 ASFQCMAAGR-AEAEFLQSLNFAFMVYKEPPTIAPPOLLRAGCPTYLQIQLNTNSIGDGPITRKCFV 264
 Qy 271 TQSBRGSGTS-NFAQOLIVREPRPRTAPPOLLGCGPTYLQIQLNANSITIGDGPITRKCFV 329
 Db 265 SQAPRGSGTSLNFAFMVYKEPPTIAPPOLLRAGCPTYLQIQLNTNSIGDGPITRKCFV 324
 Qy 330 RMTSGSWTETHAVNAPTYKLWLDPDTEYBIRULUTRECEGGTCLPGPGLITRKCFV 389
 Db 326 RMARGPWAHVSLQTYKLWLDPDTEBISVLTTRPDDGTCRGLGPISRTKCAFP 384
 Qy 390 RTPKTLKTAEQARRIAVWESLGYNITHCTFNFVTTCHYFHRS--HN-----ESRA 440
 Db 385 RAPKGLAFEAQARQTLQEWPLGNYNTVTCHTYTVSLCYHYTGSSNQTIPIVCDRAR 444
 Qy 441 CLDMDPKAPQHVVNHLPPTVNSLKMILNTPEGRKESEFTTIOQDDEPGPVPKSLOGT 500
 Db 445 CQPLHHEEAAL-----SERSREVNLNPEGRKEGVTFQDDEPGVTAESLTFT 497
 Qy 501 SFENKIPFLWKEPLEPNGLTOYEVSYSIRSSTDPAVPAQGPTQVSNLNSTHVFMHL 560
 Db 498 PLEDMIPLKWEQEOPNGLITOBISSYQIESSDPAVVAQA-TSTISKERNETYHFESNL 556
 Qy 561 HPGTTYQFQFTRASTVKGFQDATAINVNTNISAPSPLDYGVDASLNEATTIVLRLRQA 620
 Db 557 HPGTTYLFSGVARYTGKFGQQALETITVNTISAPSPLDYGMSPLGESENNTIVLRLRQA 615
 Qy 622 AKGAPISAYQIVVYQQLH-DHRTKREGAMECYQVPUVYONALSGGAPYFAAELPPGNLP 679
 Db 616 GRGAPISVQVIVBEEQGRRRLREPGGDCFPPLTPFAALRGLVYFGAELAASSLP 675
 Qy 680 EPAPFTVGORTYKGFNNDPLAPRKGNNTYQFOAMSSVEKETKQCVURATAATEPBV 739
 Db 676 EAMPFTVGOKNTYRGWNNEPLEPKAYLLYFOQASHLKGETRARKACKESKR P 735
 Qy 740 IPDPAKQTDRVKLAGISA-GILVFILLLWVVKSKR-----LAKGRKD 785
 Db 736 L-EVQSQRSEBMGLLIGICGGGLAVLILLGAIIVVIRKRDHYASYTPKPVNTK--- 790
 Qy 786 AMGNTROENTHMYNAMDRSYADOSTLHARDPLSLTEMQHNFSPRLPNPLVPTAVIDEN 845
 Db 791 ATVNYRQETTHMMSAVDRFTDQSTL--QPPGHSFMDTHGYSR-----GBQ 835
 Qy 846 HS--ATAECSRLLDVPYRCEGTSPTYQTCQHPAIRYDILQHNLANKTSQDYGPKBEY 903
 Db 8336 RSGGYTEASSLGGSPPRRCGRKSSPYHTVQLHPAVRYDADLQHINQMKTAEGYGFQKEY 895
 Qy 904 ESFFRGQSASWDVARKDQRAKNRYGNIIAYDHSRVILQVPPDSSDVTINANYIDIWLY 963
 Db 896 ESPFGS---WDATKKDKVKGSGQEPMPAYDHRVCLHPMLGDPNADYINANY---- 946
 Qy 964 RDGYORPSPHYIATGSPVHETYDFWRMVWQEOQSACIVMNTLYEVGRYKCYKWPDDTEV 1023
 Db 947 -DGTHRSNFIATQGPKPMVYDFWRMVMQEHCSIVINTKLVEAGCKCSRWPEDDT 1005
 Qy 1024 YGDFKVTCVEMEPLAETYTRTPFLERRGNEIREVKQFFGWPDHGYVYHATGLLSPIR 1083
 Db 1006 YGDJKIMLVKKTETLAEYVTRTFALERGGSARIEVROFFTAPEHGYPUHTGGLAATR 1065
 Qy 1084 RVKLSNPPSAGPIVVHCSAGAGRGCYTVIDMELDMAEREQVYDINYCVKALRSRRINMV 1143

Db 1066 RVKASTPPDAGPVIVHCAGTGTGCVYVLDVNLMAECGVTDINYCYKTLCSRVCNMI 1125
 Qy 1144 QTEEQYTFIHDALEACLGCTATPVCFCFKAAFTDMIRIDSQTNISHKDEPOTLNSVTP 1203
 Db 1126 QTEEQYTFIHDALEACLGCTTIPVSERATKYMIRIDPQSNISQUREEFQNLNSVTP 1185
 Qy 1204 RLQABEDCSTACIPLRNHDKNRMDDMLPPDRCLPPLTITDGESSYINAALMDSYRQPAAFI 1263
 Db 1186 PLDVEYESTALLPRNRDQNRSMDVLPPDRCLPPLISTGDSNNYXINNALTDTSYRRAIFI 1245
 Qy 1264 VTQYWPBEGMLRKGPVQBM 1320
 Db 1246 VTLHPLQSTTPDWRVLYVDGCTSIWMNQNSNSAMPCLQWPEPGRQYQGUMVEFIM 1305
 Qy 1321 SCNSCDVYRNPICNTRPOGQYLMWQQFOYTLQVBRQ 1380
 Db 1306 SGTADEDLVARVFRVONISRLQGHLVYRHFQPLRWSYRDTDPSKAFHLLAEDVKQ 1365
 Qy 1381 EECBEGEGRTITHCLNGGCRSGMFCAGIVVEMVKRQNVYDVPHAVKTLRNSKPNMVBAP 1440
 Db 1366 --AESGDRTIVHCLNGGRRGTSCLARTVLEMIRCHNLVDVSFAKTLRNYKPNMVBTP 1423
 Qy 1441 EQYRCPYDALEYLS 1456
 Db 1424 DQYHCPYDALEYLS 1439

RESULT 12
 US-10-087-993-34
 ; Sequence 34, Application US/10087993
 ; Publication No. US20020169303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich, Axel
 ; Aoki, Naohito
 ; Kim, Yeong Woong
 ; Wang, Hong Yang
 ; Chen, Zhengjun
 ; Naylor, Oliver
 ; Kharitonov, Alexei Igorevich
 ; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPL, CLK,
 ; AND SIRP POLYPEPTIDES AND RELATED
 ; PRODUCTS AND METHODS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/087,993
 FILING DATE: 05-Mar-2002
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/877,150
 FILING DATE: June 17, 1997
 APPLICATION NUMBER: U.S. 60/019,629
 FILING DATE: June 17, 1996
 APPLICATION NUMBER: U.S. 60/023,485
 FILING DATE: August 9, 1996
 APPLICATION NUMBER: U.S. 60/030,860
 FILING DATE: No. US20020169303A1
 APPLICATION NUMBER: U.S. 60/034,286
 FILING DATE: December 19, 1996

APPLICATION NUMBER: U.S. 60/030,964	FILING DATE: NO. US201019303Aember 15, 1996	ATTORNEY/AGENT INFORMATION:	726 SKRPU-EVSRSEENGLGICAGGLAVLILLGAIIVTRKGPEVNMTK-ATVNYROEK 783
NAME: Warburg, Richard J.			795 THMNDAMRSYADQSTLHADPLSLTFLMHNFSRLPNPDLVPTAVLDENHSATAESSR 854
REGISTRATION NUMBER: 32,327			784 THMISAVDRSFTDQSTLQEDERLGSFMDTHGSTR----- -GQRSGGTYTEASS 832
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (213) 489-1600			855 LL-DPRYLCEGETSPYOTCQLHPAIRVADLLOHTNLMTSDSYCQEKEYESFFGQSAS 913
TELEX: 67-5150			Db 833 LGGGPRRPGRKGPPHTGQFQKQEBSFFFSS--- 888
INFORMATION FOR SEQ ID NO: 34:			Qy 914 WDVAQKDQNRAKRNQGNILAYDHSEVILQPVEDDPSDYINANTIDIWLYRDGYORPSHY 973
SEQUENCE CHARACTERISTICS:			Db 889 WDATCKDKVKGSRQBPMPAYDRURVKLHMLGDNDYNTN----DGYRSNHF 942
LENGTH: 1430 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: Linear			
MOLECULE TYPE: Peptide			
SEQUENCE DESCRIPTION: SEQ ID NO: 34:			
US-10-087-993-34			
Query Match 55.4% ; Score 4325; DB 13; Length 1430;			Qy 974 IATQGPVHETVYDFTRMVWOBOSACI-LVWTLNEVGRVCKYWDDTEVYGFKVTCVE 1033
Best Local Similarity 58.1%; Pred. No. 1.9e-13;			Db 943 IATQGPKPMEVYDFTRMVWOBHCSIIIVMTKLVEGRVCKSRYNFEDSDYD1KIMLYK 1002
Matches 839; Conservative 197; Mismatches 345; Indels 64; Gaps 22;			
Qy 32 AGCTFD---DOPGACYHDQLYDDFWRVHSAQEPHYPPEMPOQSYMVVDSSNHDPGE 88			Qy 1094 GPIVHCSAGAGRTCTCYTIDIMLDMAEREGVDDLYNCYKALSRRIINMVOTEEDYIFITH 1153
Db 24 ARGCTPPEASDPAVPEYSQAXYDDQWEQVIRPGRAPADIPIGSYLMNTSCHARGQ 93			Db 1063 GPIVHCSACTGRTCTCYTIDVMLMAECGUVVDDLYNCYKTLCSRVMNIQTBEYIFITH 1122
Qy 89 KARLOLQPTMKENDTHCDFSLLYSSORGKNPCTLNLTIVRUNKPLANPWNVTGFTGRDW 148			Qy 1154 DAILEACLCETTAIEVCBKAAYFDMIRIDSQTNSHLDEFTQTNSTPRLQAEDCSIA 1213
Db 84 RAHVIFOLFSLSENDTHCQFSTFLYSLRGTC-GTLRVYVRVNGGLPLASAUNMTGSHGRQW 142			Db 1123 DAILEACLCGETTIEVSEFATYKEMIRDQIPDNNSQSLREFQTINSPPLDVBECSIA 1182
Qy 149 IAPDAELAYSTFWNEYQVTFEEAVSGRSGKIAIDDQLQSYPCDKSPHFLRIGDEVNAG 208			Qy 1214 CLPRNHDKNRFMDMLPPDRCLPFLITIDGESESSNTINAALMSYRPAFAFTVQPLNTV 1273
Db 143 HQAELAYSTFWNEYQVLFEEALISPDRGYMCDDILLSTPCAKPHFSRLGDEVNAG 202			Db 1183 LLPRRDQNSMVDUPDRCLPFLISTGDANNYNAALTDTSYTRSAFPTVLHQLSTT 1242
Qy 209 QNATFOCIATGRDAVNKLWLQRNGEDIPVQATRNIINRHPAASRQLQEVTKTQDLYR 268			Qy 1274 KDFEWFLVYDYGCTSIVMLNEVDSLQG---CPOQYNEEGMLRYGPLOVECMSMCDVIN 13330
Db 203 QNASFQCMAG-BPMQDPLJLQRQSLAVP-AGAFGTATSPATPLAAYVRAQDLYR 260			Db 1243 PDEWFNLVYDYGCTSIVMLNQNSNSAWPCLQWYBPGQOQYQMEVFMSGTADELVA 13022
Qy 269 CYTOSERGSVNSFAQLIVREPRPIAPPOLIGVGPTYLQLIQLNANSIIGDPITLKEYE 328			Qy 1331 RIFRQLNLTREPGVGLMVOQFOYLGWASHREVPVGKRSFELKLILQYEVKOECEGEGRT 1390
Db 2611 CVSQAPRG-GVSNFPELLVKEPPTIAPOLLRAQGPTLQLQNLNSIIGGPVIRKEIE 319			Db 1303 RVFRVONISLQEGDLVRFQFLFWSAVDTDPSKKAFLHLLAVIDKWO--AESGDGRT 1360
Qy 329 YRMTSGSWTTETHANATYKWLHDPETYEIRULTRPGGGTG--LPPPLYTRTKC 385			Qy 1391 ITHCLNGGRSGSMFCAIGTVYEMVRQNVYDVFHAVKTLRNSKPNMVAEIQYRCYDVA 1450
Db 320 YRMARGPAAEVAVSLSQTYKLWHLDPTDYYEISVJLTRPGGGTGEWATPHQP----- 372			Db 1361 IVHCUNGGRSGTFCACATVLEMIRCHNLVDVFFAAQTLRNYKPMNMVETMDQYHFCYDVA 1420
Qy 386 AEPMRRT---PKTLKIAEIQARIJADWESLQYNTCHPNVTCYHRG--HNEBSRA 439			Qy 1451 LEYLE 1455
Db 373 -HOMRAHEGPKGLAFIEIQARLQTLQWEPIGYNNTRVSYLQYUQGSSINQITR 431			Db 1421 LEYLE 1425
Qy 440 DCLMDMDPAPQHVNHLFPYTVNLKMLTBNPGRKESSEETIOTDVPGPVPYKSLQG 499		RESULT 13	
Db 432 ECVKTEQQVSRTIKNLPPYRNHVRVLNTBNPGRKEGKETFQIDEDVPGIAAESLTIF 491		US-10-296-115-1190	
Qy 500 TSFENKFLANKEPLENGITQYEVSYSSTSBDPAPVAGPPQTVNLNSTHVEFH 559		; Sequence 1190, Application US/10296115	
Db 492 TPLEDMFLKWEWPQEPGLTQYEISQSTESSDPAVNPGRRTISKERNETVHFSN 551		; FILE REFERENCE: 784PCT	
Qy 560 LHPGTTKOFFIRASTKFGPATAINVTNTNISAPSLLPDYEGUDASLINEATTIVLRLPA 619		; CURRENT APPLICATION NUMBER: US/10/296,115	
Db 552 LHPGTTVLFVSPVARTGKFGQQALETITNTNISAPSFDYALMPSPIGESENNTIVLRLPA 610		; PRIOR APPLICATION NUMBER: US09/488,725	
Qy 620 QAKGAPISAYQIVVEQIIPHRTKREAGAMECYQVPTYQNALSGGA---PYFAAELPP 675		; PRIOR FILING DATE: 2000-01-21	
Db 611 QRGAPASVYQVIVE--ERANGCGTTRWTGLLPSAID-LRGGAGCPRLHYFGEELAA 665		; PRIOR FILING DATE: 2000-04-25	
Qy 676 GNLEPEPAFTVGDNRTYKGFNNPLA PRKGNNYFQAMSSYKEKETKQCVRIATKAATE 735		; NUMBER OF SEQ ID NOS: 1478	
Db 666 SSPEAMMFTVGDNQTYTRGFWNPLERKAYLJYFQASHURGETNCTCIRARKACK 725		; LENGTH: 623	
Qy 736 EPEVIPDPAKOTDRVVKAGISA-GILWFILLLWVIVKSKLAKRKDAMGNTRQEM 794		; TYPE: PRT	
		; ORGANISM: Homo sapiens	
		US-10-296-115-1190	

Query Match		Score 2471.5; DB 15; Length 623;	
Best Local Similarity 72.3%; Pred. No. 1-7e-175; Matches 451; Conservative 74; Mismatches 86; Indels 13; Gaps 3;		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
Matches 451; Conservative 74; Mismatches 86; Indels 13; Gaps 3;		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
DPRVRT----HTMASDTSSLVQSHTYKKREPADVYQTGQHHPA.RVADLQLQHTQMK 64		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
834 DPLVPTAVLDENHSATARSRLIDDPVRY-LCCTESTSPYQTGOLHPAIRVADLQLQHTQMK 892		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
11 DPRVRT----HTMASDTSSLVQSHTYKKREPADVYQTGQHHPA.RVADLQLQHTQMK 64		Db 82 SRHDPEKARLOLQPTMKENDTHCIDPSYLLYSOKGKLNPGTLNLVRYTKGPLANPKWT 141	
893 TSDSYGFKEKEYESFFEGOSASWDVAKKDQNRAKNRGNIAIDYDHRSRVILQPYVDDPSSDX 952		Db 82 SRHDPEKARLOLQPTMKENDTHCIDPSYLLYSOKGKLNPGTLNLVRYTKGPLANPKWT 141	
65 CAGYGFKEKEYESFFEGOSAPWDSAKKDQNRAKNRGNIAIDYDHRSRVILQPYVDDPSSDX 124		Db 82 SRHDPEKARLOLQPTMKENDTHCIDPSYLLYSOKGKLNPGTLNLVRYTKGPLANPKWT 141	
INANYIDIWLYRGYQRSHYIATQGPHTETYDFWMMWQBOSACIVMVTNLVEGRVK 1012		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
125 INSNYI----DGYHRNHYLATQGPHQETTYDFWMMWQHENTASITMVTNLVEGRVK 178		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
1013 CYKWPDDTEVYQDFKVTCVEMPPLAEVYWRFTLERGYNTEREQFHFPWDEGVLP 1072		Db 134 GPRTTRRNRAEAIATSEFWNPYQVITYF-TTSQHGYLAIDEVKYVGHPCRTPTPHIQ 192	
179 CCKXWPDDTEVYQDFKVTCVEMPPLAEVYWRFTLERGYNTEREQFHFPWDEGVLP 1072		Db 134 GPRTTRRNRAEAIATSEFWNPYQVITYF-TTSQHGYLAIDEVKYVGHPCRTPTPHIQ 192	
DB 134 GPRTTRRNRAEAIATSEFWNPYQVITYF-TTSQHGYLAIDEVKYVGHPCRTPTPHIQ 192		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
1073 YHATGLLSFRTRVYLNSPPSAGPVLVHCSAGAGRGTGCVYVIDIMLDMAEREGVDIYNVC 1132		Db 262 TDQDLYRCVTOQSERSGSVSNFAOLTYREPRPIAPOLLGVSPTYLQJQMANSTIGDGP 321	
239 YHATGLLSFRVQVSKSPSAGPLVHCSAGAGRGTGCVYVIDIMLDMAEREGVDIYNVC 298		Db 262 TDQDLYRCVTOQSERSGSVSNFAOLTYREPRPIAPOLLGVSPTYLQJQMANSTIGDGP 321	
1133 KALRSRRRNMVQTEEQ1FTHDILEACLGCTTAIPCEKFAYFDMIRISQTNSSHLK 1192		Db 253 RDAGKRCMRTEGGISNTSYABLVKEPVPIAPPOLASATGATYWIOLNANSINGDGP 3112	
299 RELSRRRNMVQTEEQVYVTFHDALEACLGCTTSPASQVRSLSYDMDNKLDPQTNSQIK 358		Db 253 RDAGKRCMRTEGGISNTSYABLVKEPVPIAPPOLASATGATYWIOLNANSINGDGP 3112	
1193 DEFOQLNSTVPRLQAEDCSJACLPRNHDMLPDRDCFLPLTIDGESSIONYINAAL 1252		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
359 BEPTLANNMPTURVEDSIALIPRNHEKRNCDILPDRDCFLPLTIDGESSIONYINAAL 418		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
1253 MDSYROPAFAFIVTYQPLPNTVKDFWRLIVYDYGCTTSIVMLNEVDLSQGCPQWPEEGMLRY 1312		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
419 MDSYKQPZPAPFIVTQHPLNNTVKDFWRLIVYDYGCTTSIVMLNDVPAQLCPQTWENGVHRH 478		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
1313 GP1QVECMCSMDCVINIFRICNLTRPQEGYLMVQFQYLGWASHREVPSKRSPLKL 1372		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
479 GP1QVEFVSYQ1VVEERPRETTKKTTEILKCYCPVPHQFONASLLNNSOYYFAEPFDPSLQ 671		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
1373 ILQVEKNOBECFEGEGRITIHCUNGGRSGSMFCAIGIVVEMYKRONYDVPHAVKTLRNS 1432		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
539 IRQDNQEEYNGEGEGRITVHCINGGRSGTFCASIVCEMLRHQRTVDVFHAVKTLRNS 598		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
1433 KPNMVEAPEQYRFCDYALEYLES 1456		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
599 KPNMVDLIDQYKFCYEALEYNS 622		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
RESULTS 14 JS-10-296-115-1390 Sequence 1390, Application US/10296115 GENERAL INFORMATION:		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
APPLICANT: Hyseq Inc.		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
TITLE OF INVENTION: NO. US20040053248A1		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
FILE REFERENCE: 784 PCT		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
CURRENT APPLICATION NUMBER: US/10/296,115		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
CURRENT FILING DATE: 2002-11-18		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
PRIOR APPLICATION NUMBER: US09/488,725		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
PRIOR FILING DATE: 2000-01-21		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
NUMBER OF SEQ ID NOS: 1478		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
SEQ ID NO 1390 LENGTH: 815		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
TYPE: PCT		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
ORGANISM: Homo sapiens		Qy 31.6%; Score 2471.5; DB 15; Length 623;	
JS-10-296-115-1390		Db 322 1LKEYBYRM7SGSWTETHAYNAPTYKWLHDPDTYEIRVULTRGEGTGLGPPLIT 381	
Best Local Similarity 54.0%; Pred. No. 3.1e-156; Matches 409; Conservative 126; Mismatches 216; Indels 6; Gaps 4;		Qy 31.6%; Score 2471.5; DB 15; Length 623;	

PRIOR APPLICATION NUMBER: 60/186,596
 PRIOR FILING DATE: 2000-03-03
 SEQ ID NO: 114
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 1502
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-887-669-1.rabp

Query Match 19.5%; Score 1526; DB 9; Length 1502;	Qy 966 GYQRPSHYIATQGPVHETTYDFWRMIVWQEOQSACTIVMTNLVEGRVKCYKWPD-DTEVY 1024
Best Local Similarity 30.4%; Pre. No. 2.9e-104;	Db 1008 GYRRNAYIATQGPVPETEGDFWRMIVWQEOQSACTIVMTNLVEGRVKCYKWPD-DTEVY 1067
Matches 425; Conservative 211; Mismatches 476; Indels 284; Gaps 48;	Db 1025 GDFKTYTCVMEPLAEVVVRSTFTLERGYNEIREKVQFHFTCWPDQGVPYHATGLLSFIRR 1084
Qy 204 EUNAGQNTFQIATGRDAVANKWLDRNG---EDPIVQTRNINHRRFAASPTFLQEV 259	Db 1068 GFIQYLLDTELATFCVRFTSLHNGSSSEKREVQFOFTAWPDPGVPEVTPFLAFRLR 1127
Db 242 EIMPGGNVNITCVAVGSPMPYVK-WMCGAEDLTPEDMPPVG-RNV-----LELTDV 290	Qy 1085 VKLSNPPSAGPIVWHCSAGAGRITGGCIVIDIMLDMAEREGVVDINTNCVRAILSRSLINMVQ 1144
Qy 260 TKTQDQILYRCVQTQSERGSVGSNAQOLIVREPRPIAPPOLLGVGPTYLILLONANSIIGD 319	Db 1128 VRTCPDPDGPIVWCSAGVGRGTFIVIDAMLEPKTVDVGHVTLMSQANMVQ 1187
Db 291 -KDSANTHPCTVANSLLGW-IEAVAQITVSKSLPKAPTPVNTENTATSTITWDSGN---P 345	Qy 1145 TEBOYIFTHDAILEACLGCTAIPCEFKAYFDMIRIDSQTNSHLKDEFOTLNSVTPR 1204
Qy 320 GPILKVEYMRTS--GSWTETHAVNAPPTYKLWHLDPDTEYEIRVLLTRPGEGGTCLLPGP 377	Db 1188 TEDQSFHIALLEAVGCNTTEPARSLAYIQLAQVEGEHYTMELFKRL--ANSK 1245
Db 346 DPVSYYYTEYKSKSQDGPYQIKEDTTRYSIGLSPNSEYEIWU--SAVNSIGOQPPSE 403	Qy 1205 LQAEDCSIACLPRNEDKRNPRMDMLPPDRCLPFLITDG-ESSNNYNAALMDSYROPAIFI 1263
Qy 378 PLITRTRCAEPRTPTKLIQARRIAVDES-----LGNT-----416	Db 1246 AHTRSFISIANIPCKEKFKNRVLNIMYESTRVCLOPTRLGVGSDYINASFIDGYRKQKAYI 1305
Db 404 SVUTRTRGEQAPARPPRNQARMLSATMIVQWEPEVPGNLRGTVVYTMEPEHFPVGNW 463	Qy 1264 VTQYPLPNTYKDFWRLVYDYGCTSVMLNSDL--SQGCQYWPBGMILYGPVIECMS 1321
Qy 417 -----T 417 -----T 417	Db 1306 ATQPLAETEDFWRMLENNSTIVMLTKLREMREKCHQYWPMERSARYQFVDPMA 1365
Db 464 QRNNDISLITVGSLLDEDITYTVRLAFTSGDPLSDP1QVKTOQGVPCQPMNRAEA 523	Qy 1322 CSMDCDVINRIFRICNLTRPOEGY-LMVQQFQYLGWASHREVPGSKRSFSLKLJLQYEVKQ 1380
Qy 418 RCHTENVTYCZH-----YFRGHNESRADCLMDPKAPQHVNHLPPYTNTVSLK 465	Db 1366 ---ETNMPQTTLREPKVTDARDGQSRTRVROFQFTM-PEOCVPKSEGFDFIGYHHTK 1421
Db 524 RSFT-SITLWSPPROCESSIKYELLFRGHDHGIVERGTFDP-TTSVYVEDIKPNTYAFR 581	Qy 1381 BECBEGEGRTIHCLANGGRSGMPACAIGIVVEMYKRQNYVUDPHAVKTLRNSKPMVVEAP 1440
Qy 466 MILTNPG-----RKESETIILQIDDEFDVGPPVKSLOOTSPENKFLINWKEPLEN 517	Db 1422 EQFGQ-DGPISVHCASAGVGRGTGVFTLTSIVLERMVEGYVUDIFOTYKMLTORPAMVOTE 1480
Db 582 LAARSPQGLGAFTPVVRQRTLQSI-----SPKNFKWYKMINIKTS----VLSWEFFDNYN 631	Qy 1441 EQYRFCDVALEYLS 1456
Qy 518 GIITQYEVSYSSIRSFDAPVAGPPOTVSNLWNSTHVNFMHLHPCTYQFFI--RASTV 575	Db 1481 DEYQFCYQARLEYLGS 1496
Db 632 S-PTPYKIQYH-----TLDVQ-----RTTICKLITHLKPHTPINVLTINGSSL 676	Search completed: June 1, 2005, 14:02:08
Qy 576 KGF GPA-----TAINTVNTNISAPS-----PDYEGVDASLNETATTITVLLRPAQAKGAPISA 628	Job time : 140.324 secs
Db 677 GGLQQTVAWTAFNLLN--GKSVAPKPDADSF-----IMYLPDGQSP-VPQS 723	
Qy 629 YQIYVEQIUPHR-----TKRE3AMECTQ-----VPVTKQNALLSGCAYYFA- 670	
Db 724 YFIVMVPLRKSRGGQFLTPLGSPEDMLEELQDISLSSLRHSRQEYVRPTIAARF 783	
Qy 671 AELPPGPNLPEPAPFTVGDNRTRYKGFWNPPLAERKGNTNFQAMSSVEKETKTCVRIATK 730	
Db 784 SWLPP-----TYPHQGDOKQYQGFDNRQGLEPCHRIVFLAVN--LQKSEFT----FA 828	
Qy 731 AAATEEPEVI--PDPAKCTDVRVYKIAGSAGLVFLILLVYI-VIVKVKSLAKKRKDAM 787	
Db 829 ASFSDPQLDNPQVDPGEGLINVIGPVALVVICIVAILLYKKNPDSKRD- 887	
Qy 768 GNTRQEMTHNMNDRSYADQSTIHAEDPLSLTMDOHNFSPRLNDPLVTLDENHS 847	
Db 868 -----BPRTKCLANNADLAFLPHPKDPP-----	
Qy 848 ATAESSRLDVPVYLCBGTESPYQT-GCL-HPAIRVADLQLQHINLMKTSYGFKBYES 905	
Db 910 --EMRRI-----NEQTPGMSLHSHPIPADIAMAFTERKANDSKLSBEYS 953	
Qy 906 FPEGQASASWDVAKKDNONAKYKNTIAYDHSRVILQDPSDSDYINANXIDWLYRD 965	
Db 954 IDPGQQFWEHSNLEVNPKPNRYANVAYDHSRVILQFEGIMGSVDYINANXV----D 1007	

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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:40:58 ; Search time 38.7393 Seconds
 (Without alignments) 3618.750 Million cell updates/sec

Title: US-09-887-669-1

Perfect score: 78/9

Sequence: 1 MDVAARALPAFVALWLYPWN.....EAPEQYRFYCVDALBYLESS 1457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR_79;*

1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match length	DB ID	Description
1	78/9	100.0	1457	1 A48066	protein-tyrosine-p
2	7506.5	96.1	1440	2 J63112	protein-tyrosine-p
3	4812.5	61.6	1452	1 S17670	protein-tyrosine-p
4	4793.5	61.4	1452	1 S17670	protein-tyrosine-p
5	4359	59.1	1436	2 S42290	protein-tyrosine-p
6	4359	55.8	1442	2 S72441	protein-tyrosine-p
7	1516.5	19.4	1501	2 L58148	protein-tyrosine-p
8	1495	19.1	1499	2 I00212	leukocyte antigen-leukocyte antigen-protein-tyrosine-p
9	1494	19.1	1898	2 S46216	leukocyte antigen-leukocyte antigen-protein-tyrosine-p
10	1492.5	19.1	1897	1 TDHULK	protein-tyrosine-p
11	1482.5	19.0	1912	2 A56178	protein-tyrosine-p
12	1475.5	18.9	1496	1 A48758	protein-tyrosine-p
13	1453.5	18.6	1863	2 S46217	protein-tyrosine-p
14	1452.5	18.6	1691	1 I54689	protein-tyrosine-p
15	1452.5	18.6	1894	2 C54689	leucocyte common a
16	1452	18.6	1290	2 A56493	protein-tyrosine-p
17	1440.5	18.4	1907	2 S50893	protein-tyrosine-p
18	1438	18.4	2029	1 TDFEFLK	protein-tyrosine-p
19	1415.5	18.1	1231	2 S53018	probable protein-t
20	1345.5	17.2	1437	2 T31093	probable protein-t
21	1337	17.1	1585	2 T19121	receptor tyrosine
22	1311.5	16.8	2051	2 T30938	protein-tyrosine-p
23	1240	15.9	582	2 A57068	protein-tyrosine-p
24	1175.5	15.1	796	1 JC1285	protein-tyrosine-p
25	1155	14.8	802	1 A36065	protein-tyrosine-p
26	1145	14.7	832	2 JC8051	protein tyrosine p
27	1142	14.6	699	2 JC6112	protein-tyrosine-p
28	1136.5	14.6	829	1 A47373	protein-tyrosine-p
29	1127.5	14.4	700	1 S12053	protein-tyrosine-p

RESULT 1		ALIGNMENTS	
A48066	protein-tyrosine-phosphatase (BC 3.1.3.48), receptor type kappa precursor - mouse		
C;Species: Mus musculus (house mouse)			
C;Date: 21-Jan-1994 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004			
C;Accession: A48066			
R;Jiang, Y.P.; Wang, H.; DiBustachio, P.; Musacchio, J.M.; Schlessinger, J.; Sap, J.			
Mol. Cell. Biol. 13, 2942-2951, 1993			
A;Title: Cloning and characterization of R-PTP-kappa, a new member of the receptor protein kinase family			
A;Reference number: A48066; PMID:93233655; PMID:8474452			
A;Accession: A48066			
A;Molecule type: mRNA			
A;Residues: 1-1457 <JIA>			
A;Experimental source: brain			
A;Note: sequence extracted from NCBI backbone (NCBIP:1298800)			
C;Complex: after cleavage by a furin-like endopeptidase, the two chains remain associated			
C;Superfamily: proteo-tyrosine-phosphatase homology			
-tyrosine-phosphatase homology			
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor type kappa, uncleaved #status predicted <SIG>			
F;29-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, uncleaved #status predicted <EXT>			
F;29-644-755/Domain: extracellular #status predicted <EXT>			
F;29-644/Domain: immunoglobulin homology <IMM>			
F;29-377/Domain: fibronectin type III repeat homology <FN3A>			
F;29-377/Domain: fibronectin type III repeat homology <FN3B>			
F;29-644/Domain: fibronectin type III repeat homology <FN3C>			
F;644-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, chain 1 #status predicted <TMN>			
F;756-772/Domain: transmembrane #status predicted <TMN>			
F;73-1457/Domain: intracellular #status predicted <INT>			
F;841-1457/Domain: leukocyte common antigen cytosolic domain homology <LAC>			
F;122-1148/Domain: protein-tyrosine-phosphatase homology <PTP>			
F;1218-1442/Domain: protein-tyrosine-phosphatase homology <PTP>			
F;10,139-21,0,415,423,435,461,55,585,589,606,689/Binding site: carbohydrate (Asn) (cova			
F;644-1457/Domain: fibronectin type III repeat homology <FN3D>			
F;643-644/Cleavage site: Arg-Glu (furan-like endopeptidase) #status experimental			
F;1100/Active site: substrate phosphate (Arg) #status predicted intermediate #status predicted			
F;1394/Active site: Cys (phosphocysteine intermediate) #status predicted			
F;1400/Binding site: substrate phosphate (Arg) #status predicted			
Query Match Score 7809; DB 1; Length 1457;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1457; Conservative 0; Mismatches 0; Gaps 0;			
QY 1 MDVAAAAPAPVAVLWLYPWPLGSALGFSAGGCTFDGGPGACTHDLYDDPWEWVHS 60			

Db	.1 MDVAAAALPAFVALNLLYPWPILLGSALGQFSAGGGTFDGPAGCDYHQDLDDPEWVHVS	60	Qy	1141 NMVQTEEQYIFIFHDIALEAICLGETAIPICEPKAYAFDMIRIDSOTNSHHLKDFEQTLSN	1200
Qy	61 AQBPHILPPEPNQGSMIVDOSNHDEKARLQLPTMKENDTHCIDSFLILYSQKGNG	120	Db	1141 NMVQTEEQYIFIFHDIALEAICLGETAIPICEPKAYAFDMIRIDSOTNSHHLKDFEQTLSN	1200
Db	61 AQBPHILPPEPNQGSMIVDOSNHDEKARLQLPTMKENDTHCIDSFLILYSQKGNG	120	Qy	1201 VTPRLOAEDCSIACLPRNHDKNRFMDMLPDRCLPLITIDGESNYINNALMDSYROPA	1260
Qy	121 TLNILYRVNKGPLANP1WNTGFTGRDWLRALAVSTFWPNEYQVTFEAEVSGGRSGYIA	180	Db	1201 VTPRLOAEDCSIACLPRNHDKNRFMDMLPDRCLPLITIDGESNYINNALMDSYROPA	1260
Db	121 TLNILYRVNKGPLANP1WNTGFTGRDWLRALAVSTFWPNEYQVTFEAEVSGGRSGYIA	180	Qy	1261 AFIVTQYPLNTVKDFWRLYDYGCTS1WLNELQSQCPQYWHBEGMURYGPQVECM	1320
Qy	181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNLWLORRNGDIPVA	240	Db	1261 AFIVTQYPLNTVKDFWRLYDYGCTS1WLNELQSQCPQYWHBEGMURYGPQVECM	1320
Db	181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNLWLORRNGDIPVA	240	Qy	1321 SC5MCDVNR1FRICLNLTAPQEGYLMYQOFQYLQASHREVPGSKRSFLKLQLOVEKQ	1380
Qy	241 QTKNINHRPFAASFRQEVTKDQYLRYCTQSERSGVSNAQLIVREPRPIAPPOL	300	Db	1321 SC5MCDVNR1FRICLNLTAPQEGYLMQOFQYLQASHREVPGSKRSFLKLQLOVEKQ	1380
Db	241 QTKNINHRPFAASFRQEVTKDQYLRYCTQSERSGVSNAQLIVREPRPIAPPOL	300	Qy	1381 EECBEGEGRTIITHCNGGRSGMFCAGITIVEMYKRONVYDVFHAVKTLRNSKPNMVEAP	1440
Qy	3011 GVGPTYLLIQLNANSITIGDP1ILKEVEYRMTSGSWEETAVNAPTYKLWHDPTYEI	360	Db	1381 EECBEGEGRTIITHCNGGRSGMFCAGITIVEMYKRONVYDVFHAVKTLRNSKPNMVEAP	1440
Db	3011 GVGPTYLLIQLNANSITIGDP1ILKEVEYRMTSGSWEETAVNAPTYKLWHDPTYEI	360	Qy	1441 EQYRCYDVALEYLESS	1457
Qy	3661 RVLLTRPGEGGTGLPGLPGLPPLTRTKCAEPMRTPKTLKIAECAARRIAWDWSLGNTIRCH	420	Db	1441 EQYRCYDVALEYLESS	1457
Db	3661 RVLLTRPGEGGTGLPGLPGLPPLTRTKCAEPMRTPKTLKIAECAARRIAWDWSLGNTIRCH	420			
Qy	4211 TPNVTICHYFRGHSNSRADCLMDKAQPHVNHLPPTINSLMLNPEGRKESET	480		RESULT 2	
Db	4211 TPNVTICHYFRGHSNSRADCLMDKAQPHVNHLPPTINSLMLNPEGRKESET	480		JC6312	
Qy	4811 IIQTDDEVPGPVPKSLQGTSPENK1FLNWKPLEBNGIIQYEVSYSSIRSFDPAVVA	540			protein-Tyrosine-phosphatase (EC 3.1.3.48) receptor-type - human
Db	4811 IIQTDDEVPGPVPKSLQGTSPENK1FLNWKPLEBNGIIQYEVSYSSIRSFDPAVVA	540		C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000	
Qy	5411 GPPQTVSNLWNNSTHYMMLHPGTTYOFIRASTVKGFPATAINTTNISAPS1LPDYG	600		C;Accession: JC6312	
Db	5411 GPPQTVSNLWNNSTHYMMLHPGTTYOFIRASTVKGFPATAINTTNISAPS1LPDYG	600		R;Yang, Y.; Gai, M.C.; Choi, E.Y.; Park, S.H.; Pyun, K.H.; Ha, H.	
Qy	6011 LSGGAPYFAAELPPGNLBPAPFTVGDNRITYKGFWNPPLAFLRKGTNTYFOAMSYVKEI	660		Gene 186 , 77-82 , 1997	
Db	6011 LSGGAPYFAAELPPGNLBPAPFTVGDNRITYKGFWNPPLAFLRKGTNTYFOAMSYVKEI	660		A;Title: Molecular cloning and chromosomal localization of a human gene homologous to th	
Qy	6611 LSGGAPYFAAELPPGNLBPAPFTVGDNRITYKGFWNPPLAFLRKGTNTYFOAMSYVKEI	720		A;Reference number: JC6312 ; PMID:97199372;	
Db	6611 LSGGAPYFAAELPPGNLBPAPFTVGDNRITYKGFWNPPLAFLRKGTNTYFOAMSYVKEI	720		A;Accession: JC6312	
Qy	7211 KIQCVRATKAATEEPVIPDPAKOTDRIYVKGIAISAGILYFILLLWIVVCKSKLA	780		A;Species: preliminary	
Db	7211 KIQCVRATKAATEEPVIPDPAKOTDRIYVKGIAISAGILYFILLLWIVVCKSKLA	780		A;Molecule type: mRNA	
Qy	7811 KKRKDANGNTREMTMMNANDRSYADOSTLHAEDPLSITMDQHESPLBLNDLVPTA	840		A;Residues: 1-1440 <YAN>	
Db	7811 KKRKDANGNTREMTMMNANDRSYADOSTLHAEDPLSITMDQHESPLBLNDLVPTA	840		A;Cross-references: GB:177886	
Qy	8411 VLDENHSAATABESSRLIDVPRYLCLEGESPYQTGQLHAIYADLQLHINLMKTSDSYGP	900		C;Superfamily: human-tyrosine-phosphatase, receptor type mu;	
Db	8411 VLDENHSAATABESSRLIDVPRYLCLEGESPYQTGQLHAIYADLQLHINLMKTSDSYGP	900		C;Superfamily: protein-tyrosine-phosphatase, receptor type III repeat homology <IMM>	
Qy	9011 REYESFFPGQASMSWDVAKDQNRAKRYGNITAYDHSRVLQVEDPSSDYNANYIDI	960		F;31-194/Domain: MM homology <IMM>	
Db	9011 REYESFFPGQASMSWDVAKDQNRAKRYGNITAYDHSRVLQVEDPSSDYNANYIDI	960		F;209-272/Domain: fibronectin type III repeat homology <3FR>	
Qy	9611 WLYRDGYCRPSXHIAITQQPHETVYDPMWYDQESACIYVMTNLVEGRYKCYKWPDD	1020		F;294-372/Domain: fibronectin type III repeat homology <3FR>	
Db	9611 WLYRDGYCRPSXHIAITQQPHETVYDPMWYDQESACIYVMTNLVEGRYKCYKWPDD	1020		F;911-1131/Domain: protein-tyrosine-phosphatase homology	
Qy	1021 TEVYGDVKVTCYMEPLAEVYVFTLRLERGNEIREVKQPFITGWDGHGPyHATGLS	1080		Query Match Score 96.1%; DB 2; Length 1440;	
Db	1021 TEVYGDVKVTCYMEPLAEVYVFTLRLERGNEIREVKQPFITGWDGHGPyHATGLS	1080		Best Local Similarity 96.1%; Pred No. 0;	
Qy	1081 FIRRVKLSNPPSAGPITVHCSAGAGRTCTCYIVIDIMDMAREGVYDINYCKVAKLSR	1140		Matches 1404; Conservative 19%; Mi smatches 16; Indels 19; Gaps 3;	
Db	1081 FIRRVKLSNPPSAGPITVHCSAGAGRTCTCYIVIDIMDMAREGVYDINYCKVAKLSR	1140		Qy 1 MD-VAAAALPAFVALNLLYPWPILLGSALGQFSAGGGTFDGPAGCDYHQDLDDPEWVHVS	59
Qy	9612 GTLNILYRVNKGPLANP1WNTGFLRALKLAVSTFWPNEYQVFEAVSGGRSGYI	180		Db 1 MDTRAAAAPFVALNLLSPWPLQGQFSAGGCTEDDGPAGCDYHQDLDDPEWVHVS	60
Qy	121 GTLNILYRVNKGPLANP1WNTGFLRALKLAVSTFWPNEYQVFEAVSGGRSGYI	180		Qy 60 SAQEPHILPPMPMQGSMYVDSNHPGEKARLQPTMKENDTHCDFSYLILYSQKGLN	119
Db	121 GTLNILYRVNKGPLANP1WNTGFLRALKLAVSTFWPNEYQVFEAVSGGRSGYI	180		Db 61 SAQEPHILPPMPMQGSMYVDSNHPGEKARLQPTMKENDTHCDFSYLILYSQKGLN	120
Qy	180 ADDIQQLSYPCKSPHFLRLGDVYENAGONATFQCIATGRDAVHNKLWLRNRRGDI	239		Qy 120 CTLNLVRYNKGPLANP1WNTGFLRALKLAVSTFWPNEYQVFEAVSGGRSGYI	179
Db	180 ADDIQQLSYPCKSPHFLRLGDVYENAGONATFQCIATGRDAVHNKLWLRNRRGDI	239		Db 121 GTLNILYRVNKGPLANP1WNTGFLRALKLAVSTFWPNEYQVFEAVSGGRSGYI	180
Qy	181 ADDIQQLSYPCKSPHFLRLGDVYENAGONATFQCIATGRDAVHNKLWLRNRRGDI	240		Qy 180 ADDIQQLSYPCKSPHFLRLGDVYENAGONATFQCIATGRDAVHNKLWLRNRRGDI	240
Db	181 ADDIQQLSYPCKSPHFLRLGDVYENAGONATFQCIATGRDAVHNKLWLRNRRGDI	240		Db 181 ADDIQQLSYPCKSPHFLRLGDVYENAGONATFQCIATGRDAVHNKLWLRNRRGDI	240
Qy	240 ACTKNTNHRRAAASFRLQEVTKDQDLYRCVTSQSGVSNPAQIVTREPRPPIAPPOL	299			
Db	241 ACTKNTNHRRAAASFRLQEVTKDQDLYRCVTSQSGVSNPAQIVTREPRPPIAPPOL	300			

253	RDAKYRCMIRTEGGVGISNYAELUVVKEPVPPVAPPQLASVATYLMQLNANSINGDGP	312	Db	11321 EDIISIRIYRNARAPQDGYRMQQFGLGMPWYKTRDPYKSRSTPLKLTRQVDKHNQOEYNG		
322	IIIKEVEYRMTGSWTTAHHNAPTYKILWHDDTEYETRVLILTRGEKGFTGGLPGPPLIT	381	Qy	1386 GEGRTTICLNGGRSGMFCAGTIVEMVYKRTNTDVFAVKTLRNSKRNMFVAPBQYRF		
313	IIVREVEYRMTGSWTTAHHNAPTYKILWHDDTEYETRVLILTRGEKGFTGGLPGPPLIT	372	Db	1445 GEGFTVHCLNGGRSGTFCATISVCEMRHQTVDVFAVKTLRNNKNMVDDLDQYRF		
382	RTKCAEPNMRTPKTKIAEIQARRIAVDFWESLGYNITRCHTENTVNTICHYFRGNESRAD-	440	Qy	1446 CTDVALEYLES 1456		
373	RTKCADPNRGPKRPLEWEVVKSRQQTIRMEPFQNVTRCHSYNLTVHCVYQVCGEQYQRE	432	Db	1441 CYEVALEYLNS 1451		
441	-CLDDMDPKAQHQVHNHLPPYTNVSLMLTNPGRKRSSEETIQTDEIVGPVPUKSLQ	499	RESULT 4			
433	VSMDTENSHPOHTITNLSPYTNTVSQKLIMNNPGRKSQELIQTQDDELPAGVPTESTQG	492	SI17670	protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor [validated] - mouse		
500	TSPEKNFLNWKRPELEPNQGIIOTYEVSYSIRSFSDFPAVVAQPOTVSNLNNSTHVFHM	559	CtSpecies	Mus musculus (house mouse)		
493	SPIBEKFLQWRPEPTQTYVITIEITYKAVSSDPEIDLSRSGRVSKLGNETHIFGG	552	CtDate	22-Nov-1993 #sequence_revision 08-Feb-1996 #Text_change 09-Jul-2004		
560	LAPGTTQFPIRASSTVKFGPATAINVTNISAPSLPDYEGDASLNETATTITVLLRPA	619	CtAccession	SI17670		
553	LAPGTTQFPIRASSTVKFGPATAINVTNISAPSLPDYEGDASLNETATTITVLLRPA	611	A.Title	Cloning, expression and chromosomal localization of a new putative receptor-link		
620	QAQGAPISAYQVQIVQEQLPHEPRTREREAGNECYQVPTVQNAISGGAPYFAAELPPGNL	679	A.Reference	SI17669; PMID:92008644; PMID:1655529		
612	HSGCAPVSYQIVVEERPRRKTTIELKCYPPVPHQNASLINSQYFAAEFPADSQI	671	A.Molecule	Product: protein-tyrosine-phosphatase, receptor type mu #status predicted		
680	EPAFPVTCGDNRTYKGFWNNPLAPRKGTNTYFOAMSSVERETKQTQVRIATAAATEEEPEV	739	A.Residues	MAA-1452 #status predicted <GEB>		
672	AADPFTIGGKNTQYWTPLPKSYRYFQQAQRANGEIKTDCVQVATKGATPKEF-	729	A;Cross-references	UNIPROT:P28828; EMBL:X58287; PIDN:CAA41225_1; PID:953235		
740	IPDPAKQDTRVVKIAGSAGLYFILLLAVVIVTVKVKSLAKRKDKANGNTROEMTHMV	799	C;Superfamily	proteins: proteine-tyrosine-phosphatase, receptor type mu; Fibronectin type III repeat homology <FN3A>		
730	VPEPEKQDQHTVKLAGVAGLFLVIFGQVWVKCERKAKERKETMSSTRQEMTVNN	789	F;84-470/Domain	fibronectin type III repeat homology <FN3B>		
800	AMDRSYAODTQDHAEDPLSLTMQDHNSPSRLNDP-----LVPITAVL-DENH	846	F;746-747/Domain	fibronectin type III repeat homology <FN3C>		
790	SMDKSYAEGCTNCDE--AFSEFDTHNLGRSYSSPSFSTMKNTLSTSVPNSYYPDETH	846	F;746-762/Domain	transmembrane #status predicted <TMN>		
847	SATAESSRLLDVPRY-LCGETESPYQTGQGHPAIRVADLQHINLMKTSDSYGFKEEYES	905	F;842-1452/Domain	leukocyte common antigen cytosolic domain homology <LAC>		
847	: : : : : : : : : : : : : : : : : : : : :	906	F;923-1143/Domain	protein-tyrosine-phosphatase homology <PTP1>		
906	FPEQQSASWDVAKKDQNTZRKNRGNITIADWHSRVTQLOPVEDDSSDYINANVIDIWLRD	965	F;712-9213-1437/Domain	protein-tirosine-phosphatase homology <PTP2>		
907	FPEEQQSAPDSACKDENMKRGNITIADWSRVTQLOTEGDTNSDYNGNYI-----D	960	F;206-260/Disulfide bonds:	#status predicted		
966	GYQRPNTIATQGPHVETWVWVWQQSACTIVMVTLVVEGRVKCYKWDDDETEYG	1025	F;1095/Active site:	Cys (phosphocysteine intermediate) #status predicted		
961	GYHRPNHYIATQGPMQETIYDFWRMWHTENTASIMTMNLVVEGRVKCCCKYWDDDETEYK	1020	F;1101/Binding site:	substrate phospho-Arg (Arg) #status predicted		
1026	DFKWTCVMEWPLAXYVVRPTTLEAQLGETAVRKYIREYKQFHFTGWPDHGPVYTHATGILSFIRR	1085	F;1389/Active site:	Cys (phosphocysteine intermediate) #status predicted		
1021	DIVRVLTEBLLAIVYVIRTPADPVEYQTCRLLQHLLPQKLNQVYKQKKEVYBS	906	F;1395/Binding site:	substrate phosphate (Arg) #status predicted		
1086	KLSNPPSAGAPIVYHCSAGAGRGTGCVYDIDLMDAEREQEVDDLYNCVKALESRRRNMVYCT	1145	Query	61.4%; Score 4793.5; DB 1; Length 1452;		
1081	KSKSPPSAGAPIVYHCSAGAGRGTGCVYDIDLMDAEREQEVDDLYNCVKALESRRRNMVYCT	1140	Best Local Similarity	61.3%; Pred. No. 1.4e-314;		
1144	EEQVTFIHADLLEAQLGETAVRKYIREYKQFHFTGWPDHGPVYTHATGILSFIRR	1205	Matches	Mis matches 325; Indels 29; Gaps 9;		
1141	EEQVTFIHADLLEAQLGETAVRKYIREYKQFHFTGWPDHGPVYTHATGILSFIRR	1200	Qy	22 LIGSALGQPSAGGCTPDDGQACDWHQDLDDPFTVHVSQAEQPHLPPENPQGSYMWDS 81		
1206	QAEDCSIACLPRNHDKNRFDMDPLPDRCLPFLTIDGESSNYINAALMDSYROPAAFVTT	1265	Db	14 LLLTAGETFSGGCFDEPYSTCGFSQADEDDENWBEQVNTLTKPTPSDPMNGPSGMVNT 73		
1201	RVEQVTFIHADLLEAQLGETAVRKYIREYKQFHFTGWPDHGPVYTHATGILSFIRR	1205	Qy	82 SNHDFGEKARLQLQPMKENDTHCIDSYSLLYSOKGLNPGLTUNLVTRVNKGPLANTPWNT 141		
1201	DIVRVLTEBLLAIVYVIRTPADPVEYQTCRLLQHLLPQKLNQVYKQKKEVYBS	906	Db	74 SGKPGQRAHLLPLKENDTHCIFDHYFVSSKSAAPGLUNVTVKVNNGPLGNPNTWNIS 133		
1201	DIVRVLTEBLLAIVYVIRTPADPVEYQTCRLLQHLLPQKLNQVYKQKKEVYBS	1080	Qy	202 DVEYNAQWATFOCATGDAVHNKLWLQRNGEIPVQATKRNHFRPASFRLOEVTK		
1141	EEQVTFIHADLLEAQLGETAVRKYIREYKQFHFTGWPDHGPVYTHATGILSFIRR	1200	Db	142 GFTGRDWLRAELAVSTFWPNEYQVIFEAEGGGRSGYIAADDIQVLSYPCDKSPHFLRLG 201		
1206	QAEDCSIACLPRNHDKNRFDMDPLPDRCLPFLTIDGESSNYINAALMDSYROPAAFVTT	1265	Qy	134 GDPTTWHRAELAISTFWPNEYQVTFEV-VTSQHGPCTTRPFLRIO 192		
1201	RVEQVTFIHADLLEAQLGETAVRKYIREYKQFHFTGWPDHGPVYTHATGILSFIRR	1260	Db	126 TDQDLYRCVTOQSERSGVSNFAOLIVREPRPPIAPPQLLGVPYTLQIONANS1GDP 321		
1266	QYPLPNTYKDFWRLUYDGCSTIUMNVEDSLQSCOPWYEGMRLYGPQECMSCMD	1325	Qy	193 NVEYAGQAFATFOQSAGITVAGDYLWLGIDVRAPIKEIVTSSRRETFASENVNTTK 252		
1261	QHP4LPNTVDFWRLUYDGCSTIUMNVEDSLQSCOPWYEGMRLYGPQECMSCMD	1320	Db	253 RDAGYRCMTCETGGVGISYNAELUVVKEPVPPVAPPQLASVATYLMQLNANSINGDGP 312		

Qy	322 IILKEVYRMTGSWTTETHAVNAPTYKLLWILDPEPTEYEIRVLLTRPGECGTGLPGPPPLIT	381	Db	1381 GEGPTVHCLNGGRSGTCAISIVCEMLRHQRVTDVHAKTILRNKNPVMVDLIDQYKF	1440
Db	313 IVAREVECTASGSYNDRPUDETSYKIGHLDPDTEYESVLLTRPGECGTGSGPALIT	372	Qy	1446 CYDVALEYLES 1456	
Qy	382 RTKCAABPMRTPEKTLKIAEIQARRIAYDWESIGNYNTCRCHTFENNTICHYFRGHINESRAD-	440	Db	1441 CYEVALEYNS 1451	
Db	373 RTKCADPMGRPKLVEEVKRSQITIRWEPFGYNTCRCHSYNLTHYGTQVGGEQVRE	432			
Qy	441 -CLMDPKAQCQHVUNHLPPTYNVSLKMILNPREGKESESETIQTQDYPGPVVKSLG	499			
Db	433 VSWDTDNSHQQTHTNLSPPTYNVSKLILNPREGKESEQBLTIVQDLEPGAVTSTG	492			
Qy	500 TSFENKIFLWKEPPLPQNGGITQDVEVSYSIISRSDPAVYAGPPOTVSILWNSTHVFNH	559			
Db	493 SAFEKKIFLQMRREPPTQGYVILIEITYKAVSSFDPEIDLSNQSGRVSLGNETHFLFG	552			
Qy	560 LHPGTYOFFRASYTKGFGPATAINVTNTNISAPSALPDYEGVDASLNFTATTITVLLRPA	619			
Db	553 LYPGTYSFTIRASTAKGFPATNQFTKISAPSMPATE-FETPLNQTDNTTVMLKEA	611			
Qy	620 QAKGAPIASQYQIVYBOLHPHRTKREAGABCYQVFTYQNALSGAPPTFAAEELPPGNIP	679			
Db	612 QSRGPVSYQIVVEERPARTKCTEILCKCYPPIFHQNATILNSQYFAAERPDSI-LQ	671			
Qy	680 EPAPETVGDNRTYKGFWNPPLAPRKGYNTYQFOAMSSVEGETKTQCVRIATAEPEPV	739			
Db	672 AAQPPTIDGNKTYQWNTPLPHPSKSYRIVYQASRANGEKIDCVRATVKAVTPKP--	729			
Qy	740 IPDAKQTDRVKLAGISAGILVFILLVVIVVTKSKKLAKERKDAMGNTROEMTHMN	799			
Db	730 VPEPEKQTDTVKLAGIVAGILFVIFGVLYMKKRCLAKERKETMSSTRQEMTMVN	789			
Qy	800 AMDSYADQSTLHAEDPLSLTMDOHNFSPRLNDP-----LYPTAVL-DENH	846			
Db	790 SMDISYAEQSTNCDE--AFSFMGTHNGLNRGSVSSPSSFTMKINTLSTSVPNSYYPDETH	846			
Qy	847 SATAESRRLLDVPY-LC83ETSYQTGQHPAIRVADLQLQHNTMKTSDSYGFKEYES	905			
Db	847 TMASDTSSLAQPHTYKKGREADAVPQTGQHPAIRVADLQLQHNTMKTSDSYGFKEYES	906			
Qy	906 FFEQGOSASWDVAKKDNRAKRNRYGNLIAVDHSRVLQPYEDDPSDDYINANYIDIWLYRD	965			
Db	907 FFEQGOSAPDSDAKPSACKDENSRMNQNYGNLIAVDHSRVLQMDNNSDTINGNYI-----D	960			
Qy	966 GYQPRSHYIATQGPYHETVDFWRNWQEOSACIYMWTLIVEGRVVKCYKWPDDTEVY	1025			
Db	961 GHREPHNYIATQGPQETI DFWRMWVWHENTASIMMVNEGRVKCCCKWPDDTEYK	1020			
Qy	1026 DFKVTCVEMPLAETVVRFTLERRGYNEIREVKOFHFTCPWDHGVPYHATGLLFSIRV	1085			
Db	1021 DIKVTLDITELLAEVIRPAVEKGIIHIREIROFHFCTWPWDHGVPYHATGLLFSIRV	1080			
Qy	1086 KLSNPPSAQPTVWCHCSAGAGRFTGCVIVIDIMLDMBAREGCVYDIYNCVKALRSRINMYCT	1145			
Db	1081 KSKSPNAGPLVVCWCSAGAGRFTGCVIVIDIMLDMBAREGCVYDIYNCVRELRSSRNNYCT	1140			
Qy	1146 BEQYIPIHDALEALCGEPAIPCEBFKAAYFDMIRDSCTNSHLLKDFQTLNSVTPL	1205			
Db	1141 BEQYIPIHDALEALCGDTSIPASQVRSIYDANKLDDQTNSSQIKEFRTLNMTPL	1200			
Qy	1206 QAEDCSIACLPRNHDQKRNFDMLPPDRCLPLFLITDGEESNNYNAALMDSYROPAFTW	1265			
Db	1201 RVEDCSIALLPRNHEQRNCDLPPDRCLPLFLITDGEESNNYNAALMDSYKQPSAFTW	1260			
Qy	1266 QYPLNPTVXDFWRLTYDGGCTSIYMLNEYDLSQGCPQYHNGPMLRYGPQYECMSCMD	1325			
Db	1261 QHPLNPTVDFWRLYDHTCTSVMLNDTPAOLCPQYHNGPMLRYGPQYECMSCMD	1320			
Qy	1326 CDDVNRIFRCNLTRPQEGLYVQOFQYLGWASHREVPSPSKRSFKLIIQVKWQEECB	1385			
Db	1321 EDILSRIFRYNAASPQDGHMVOQFQLGWPMTDTPSKRSFKLIIQVKDQEEYNG	1380			
Qy	1386 GEGRTIHLNGGRSGMFCAIGIVVEMYKRNQYNTDVFAVKTLRNRSKCNMVEAPEQYRF	1445			
Db	384 MRAPGLAPEIQRQLTQWEPLGVNTIRECVKTE	443			

RESULT 5

JCS290 protein-tyrosine-phosphatase (EC 3.1.3.48) - human

N;Alternate names: Phosphotyrosine phosphatase

C;Species: Homo sapiens (man)

C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C;Accession: JCS290

A;Reference number: JCS290; MUID:90723402; PMID:9070223

A;Accession: JCS290

A;Molecule type: mRNA

A;Residues: 1-1436

A;Cross-references: UNIPROT:000197; GB:U73727; NID:91923222; PID:AA851343.1; PID:919232

C;Comment: This enzyme belongs to type II receptor protein tyrosine phosphatase which mainly consists of an immunoglobulin-like domains.

C;Genetics:

C;Gene: hPTP-J

C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat -tyrosine-phosphatase homology <WAN>

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatases

F;203-266/Domain: immunoglobulin homology <IMM>

F;288-366/Domain: fibronectin type III repeat homology <3PR>

F;826-1436/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F;903-1123/Domain: protein-tyrosine-phosphatase homology <PTP1>

F;1193-1418/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;1075/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1081/Binding site: substrate phosphate (Arg) #status predicted

F;1376/Binding site: Cys (phosphocysteine intermediate) #status predicted

Query Match 59.1%; Score 4619; DB 2; Length 1436;

Best Local Similarity 60.4%; Pred. No. 8.2e-303; Matches 866; Conservative 203; Mismatches 329; Indels 36; Gaps 12;

Query Match 32 AGGTCTFD---DGGCACDYHQDLYDFFENYVSAQEPHYPPEMQGSYMVVDSSNNHDGSE 88

Db 24 AAGCTTEEASDPAVCEYSSQAQYDFOEQVRIHPGTRAPADLPHGSTYLMVNTSQHAPGQ 83

Qy 89 KARLOLPTMKENDTCHIDSYLILYSQKGLNPGTILILYRVKGQLANP1WNVTFGTGRDW 148

Db 84 RAHVTFQSLSENDDTCVQFSYFLYSDRGHSPTLGGVYRVMGFLPSATWMMTGSHGROW 143

Qy 149 LRAEALAVSTFWPNKEYQVIFPEAEVSGGRSGXIAIDDIQVLSYPCDKSPHFLRLGIVEVNAG 208

Db 144 HQAEALAVSTFWPNKEYQVLFPEALISPDRTSYGMGLDILLSSYPCAKAPHSRLGIVEVNAG 203

Qy 209 QNATFQCIATGRDAVHNKLQQRNGEDI1PVAQTKINHRRFAASFRLOEVTKTDQDLYR 268

Db 204 QNASFQCMAGRAEAERFLLQRLQGALVPAAGYTRISHRRELATPLAAVSRAEDQLYR 263

Qy 269 CVTOSERGSGVSNPAQLIVREPPPAPQLLGGVPTYLQIANS1IGDPLILKEV 328

Db 264 CVSQDAPRGAGVSNPAELIVKEPPTIAPQOLLRGGPTLIIQIANTS1IGDPLIVRKE 323

Qy 329 YRMTSWSNTETHAVNAPTYKWLHDPDTEYEIRVLLTRPGEGTGCPGPPLITRKCAEP 388

Db 324 YRMARGPWAHVLSQTYKWLHDPDTEYEISVSLTRGQDGGTQGPPLISKRCAEP 383

Qy 389 MRTPKTLKIAEIQRARIADVWESLUGYNTRCHTFENVTICHYFRG--HNESRADOLDMDP 446

Db 384 MRAPGLAPEIQRQLTQWEPLGVNTIRECVKTE

Qy 388 GEGRTIHLNGGRSGMFCAIGIVVEMYKRNQYNTDVFAVKTLRNRSKCNMVEAPEQYRF 443

Qy 447 KAPQHVNHLPPYTNSLKMILTNPGRKESEETIQTDEDVPGPVVKSLQGTFSFNK 506
 Db 448 GVSRTYKINNLRYRNVRVLITNPSRKEGVTFQTDVEVPSGAAESTFTPLEDMI 503
 Qy 507 FLWKEDPEJEPNGLITQYEVSSIRSFDPAVAGRPOTYSNLNSTTHYFMMHLHPGTY 566
 Db 504 FLKWEEOQPNGLITQYEVSTOSIESSDPAVNVPGRRTISKLRLNETHYFNSLHPTGY 563
 Qy 567 QFFIRASTVKRGCPATAINTNTNISPLPDYEGVDAISLBETATITVLRPAQKGAPI 626
 Db 564 LFSVRARTGKGFQQAALTEITNTNISAPF-DYADMSPLGESENNTVLRPAQSGAPI 622
 Qy 627 SAYQIVIVEQLPHRTKREBAGAMECYQPVTVYDGGAPPAELPGLNLPPEAPFTV 686
 Db 623 SYQVIVBEERARRLRRPGODCFPPITEAALRGLVHFGAHLAASSLPEAMPFTV 682
 Qy 687 GDNRTYKGFWNPPLAPRKGNYIQFOAMSVEKETKTOCVRATAATEEPEVTPDKQ 746
 Db 688 GDNQTYRGFWNPPLPERKAYLITYFQARASHLKGDTRLNCRARKACKERSKRPL-EVSQR 741
 Qy 747 TDRVVKTAGISA-GILVFLILLVVVTKSKLAKKRKDAMNTQEMTMVNAMDRSY 805
 Db 742 SEEMGLLIGICGGLLAVILLGIGLAVIIVTRGKPYNMTC-ATVNTROEKTHMMSAVDRS 800
 Qy 806 ADOSTLHAEDPLSLTFMDQHNSPRLEPLNDPLVPTAVLDENHSATAESSRL-DVPRYLC 864
 Db 801 TDOSTLDEDERGLSFMDTHGYSTR-----GDRQRCGVTIASLIGGSPPRPCG 849
 Qy 865 GTESPYQTGOLHPAIRYDILQHINLMKTSDSYGFKEEYESFFEGQSAASNDVAKKDQNR 924
 Db 850 RKGSPTXHTGOLHPAVRYDILQHINQNKTAEGFKQEYESFFEG---WDATEKKDKV 905
 Qy 925 KRYGNITAYDHSRVLQPVEDPSSDXYINANYIDWLWYRIGYQPSHXYIATQGPVHETV 984
 Db 906 GSRQEPMPAYDRHVKLHPMLGDPNADYNTNANY----DGYHRENHFIATOGPKPEMV 959
 Qy 985 YDFWRMWYQEQSACIVMTNLVEGVRKYCKYKWPDDTEVYGFDTKVFCVMEPLAETVVRT 1044
 Db 960 YDFWRMWYQEHCSIVNTKLVEGVRYKCSRWPEDDTGAIKIMLVKTTLAETVVRT 1019
 Qy 1045 FTLLRGYNEIREVKOPHIFTGMWDHGYPYHATGLLSPTRVYKLSLQVPLTAASTPDA 1104
 Db 1020 FALTERRGYSARHEVRQFHTAWPEHGYHATGLATRRASTPDAGPVVIHCSGT 1079
 Qy 1105 GRIGCYTYDILDMAEREGVUDYNTCKALRSRRIMVOTEQYIFHDIALEACIGE 1164
 Db 1080 GRIGCYTYDILDMAESEGVDIYNCVKTLCSSRVNMTCIOTQYIFHDIALEACIGE 1139
 Qy 1165 TAIPVCEKTAAYFDMIRLDSQTSNLSH1RDEFOTLNSVTPRLOADECSACIPLRNHDKNRF 1224
 Db 1140 TIPVSEKATYKEMIRDQPSNMSQUREEFQTLNSVTPPLDVECSALLPRNDRKNS 1199
 Qy 1225 MDMLPPDRCLPFLITIDGESNNYINAALMDSYRQPAFVTOYPLNTVDFWRLVYDYG 1284
 Db 1200 MDLTPPDRCLPFLISTDSDNNYINAALTDSYRQPAFVTOYPLNTVDFWRLVYDYG 1259
 Qy 1285 CTSIVMLNEVDLSQG---CPOYTPERGMLRYGPQVOEMCSMDCDVINRFRICNLTRP 1341
 Db 1260 CTSIVMLNQLNQNSNSANVCLQWPEPGRQYQGIMEVEFMGTADEDLVAVFVONISRL 1319
 Qy 1342 QEGYLMYQFOQTGLWASHREVPGSKRSFLKLQVKEWQEEBEGEGRSTIHCLNGGRS 1401
 Db 1320 QESHLVVFHQFQFLRWSAARDTDSKKAHLHLLAEVDKMQ-AESGDRITVHCLNGGRS 1377
 Qy 1402 GMFCAIGIGVYEMVKRONTYDVFHAKTURSKENMYTAPEQYRFCYDVALEYLE 1455
 Db 1378 GTECACATVLEMRCHNLNVDVEFAAKTURSKENMVTMDQYHFCYDVALEYLE 1431
 Qy 1456 PLEDMLFLKWEQPOENGLTQYEVQYQIEVYDQYEGVDAISLNETATTIVLRLPAQ 620
 Db 1445 CQPLHHEPAAU-----SERSREYVLTNPEGRKEKGKEYVFTQDDEDPVPSGIAAESLFT 497
 Qy 1501 SFENKEFLWNKEPLEPENGITQYEVSYSRSFDPAVPVAGPPQTVSNLWMSTHLYFMHL 560
 Db 385 RAPKGLAFABIQARQQLQWEPLGNVTRCHTYTSLCYHTLGSSHINQTPRVCEDRDR 444
 Qy 441 CLDMDDKAQPHVNVNHPYPYTNLSKMLTNPEGRKESBTIQTDDVPGPVVKSLQGT 500
 Db 445 CQPLHHEPAAU-----SERSREYVLTNPEGRKEKGKEYVFTQDDEDPVPSGIAAESLFT 497
 Qy 561 HPGTYLTOFFRASVYKFGPATAINVNTNISPLPDYEGVDAISLNETATTIVLRLPAQ 620
 Db 557 HPGTYLFLSVGARTGKGFQQAALTEITVYISAPS-LDYADMPSPLGESENNTVILRLPAQ 615
 Qy 621 AKGAPISAYQIVVEQLH-PHRTKREAGAMECYQPVPTYQNALSGGAPYFYAELPPONLP 679
 Db 616 GRGAPISVQVTEEQGSRRLRREPQGQDCCFPVPLTFEAALARGVLDYFGBLAASSLP 675

QY 680 EPAPPTVGDNRTRYKGFWNPIPLAPRKGYNTYFOAMSSVEKETKTOCVRITALKAATEEPPV 739
 Db 676 EAMPPTVGDNKTYGRWNPPIPLEPKAYLYFQAASHLKGTRUNCIKARRAACKESRP 735

QY 740 IPDPAKQTDRVKLAGISA-GILYPILLIIVVIVKKS------LAKRKKD 785
 Db 736 L-EVSQRSEBMLGLIGCAAGLAVLILLGAIIVIRKRDHYASYYPKPVNMTK--- 790

QY 786 AMGNTROENTHMDNAMDRSYADOSTHLAEDPLSLTMDQHNSPRLPNPBLVPTAVLDEN 845
 Db 791 ATVNRYQEKTTHMMSAVDRTSDTSL---OPPGLSFEMDTGHYSR-----GPQ 835

QY 846 HS--ATAEESRLLDVPRYLQEGTESPYQTCQLHPAIRVADLQHTNLMTKIDSYGFKBEY 903
 Db 836 RSGGYTEASSLGGSPRPGRKGSPPYHVTQHLPAVRDILQHINQMTKAEGYFKQY 895

QY 904 ESFFEGQASASWDVAKDKDQNRKARYGNIAYDHSRVILQVPEVDPPSSDYINANYIDIMW 963
 Db 896 ESFFEG---WDAEKKKDKVKGSRQBPMPAYDHRVHLQHEMLGDENADINYI--- 946

QY 964 RDGYTORPSHYIATQCPVHETVYDFTRMWVHQEQAISACIUMTNLVYEGRYCCKWPDDEY 1023
 Db 947 -DGYHRSNRFIATQCPKPEMVYDFKRMWQEHCSISIIMTKLVEYAGCCKCSRWYEDSET 1005

QY 1024 YGDFKVTCTVEMPLAEYVVTFTLERRGNEIREVKOFFGWDHGTVYHATGCLSFR 1083
 Db 1006 YGDKIMLKVKTTETLAEVVTTFALEERRGYSARYEVQFFTAPEHGVYHTTLLAFLR 1065

QY 1084 RVKLSNPPSAGPTVYHCAGAGRTGCTYVTDIMLDMAREGVYDIDNCYKALRSRRIMWV 1143
 Db 1066 RVKASTTPDAGPIVHCSCAGTGRGTCYVTDVMDMABEGWVDIYCNCKTKLCSRVCNM 1125

QY 1144 QTEBOXIFHDIALEACIGGETAIPVCEKKAAYFDMIRDQSQNSHSLKDEFQTLNSVTP 1203
 Db 1126 QTEEQYIIFHDIALEACIGGETTIPVSEPKATYKEMIRDQPSNNSQSLREFTQTLNSVTP 1185

QY 1204 RLQABDCSIACLPANHDKRFMDMLPPDCPLPFLITDSSNTNAALMDSTYRQPAFT 1263
 Db 1186 PLDVEEYSAALLPNRNDQRSMVDPDRCPLFLISTDGSNNYINAALTDTSYRSAFI 1245

QY 1264 VTOYPLPLNTVKDFPLRVLVYDGTCTSVLMNJEVDSQG---CPOYWPEEGMLRYGP10ECM 1320
 Db 1246 VTUHPLQSTPDEFWRLVYDGTCTSVLMNQNSAWCLQTWPEPGRQQYGLMEVFIM 1305

QY 1321 SCSMDCDVNRIPRICLNTRPOEGYLMYCOFOQIIGWASHREVPOSKRSFLKLQVETKQ 1380
 Db 1306 SGTADEDLIVARFVYQNTSRQSLQEGHLLVHEOFLRWSAYRTDPSEKAFLHLLAEDKMQ 1365

QY 1381 BECGEGEQTIIHCLNGGRSGMFCAGIIVVEMYKRONVVDYPAVAKTLRNSPKNMVEAP 1440
 Db 1366 -AESGDGRTIVHCLNGGRGRTSCALRTYLEMRCHNLVDSPAAKTLRNPKNMVETM 1423

QY 1441 EOXYFCYDVALEYLES 1456
 Db 1424 DQYHFCYDVALEYLES 1439

RESULT 7
 150148 protein-tirosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R;Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
 Neuron 11, 387-400, 1993
 A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogenesis
 A;Accession: 150148; MUID:93357030; PMID:8352946
 A;Status: Approved; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1501 <WAL>
 A;Cross-references: UNIPROT:Q64605; GB:L19933; NID:9310242; PID:AAA42309.1; PID:9310243

QY 595 NVTTNISAPS-----LPD-----YEGYDASLN-ETATTIT 613
 Db 596 VCBTQLQASPKNEVKRMIMKTSVLSFPDYNSSPPYKIQYNGLTLVDGRTKLL 655

QY 614 VLLRP-----AQAKGAPISAYQIVVEOLPHRTKREA-----GAME 649
 Db 656 THLKPHTYFNFLVNGSSLGGHQQTV-----TARTAFNMUSGKPSVAKPDNDGSLV 708

QY 650 CY---QVPVTKONALSGCAPYPAELP-----PGNLP-----679
 Db 709 VYLPDGQSPVTVQN-----YFIVMVPLRKSRGGQPILLGSPDMDBELIQDLSRL 760

QY 680 -----EPAPFTVGDNRTRYKGFWNPLAPKGKYNFYQAMSS 715
 Db 761 QRRLRHSRQLEVERPYIAARFSILPAVEHPGNQKXQGGFDNRGLBEPGRYVLFVLA V-- 818

Qy	749	RVVKLAGISAGILVFILLVVIT-VIVKKSKLAKKRKDAMGNTQEMTMVNAMDRTSYAD	807	A; Molecule type: mRNA A; Residues: 1361-1604; '1649-1898 <HAS> R; Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
Db	847	GBEGLIWIWGVLAFFVPIICIVIALLYKKRPDKDSRKDKS-----	885	J. Biol. Chem. 266, 19688-19696 1991 A; Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic domain of the rat G-protein α_i1₁ protein kinase A; Reference number: A41032; MUID: 92011772; PMID: 1918076
Qy	808	QSTLHADPLSLTMDQHNFSPRLPNDPLPTAVLDENHNSATAECSRLLDPRVLCEGTE	867	A; Molecule type: mRNA A; Residues: 1035-1072; 'S', 'T', '1074-1433; 'T', '1435-1638; 'N', '1640-1642; 'HT', '1645-1898 <PO2>
Db	886	-----EPRTKCLINNAELTPHHPKDPV-----	912	A; Cross-references: GB:M6103; PID:9205130; PID: AAC37655.1; PMID: 9205131 R; Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E. submitted to the Protein Sequence Database, December 1990
Qy	868	SPYQT-GQL-HPAIRVADLQHINMKTSDSYGKPEBYESSEFGEGASASDVAKEKDQNRAK	925	A; Molecule type: mRNA A; Residues: 1035-1072; 'S', 'T', '1074-1433; 'T', '1435-1638; 'N', '1640-1642; 'HT', '1645-1898 <PO2>
Db	913	-NFQTPGMLSHSPPIPSELLAETHEHLKANDNLKLQSBEYESIDPGQOPTNEHSNLEVNPK	971	R; Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
Qy	926	NRYGNLTAYDHSRSVTLQPVEDDPSSDYYTINANVYD1WLYRDGYQRPSPHYATQGPVHETYY	985	A; Reference number: A33154 A; Accession: A33154 A; Molecule type: mRNA A; Residues: 1035-1072; 'S', 'T', '1074-1433; 'T', '1435-1638; 'N', '1640-1642; 'HT', '1645-1898 <PO2>
Db	972	NRYANVIAYDHSRSVLLPIBGSIVGSDBYINANVY-----DGYRKONAYATQGPVLPETRG	1025	C; Comment: Only the first of the two domains homologous with protein tyrosine phosphatases C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy
Qy	986	DFWRMWQEQSACIUMVNTLVYEVGRVKCYXWPD-DTEVYGDPRVTCVMEPLAEVYVRT	1044	C; Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; t
Db	1026	DFWRMWQEQSACIUMVNTLVYEVGRVKCYXWPD-DTEVYGDPRVTCVMEPLAEVYVRT	1085	F; 1-27/Domain: (or 1-26) signal sequence #status predicted <SIG> F; 28-125/Domain: (or 27-125) leukocyte antigen-related protein #status predicted <MAT> F; 41-109/Domain: (or 27-125) extracellular #status predicted <EXT>
Qy	1045	FTLERRGYNEREVQFHFGWPDIGVPHATGLLSFIRVKLNSLPPSGACPIVVHCSAGA	1104	F; 149-203/Domain: immunoglobulin homology <IMM1>
Db	1086	FSLHKNGSSERKREVQFQTAWPDGVPVTPPFLAFLRKVKTNPPDGVPVIVHCSAGV	1145	F; 246-300/Domain: immunoglobulin homology <IMM2>
Qy	1105	GRTCGYCIVTDIMLDMAEREQSYVDIYNCVKALRSRRINMMQTEQYIFHDALEAACLGEE	1164	F; 318-400/Domain: immunoglobulin homology <IMM3>
Db	1146	GRTCGYCIVTDIMDLERKFLTIDG-ESSNTYALMDSYROPAAFVTOPLPNVTKDFRVLVYX	1205	F; 413-492/Domain: fibronectin type III repeat homology <FN3A>
Qy	1165	TAIPVCEFKAYFDMDMIRSDQTNSSHLDQFQTLNSVTPLQAEDCSIACLPRMHDKNPF	1224	F; 511-591/Domain: fibronectin type III repeat homology <FN3B>
Db	1206	TEVAPRNLYTYIOKLAQIEVHGTMGELEFKRL--ANSKAHTSRFISIANLPCNKFKNFL	1263	F; 606-691/Domain: fibronectin type III repeat homology <FN3C>
Qy	1225	MDMLPDRCLPFLTIDG-ESSNTYALMDSYROPAAFVTOPLPNVTKDFRVLVYX	1283	F; 708-798/Domain: fibronectin type III repeat homology <FN3D>
Db	1264	VNINPYETTAVCLQPFRGEGSDTINASFDGTRQKANATQPLAETEDFIRMLWN	1323	F; 1276-1898/Domain: intracellular #status predicted <INT>
Qy	1284	GCTSTVMLNEVDL--SOGCCPQYWPEGMRLYQLOVECMSCSMCDVIRTRIFCNLTP	1341	F; 1386-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>
Db	1324	NSTIVVMLTQLREMGREKCHQYWPAERSARYQFVVDPA--SYNNMPQYLRFKVTA	1380	F; 1366-1878/Domain: protein tyrosine-phosphatase homology <PTP1>
Qy	1342	QEGY-LMVQOFOQYLGWASHREVPSSKRSFLKLLOVVKYQEBCBEGEGFTIHFLNGGR	1400	F; 1655-1878/Domain: protein tyrosine-phosphatase homology <PTP2>
Db	1381	RDGQSRTVNRQFOFTDW-PEGQVPKSGEGFDFIGQVHKTEQFGQ-DGPISVHCSCAGVR	1438	F; 1702-1079/Domain: fibronectin type III repeat homology <FN3H>
Qy	1401	SGMFRAIGITVWYKRNQVNYDVFHVAKTRKTRNSKPSNKEPEQTRCYDALEYLES	1456	F; 1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TMM>
Db	1439	TGVFITLSSLVLEMRYEGTWDIFQTVKMLR-TQPMVQFDETCYQDALEYLS	1493	F; 1276-1898/Domain: intracellular #status predicted <INT>
RESULT 9				
S4616		lenkocyte antigen-related protein precursor - rat		
N		Alternative names: leukocyte common antigen homolog		
N		Contains: protein-tyrosine phosphatase (EC 3.1.3.48)		
C		Species: Rat/ mouse/ human (Norway rat)		
C		Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004		
R	Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.	Accession: S46216; S23225; A41032; A33154	163 -YQVIFAEVSGGRGSGYIADDIQVLSPYC-DKSP-----HFLRLGDEVVNAG-----Q	241 QTRNINHRFAASFRQEVTKTDDOLYRCVTSERGSGVSNFQQLIVRBPPTAPPOLL 300
Biochem.	J. 302, 39-47, 1994	Biochem. J. 302, 39-47, 1994	487 RVIATFAVEDGPPPTQVPAQ-----ADFOQAK--ABSRTDQLSLWLPQERI 540	658 VVDS-----REHSSWDLGGEBKMTPEYVMVRAHSDLGVGVTPTVB 598
A	Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho	Accession number: S46216; MUID: 94347119; PMID: 8068021	541 IKVELVWVAAADEQHQKVTEDPTS--SYTLEDIKPDLYHFQLAARSDSLGVGVTPTVB 598	716 EVEPLNSTAVHVSWKLPVFNKQHQIRGQYQTVYRLENGEPRGQPIQD--VNLAAEAQET 773
A	nucleic acid sequence not shown	Accession: S46216	210 NATFQ-----CIATGRDAVHNKLWL---QREN-----GEDIPVA 240	
A	nucleic acid sequence not shown	Accession: S46216	599 ACTAQSTSAPPQKVTCSTGSTVRS-WVPPPADSRSGNITTOYSVAYAVDGE DRKHH 657	
A	Residues: 1-1898 <ZHA>	Accession: S46216	600 -----TFLLI-----QLNANSIIGDGPILIKEVYR 330	
R	Cross-references: UNIPROT:Q64604; EMBL:L11586; PID:9205132; PID: AAC37655.1; PMID: 9205131	Accession: S23126; MUID: 92287069; PMID: 1599938	601 GVGP-----TFLLI-----QLNANSIIGDGPILIKEVYR 330	
A	Reference number: S23126; MUID: 92287069; PMID: 1599938	Accession: S23252	602 -----EVEPLNSTAVHVSWKLPVFNKQHQIRGQYQTVYRLENGEPRGQPIQD--VNLAAEAQET 773	

Qy	331 MTSGSWTEETHAVNAPTYKLWHLDPDTEYEXIYV-LITRPGEGGTGLPGPLITRTKCAEPM	389	Qy	1264 VTOYPLPLNTVKDFWRLVYDYGCTSSVMLNEDVL-SQGCPOYWPERGMRLRYGPIOVECMS	1321
Db	774 TISG-----LTPETTYSITVAAYTTKGIDAR--SKPKVVTITGAVPG	813	Db	1702 ATQGLAEESTEDFWMLWEINSTIVMLFLREMREREKCHQYWPERMRSAYQKFVDPMA	1761
Qy	390 RTPKTLKIAEIQARRIAVDW-----ESGYNINTRCHITPNTVNTCYHYPFGHNESRADC	441	Qy	1322 CSMDCDVINRIFRICNLTRPOEGY-LMVQQFOYLGLWASHREPGSKRSFSLKLILQVEKWQ	1380
Db	814 R-PTMNVSTTAMHTAILQHIPPKEPLPGELLYGR-----QYRDAEARPNT	858	Db	1762 --ETMPQTLREKFTDARDGQTIROFQFTW-P-EQGVPKGEGPFDIGGPHHKTK 1817	
Qy	442 LDMDPKAPQHVNHLPPYTNSLKMILNPBGRKESBETLIQTDDEBPGPVP----VKS	497	Qy	1381 BECBCEGTRTHACNGGSRGMFCAGIGIVEMURQNVUDVFHAKVTKLBNSKPMEAP	1440
Db	859 IDFGKDQDHFTTGLHKGATYIFRLAKRNKGPFSEFEKETTPEDAPSFPQNLRVTGL	918	Db	1818 EQFGQ-DGPITVHCCSAGVGRTGVFTLTSIVLERMRYEGVUDMFQTVKTLTQRPMVQTE	1876
Qy	498 QGTSFENKIFLNKEPLI-EPNGITIQEVSYSSIRSFSDFPAPVAGPPOTVSNLWNNSTHH	555	Qy	1441 EQYRFCDYVALEYLS	1456
Db	919 TISTE---LAQDPPVLAERNGRITNTVYRDINS-----QHELQNVYGDVHL	964	Db	1877 DQQLCYRALEYLS	1892
Qy	556 VFMHLHPGCTYOFFIRASTVKFCGP-----ATAINVTINISAPS	594	RESULT 10		
Db	965 TLGLKEDPTTDIKVRAHTSKGAGPLSPSTIQSRTMPEQVFAKNFRVAAMKTSVILSWE	1024	TDHUIK	leukocyte antigen-related protein precursor - human	
Qy	595 LPD-----YEVDASLN-----BTATTITVLRPAQAKG-----623		N; Contains:	leukocyte common antigen homolog	
Db	1025 VPSYKSAAVPFKILYNGQSVEUDGHSMRKLIADLQNTTEVSFLNMRGTSGGLOHLVSI	1084	C; Species:	Homo sapiens (man)	
Qy	624 -----APISA-----YIIVV-----633		C; Date:	31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004	
Db	1085 RTAPDILPQKPLPASAFTEDREFSLSNPQVODPSLVRWFTIVVVVPIDRVGGNLLAIPRWT	1144	C; Accession:	S03844; JLU051	
Qy	634 -EQLH-----PHTKRSAGAMECYQPVTYQNALSGGAPYYFAELPPGNL	678	R; Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.		
Db	1145 PEELELDLEIAEQGEKERRQRRQAERLK-----PYVAAQV-DEL	1185	J. Exp. Med. 168, 1523-1530, 1988		
Qy	679 PEPAPFTVGDNTYKGFWNPPLAPRKGNUNYQAMSSVXETK-----TQCYRIATK	730	A; Title:	A new member of the immunoglobulin superfamily that has a cytoplasmic region hc	
Db	1186 PE-TFTLGDKNNYRGFYNRPLPSLSDYQCFWVLAISLKEPDMQRYASSPSDEIVVQVTP	1243	A; Reference number:	JL0051; MUID:89035578; PMID:2872792	
Qy	731 AAATEEPVIPDPAKQDTDVKLAGISAGILVILLVVIVVKSKLAKRKDAMGNT	790	A; Accession:	S03841	
Db	1244 AQQQEEPEML-----WVTPGLAVILILIVAI-----LJFPRK-----1278		A; Status:	nucleic acid sequence not shown	
Qy	791 ROEMTMVNAMDR--SYADQSTLHAEDPLSLTMQDNFSPRLNDPLVPTAVLDENHS	847	A; Molecular type:	mRNA	
Db	1279 --RTHSSPSXDEQSLICKDSLLAHSSDPMVRRLN-----1311		A; Residues:	1-189 <STR>	
Qy	848 ATAESSRLLDVPRYLECEGTESPYQTGOL--HPAIRVADLLOHNMKTSGYFKEYES	905	A; Cross-references:	UNIPROT:P10586; EMBL:Y00815; PID:CAA68754.1; PID:934267	
Db	1312 -----YQTPGMDHPIPITDLDNIEERLKAQDGLKFSOEYES	1349	C; Genetics:		
Qy	906 FPEQGOSAWWDVAKDONRAKRNQGNTIAYDHSRSVILQVEDDPSSDYTINANYIDIWYRD	965	F; Map position:	1p34-1p34	
Db	1350 IDPGQQPTWENSEVNPKPNYANVAYDHSRSVILQVEDDPSSDYTINANYIDIWYRD	1403	C; Superfamily:	leukocyte antigen-related protein, fibronectin type III repeat homology; C; Subfamily:	
Qy	96 GYORPHSHYIATQGPVHETVYDFWRMWTQEoSACIVMNTNLVEGGRVTKCYKWP-DDTEVY	1024	C; Keywords:	glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane	
Db	1404 GYRKONAYIATQGPVHETVYDFWRMWTQEoSACIVMNTNLVEGGRVTKCYKWP-DDTEVY	1463	F; 1-16/Domain:	glycan sequence #status predicted <SIG>	
Qy	1025 GDFKVTCVEMEPLAETYVFTLERRSYNEREVKOFHTGMPDHCVYPHANTGLUSPIR	1084	F; 17-189/Domain:	leukocyte antigen-related protein #status predicted <MAT>	
Db	1464 GLIQTIVLVDTVELATYMTMFLAHKGSSSERLQFQEMAPDHGVPEYPTPILAFIRR	1523	F; 17-125/Domain:	extracellular #status predicted <EXT>	
Qy	1085 VRLSNPPSAGPIVHCSAGAGRTGCVIYD1MIDMAEREGVYD1NCVKALRSRINMVQ	1144	F; 17-99/Domain:	immunoglobulin homology <IMM1>	
Db	1524 VKAQNPLDAGPMVHCSAGVGTGCFIVIDANLEMKHTDQFVLTQPRGEVDYTNASVTPR	1204	F; 139-199/Domain:	immunoglycoprotein; phosphoric monoester hydrolase; transmembrane	
Qy	1145 TEEQYIPTHDIALEACIGETAIPVCEFKAAFDMDIRIDSQTSQNSHSLKDEFQTLNSVTPR	1204	F; 1-16/Domain:	immunoglycoprotein; phosphoric monoester hydrolase; transmembrane	
Db	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1-16/Domain:	immunoglycoprotein; phosphoric monoester hydrolase; transmembrane	
Qy	1205 LOAEDCSIACLPRNHDKRFRMMDLPPDRBLPLITDG-ESSNYTAALMDSYROPAIFI	1263	F; 1367-158/Domain:	protein-tirosine-phosphatase homology <PTP1>	
Db	1642 APASRFISANTLPCNKFCKRNLVIMPYELTRVCIQPTRGVEGSDYTNASVTPR	1701	F; 1654-187/Domain:	protein-tirosine-phosphatase homology <PTP2>	
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 44-57,16-19/243-388/Disulfide bonds:	#status predicted	
Db	1829 Active site: Cys (phosphochysteine intermediate) #status predicted		F; 1001-1018/Domain:	carbohydrate (Asn) (covalent) #status predicted	
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1251-1274/Domain:	fibronectin type III repeat homology <FN3H>	
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 1275-1589/Domain:	transmembrane #status predicted <INT>	
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1285-189/Domain:	intracellular #status predicted <INT>	
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 1367-158/Domain:	leukocyte common antigen cytosolic domain homology <LAC>	
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1367-158/Domain:	leukocyte common antigen cytosolic domain homology <LAC>	
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 1654-187/Domain:	protein-tirosine-phosphatase homology <PTP1>	
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 44-57,16-19/243-388/Disulfide bonds:	#status predicted	
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 107-240,285,711,936/Binding site: carboxyhydrate (Asn) (covalent) #status predicted		
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1538/Active site: Cys (phosphochysteine intermediate) #status predicted		
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 1544/Binding site: substrate phosphate (Asp) #status predicted		
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1829/Active site: Cys (phosphochysteine intermediate) #status predicted		
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 1835/Binding site: substrate phosphate (Asp) #status predicted		
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	Query Match 19.1%; Score 1492.5; Length 1897;		
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		Best Local Similarity 28.9%; Pred. No. 9.6e-92;		
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	Matches 469; Conservative 211; Mi matches 551; Indels 393; Gaps 59;		
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		F; 1829/Active site: Cys (phosphochysteine intermediate) #status predicted		
Qy	1584 TEDQYVFTHEALLEAAMGHTEVARNIYAH1QKLGYOPGESVTAMELFKL--AGSK	1641	F; 1835/Binding site: substrate phosphate (Asp) #status predicted		
Db	1835 Binding site: substrate phosphate (Asp) #status predicted		Query 68 PPEMPQG-----SYMVVDS-----SNHDPGEKARLOPLTMKENDTHCIDFS--YL 110		

A; Experimental source: Pre-B cell NALM-6	581	-----ATAINTVNISAPSPLPD-----	YEVVDASL 605
A; Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBI:P:78087)	1008	SVQFTTLIPIDQVFAKNEFVKAVMRKTSVLSWEIPEYNAMPPFKLYDDGKRAVEVDGRA 1067	Db
C; Genetics:	625		
A; Gene: GDB:PTPRD	606	NETATTITVLLRPA-----AKGAP-----	Qy
A; Cross-references: GDB:131384; OMIM:601598	1068	:-----TQ----KLIVNLKPESPKSYFVLNNGNSAGGLQHRVTAKPADVLTKPAFIGTNLDGM 1124	Db
A; Superfamily: 9p24-9p24	626	-----ISAYQIVVEQLHLHRTK----REAGAMECYQ-----PVTYON 659	Qy
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology	1125	TQQLPEPV PANENIKCXYVLLVPLKRSRGKPKWESPDMEDELLEILKEISKRRSIRYGR 1184	Db
Ogy	660	ALSGGAPYFAAELPGNLBEPAPPTVGDNRTYKFWNPPLAPRKGINYVQAMSVERE 719	Qy
C; Keywords: Glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane	1185	:-----EVB-LKPYIAAHFD---WLPTETLGDKHYGFTPNKOLQSGBY-VFVFLAYMEHA 1237	Db
F; 38-100/Domain: immunoglobulin homology <IMM1>	720	TKTQCVRATKAATTEPEVTPDPKOTDRVKLAGISAGL----VFILLLUVTVKKS 777	Qy
F; 140-209/Domain: immunoglobulin homology <IMM2>	1238	SK---MYATSPSSPVVSNDLDPDPEITDEBGLWVGVPLAVYFICIVIAILYKRK 1293	Db
F; 250-304/Domain: immunoglobulin homology <IMM3>	778	KL-ARKRKDAGNTFQEMTHMVNANDRSYADQSTIHAEDBLSLTMDQHNFSPRLNDPL 836	Qy
P; 711-811/Domain: fibronectin type III repeat homology <3FR>	1294	RAESRSRKSS1PNNCKIPSH-----HPTDPVELRLN-----1325	Db
P; 129-192/Domain: leukocyte common antigen cytosolic domain homology <LA C>	1326	-----POTPGKMSHP-----	Db
P; 1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>	837	VPTAVLDENHSATABSSRLLDVPRYLCEGTESPYQGQ-----	Qy
P; 1553/Active site: Cys (phosphocysteine intermediate) #status predicted	1354	-----HQPAIRVADLQLQHINLMKTS 894	Db
P; 1844/Binding site: substrate phosphate (Arg) #status predicted	1355	-----POTPGKMSHP-----	Db
P; 1850/Binding site: substrate phosphate (Arg) #status predicted	1356	-----	Qy
Query Match	19.0%	Score 1482.5; DB 2; Length 1912;	
Best Local Similarity	27.2%	Pred. No. 4.6e-91; Mismatches 534; Indels 487; Gaps 57;	
Matches 464; Conservative 222; Mismatches 534; Indels 487; Gaps 57;			
Qy 51 YDDFEW-----VHVSQAOPHYLE-----PEMPQ 73			
Db 386 YSDYEFRVAVNNIGRGPSEPVLTQTSQEAPSSARDVQARMLSLSTTLLQWKEPEEPN 445			
Qy 74 GS-----YMWVDSNHFDPGEKARLQLPTMKEN--DTHCIDFSYLL---YSQKGLNPGT 121			
Db 446 GOIQGYRYYTMPTQHVN-----WMKHNVNAISOQTITIGNLVPKQTYSVKV-----493			
Qy 122 LNLIYRVNKGPLANPTNWVTFGTGRDWLRAELAVSTFWPNEXQVTFEAEVSGGRGSIYAI 181			
Db 494 --APTSIGDGPSSDI-----QVITQTVPG-----517			
Qy 182 DDIQVLSYPCD-KSPHFLRLGDVEVNAGQNATFOCIATGRDAVHNKLWLRQRNGEDIPVA 240			
Db 518 --QPLNFKAEPESETSSILLSWTPRSDTIANTELVY---KDGEH-----GEE-----559			
Qy 241 QTKNINHRRFAASPRLOBEVTKTDQDLYRCTOSERGGSVNSFAQLIVR-PPRPPIAPPQL 299			
Db 560 QRTIEP---GNSYRLQGKPNISLYTFLAARSPOGIGAST-AEISARTMQSKPSAPQD 615			
Qy 300 LGV---GFTYLITQLNANSIIGDGPITLK-EVEYRTGSMTETHAV-----NAPYTKLW 350			
Db 616 ISCTSPSTSILSVWQPPVEKONGTIEYSIKYTAVDGEDDKPHELGIPSDTKYL 675			
Qy 351 HLDPDTBEVIRLTLTRPEGGTGLPGPLITRKCABPMTPTKTLKIAEIARRIAVDE 410			
Db 676 QLEKWTYY--RITVTAHTDVGPGPESTLVSUPLRKTNTEDPSGPBRKVEAVNSTSVKWSWR 733			
Qy 411 S-----LGYNITRCHTFNVTICHYFRGHN-----435			
Db 734 SPVPNKQFGQIREXQV-----HYRMENGKRGQFQMLKDVMЛАAQWEFDDTT 781			
Qy 436 -----ESRADLDMDPK-----APDHVVNHLPPTVNV 463			
Db 782 EHDMIISLQPETSYSLTVTAYTKGDBARSKPVLVSTGAVPGKPRVINH---TQMN 837			
Qy 464 LRMILTNP-----GRK-----ESEETIICD-----485			
Db 838 TALIQWHBPVDTGFLQCYRLKGDKDMEPLTLEFSKEDIFTADIHKGASYVRLSA 897			
Qy 486 -----EDVGPVPUVKSLOGTSFENKFLNKEPL--EPNGLIIQYEV 526			
Db 898 RNKVGFGGEEMVKRISIPEBVPTGCFPONLHSEGSTSTSVOLOSSKPPVLAERNGLITYKYL 957			
Qy 527 YSSIRSFFDPAVPGAG--PPQTVSNLNWNSTHAYFMHILHGTYQFFTRASTVKGFGP---580			
Db 958 YRDINI--PLLPMEQLIVIUPADTTMTLTC-----LKPDITTYDVKURAHTSKGPFYSP 1007			
RESULT 12			
A48758 RNSKPNVNEAPEQYRCYDVALEYLES 1456			
Db 1765 RYQYFVUDPM-----EYNMPOYTLREPKVTNDARQSRTRVQFFDTW-PEOGVPKGEGP 1820			
Qy 1370 LKLILLOVEKWBECBEGERTLICHNGGRSGMFCAGIGIVVEMVRQNTVDFEHAVKTL 1429			
Db 1705 IDGyroQKAYATQGPAAETEDFWMLWEINSTVVMLTKLREMGREKCHQYWAERSA 1764			
Qy 1311 RYGPQVECMCSMCDVINVPLFICNLTROEGY-LMVQOQYQLGWASHREPVGSKRSF 1369			
Db 1766 EFKRAS--SKAHTSFISIANLPCFKENPKNLUNVNPYESTRVCLQ-----			
Qy 1253 MDSYRPAAFIVTOYPLNPTVKDFWRLYDGTCTIVMLNEVDL--SQGCPOYWPREGML 1646			
Db 1587 LMRAQNYMOTEDOYIFIFHDALLAETCCTENTEPARNLYTAYQLQTLQIEGENTTGME 1586			
Qy 1194 EFQTMNSVTPLQAOEDCSIACLPRHDKNRFMDMLPDRCLPFLITDG-ESSNINNAL 1252			
Db 1647 EFKRAS--SKAHTSFISIANLPCFKENPKNLUNVNPYESTRVCLQ-----			
Qy 1074 HATGLLSFTTRVKLSNPPSAGPIVHCSAGAGRGTGCVIVDILMAEREQVWIDYNCVK 1133			
Db 1527 HPTPFLAFLRVKTNCPDPGMVHCSAGYGRGTFIVIDAMLERIKHEKTVDFIGHVT 1586			
Qy 1134 ALRSBRINNMOTEEQYIIFIDAILFACLGSTIAIPCEKFKAAYFMDMIRIDSQTSNSSLKD 1193			
Db 1587 IMAQNYMOTEDOYIFIFHDALLAETCCTENTEPARNLYTAYQLQTLQIEGENTTGME 1646			
Qy 300 LGEV-----GFTYLITQLNANSIIGDGPITLK-EVEYRTGSMTETHAV-----NAPYTKLW 350			
Db 560 QRTIEP---GNSYRLQGKPNISLYTFLAARSPOGIGAST-AEISARTMQSKPSAPQD 615			
Qy 351 HLDPDTBEVIRLTLTRPEGGTGLPGPLITRKCABPMTPTKTLKIAEIARRIAVDE 410			
Db 676 QLEKWTYY--RITVTAHTDVGPGPESTLVSUPLRKTNTEDPSGPBRKVEAVNSTSVKWSWR 733			
Qy 411 S-----LGYNITRCHTFNVTICHYFRGHN-----435			
Db 734 SPVPNKQFGQIREXQV-----HYRMENGKRGQFQMLKDVMЛАAQWEFDDTT 781			
Qy 436 -----ESRADLDMDPK-----APDHVVNHLPPTVNV 463			
Db 782 EHDMIISLQPETSYSLTVTAYTKGDBARSKPVLVSTGAVPGKPRVINH---TQMN 837			
Qy 464 LRMILTNP-----GRK-----ESEETIICD-----485			
Db 838 TALIQWHBPVDTGFLQCYRLKGDKDMEPLTLEFSKEDIFTADIHKGASYVRLSA 897			
Qy 486 -----EDVGPVPUVKSLOGTSFENKFLNKEPL--EPNGLIIQYEV 526			
Db 898 RNKVGFGGEEMVKRISIPEBVPTGCFPONLHSEGSTSTSVOLOSSKPPVLAERNGLITYKYL 957			
Qy 527 YSSIRSFFDPAVPGAG--PPQTVSNLNWNSTHAYFMHILHGTYQFFTRASTVKGFGP---580			
Db 958 YRDINI--PLLPMEQLIVIUPADTTMTLTC-----LKPDITTYDVKURAHTSKGPFYSP 1007			
Species: Rattus norvegicus (Norway rat)			

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	QY	681 -----PAPPTVGDNRTTYKGFWNPLPLAIPKGYNIVFQAMSSV 716
C:Accession: A48758	Db	760 RRSRHSRROLEVPPIAARFSTLPAVFGNQKQYGGDNRNGLPGRHRYVLFAV--L 817
R:Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.		
J: Biol. Chem. 268, 1984-19291, 1993		
A:Title: Cloning and expression of two structurally distinct receptor-linked protein-typ	QY	717 EKETKTQCVTRIATAATEPEV-----PDAKQTDTRVKVIAAGILVPLILLVVI-VI 773
A:Reference number: A48758; PMID:8396131	Db	818 QKNEPT-----PAASPSDPFDQLNDPDEQPIVGEELWIGPVLAIVLICIVIAIL 871
A:Status: preliminary	QY	774 VKGSKRLAKERKDANGNTQEMTMVNAAMDTSYADQSTLHAEDPLSLTPMDQHNSPRLPN 833
A:Molecule type: mRNA	Db	872 LYKXNPLDADLAPPHPK 903
A:Residues: 1-1496 <PAN>	QY	834 DPLVPTAVLDENHSATABSSRLIDVPRVLCGETTESPYOT-GQL-HPAIRVADLQHINLM 891
A:Cross-references: GB:L19180	Db	904 DPV-----EMRRI-----NFQPGMUSHPPLIPITDMABHMERL 936
A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as Gl		
as Phe		
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;		
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; transm	QY	892 KTSDSYGFKEEYESPFFEGOSASMWDAAKKDQNRAKKNRYGMIAVDHSRVTLPQVEDDPSSD 951
F:149-209/Domain: immunoglobulin homology <IMM1>	Db	937 KANDSLKLUSQEYESSIDPGQQFTWEHSNLNEAKNCPRNRYANVIAVDHSRVTLPQLEGIMSSD 996
F:246-300/Domain: immunoglobulin homology <IMM2>		
F:318-405/Domain: fibronectin type III repeat homology <FN3A>	QY	952 YINANYIDIIWLGYQRPSPHYIATQGPVHETYYDFWMTWVQBSACITVMVTNIVVEGRV 1011
F:411-504/Domain: fibronectin type III repeat homology <FN3B>	Db	997 YINANYV----DGYRRONAYIATQGPPIPETGDFWRMWWEQSATVMMTRLEKSRV 1050
F:509-599/Domain: fibronectin type III repeat homology <FN3C>		
F:600-684/Domain: fibronectin type III repeat homology <FN3H>	QY	1012 KCVXWPD-DTEVYGFDFKVTCVEMEPLEYWVTFLLERRGNEIREYKQFHFTGWPDHG 1070
F:1256-1497/Domain: leukocyte common antigen cytosolic domain homology <LAC>	Db	1051 KCDGQWPNRGTTGFQVTLQDLMELATPCVTFSLHKGSSKREYRHFQFTAWPDG 1110
F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted	QY	1071 VPIHATGLLSFIRRVKLSNPPSAGPPIVYHCSAGAGRTGCVIYIDIMILDMAEREQVYDYN 1130
F:1146/Binding site: substrate phosphate (Arg) #status predicted	Db	1111 VPEPYPTPFLAFURVKTCPNPDPGVVYHCSAGYGRGTFIVIDAMLERIRTEXTVDYG 1170
F:1449/Active site: Cys (phosphocysteine intermediate) #status predicted	QY	1131 CVKALRSRRINMVQTEEQVIFIDIAILBACLGTEATIPVCEFAKAYFDMIRIDSQTNSHH 1190
F:1435/Binding site: substrate phosphate (Arg) #status predicted	Db	1171 HVTLMRSQRNYMVTQEDYSQSFHNEALLEAVCGCTNTEVARSILYIQLAQVEPGEHTVG 1220
Query Match Score: 18.9%; Best Local Similarity 29.5%; Pred. No. 9.3e-91; Matches 415; Conservative 202; Mismatches 473; Indels 315; Gaps 46;	QY	1250 AALMDSYRQPAAFITVTOYPLPNTYKDFWRLVYDYGCTSTVMLNEVDL-SQGCBQYWPE 1307
Db	242 EIMPEGGNVNTICVANGSPPIVK-WMQGAEDLTBDMMVG--RNV-----LELT 288	
QY	1191 LKDDEFQTLNSVTPLRQAEDCSTACLPRTNDKDRFMDMLIPFDRCILPFLITDG-ES-SNTYN 1249	
Db	260 TKTDDOLYRCVTOSERGSVSNSFAQLIVEPPIRPIAPPQLGVGCPYTLIQLNANSITGD 319	
QY	1289 ASFDGTRQKQVATQGQPLAETTEDPFRALWENNNTSTIVVMLTKLREMGREKCHQYWPAE 1348	
Db	289 DVDSANYPQCVAMSSLGV-IEAVADITYKSLPKAIPGTPVTENTATSTTVWDAGNPPV 347	
QY	1308 GMRYGPQVECMNSCSMDCDVIRFRICCNLTQPGYLMQOFQYLWASHRHEPGSKR 1367	
Db	320 GPILKEVYRMTSGSWTETHAVNAPTYKLWHDPETEVIRY-LLTREGEGTGLPP 378	
QY	1349 RSARYQYFVDPMA--EYNMPEYLREFKUTDGSQRTVR-QFTDW-PEQGAPKSGB 1403	
Db	348 SYVYLSIIKARM- GRISRKKTSTTRISIGGLSPNSTEITWSAVNSQGA---PSES 401	
QY	1368 SFUKLILQEVKWWBECBERGEGRITLHCUNGGRSGRMGCAIGTYVEMVRQNYDVFHAVK 1427	
Db	379 LITETKCAFPMRPTPLTKIAETQARRATDWS-----LGYNITRCHTFNTVTCYH 430	
Db	402 VVTRTGEOQAPASAPNQARMSATTTMIVQWEEPVEPNGLIRGRV-----Y 448	
QY	1404 GFIDPFGIVQHKTKEQFGQ-DGP-TSVHCSAGVGTGVFTLTSIVLRMRYEGVVDFQTVK 1462	
Db	431 FRGNESRADCLDMDPKAPAOHVNVHLPPYTNVSLKMILTNPEGRKESEETIQT-----484	
QY	1428 TIRNSKPNMVAEAQYRSCYDVALE 1452	
Db	449 Y-----TMEPEHPVGNWOKH-NVD-DSLITVGSLEDETYTVRLAFTSV 492	
QY	1463 VLRTQRSPMVQTEDYQFCFOAAL 1487	
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QY	RESULT 13	
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QY	586 VTTNISAPS-----LPD-----YEVDASLN-ETATTIV 614	
Db	595 RQITLQAI8PKNFVKMINTKTSVLSWEPTDNNTSPTPKIQNGLTLVDGRITKLLT 654	
QY	615 LLRP-----AQKQAPASAYQIVVBLPHPRPKREA-----GAMC 650	
Db	655 HLKPTHTPYFLVNRGSSIGGLQQTW-----TARTAFMNLSGKPSVAPKPDNDGSIV 707	
QY	651 Y----QVPTTYQNALSGGAPYFYAELP-----PONLPE----- 680	
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A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Cross-references: UNIPROT:Q64605; EMBL:L11587

S44217 protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
 N:Alternate names: leukocyte common antigen-related phosphatase
 C:Species: Rattus norvegicus (Norway rat)
 C:Accession: S46217; S51174; A49104
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phot
 A:Reference number: S46216; MUID:94347119; PMID:8068021
 A:Accession: S46217

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Cross-references: UNIPROT:Q64605; EMBL:L11587

R; Goldstein, B. J.	Submitted to the EMBL Data Library, February 1993
A; Reference number: S51174	
A; Accession: S51174	
A; Molecule type: mRNA	
A; Cross-references: EMBL:Li1788; 'G', 1790-1863 <COL>	
A; Residues: 1-1788; 'G', 1790-1863; PID: g205134; PID: AAC37656_1; PID: g205135	
R; Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J. M.; Silverstein, J. Biol. Chem. 266, 24880-24886, 1991	
A; Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the nervous system	
A; Note: sequence extracted from NCBI backbone (NCBIPR:139669)	
A; Status: preliminary; not compared with conceptual translation	
A; Molecule type: nucleic acid	
A; Residues: 1-596; 'R', 598-603; 'I', 967-1788; 'G', 1790-1863 <YAN>	
A; Experimental source: brain	
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology	
C; Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrolysis	
F; 1-26/Domain: signal sequence #status predicted <SIG>	
F; 27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>	
F; 149-209/Domain: immunoglobulin homology <IMM1>	
F; 246-300/Domain: immunoglobulin homology <IMM2>	
F; 318-400/Domain: fibronectin type III repeat homology <FN3A>	
F; 413-499/Domain: fibronectin type III repeat homology <FN3B>	
F; 511-592/Domain: fibronectin type III repeat homology <FN3C>	
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F; 1504/Active site: Cys (phosphocysteine intermediate) #status predicted	
F; 1510/Binding site: substrate phosphate (Arg) #status predicted	
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Best Local Similarity 27.5%; Pred. No. 4e-89; Matches 215; Mismatches 489; Indels 485; Gaps 57;	
Matches 451; Conservative 215; MisMatches 489; Indels 485; Gaps 57;	
67 LPPEMPQSYMDSSNHDPGEKARQLQOPTMKENDTHCIDSYLLYSQKGQINPGTINIL- 125	
Db 453 MEPEHPYGWNW----QKHNVDQDSLTLTVGSLEDETY- -TVRLVA 490	
Qy 126 -VRVNKGPLANPIWNT-GFTGRDW-LRAELAVSTFWPNEXYQVIFEAEGSGRSSYIAI 181	
Db 491 FTSVGBGPQLSDP1QVKTQGYPQGPQHNPBARA----KSEFISIGLS WSAP 535	
Qy 182 DDQIVLSPYPCDKSPHFLRLGDIYEVNAQNATFOCIATGRDAVNKLWLRQRNGEDIPVAQ 241	
Db 536 ROBSVIXEL----LFRFGD----RGREV----- 556	
Qy 242 TKNINIRRF--AASFRQLEQVTKTQDLYRCVTCQTSERSGSVNSNFAQLIRE--PPRIAPP 297	
Db 557 ----GRTFDPTTAFFVVEDLKENTEYAFRLAARSPOGLGA--FTAVVCORTLQAKSAPP 609	
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Db 610 QDVVKCTSLRSRPLAIIA-----LERTWTEYVAVAYEV----- 645	
Qy 355 DTEYEITRVLLTRPGEETGLGPPLITRKCAEPMTPTKTKIAEIQARRIAWDWES-- 411	
Db 646 -----GPGBPSSPVVTRTDEDPSSAPPKVEEAALNATAIRVLWESPTP 689	
Qy 412 -----LGYNINTRCHTFNVTCYHYPRGH-NESRA---DCLMDPDKAQHVNHLPP 458	
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Qy 459 YTNVSL---KMIIT-----NPEGR----- 474	
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Qy 475 -----KESEETTIQT 484	
Db 796 PVIGYRLQFGREDAAPATELAAWERERAFAAHKGATYVFLAARGRAGLCEBASALSI 855	
Qy 485 DBDVPGPVP-VKSLOGTSFENKIFLNWKPEPL--EPNGIITQOEVYSSYSSIRSFDPA---v 537	
Db 856 PEDARPGFPQOLGPAGNVSAQSIVRLPPVAENGAIKYTKYTVSREAGTPGPATEL 915	
Qy 538 PVAGGPQTVSMLWNNSTHAVPMFHLDGTIOFFIRASTVKFGFP-- 580	
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Qy 581 ---ATAINTVNINISPLPD-----YEGDASLN-ETATTITVLLRP----- 618	
Db 970 NFKVUMIMKTSVLLSWEFPDMYNSPTPYKIQYNGLTLDVGRTXKLITHLKPHTFYNFV 1029	
Qy 619 AQAKGAPISAYQIVYBQLHPHTKREA-----JAMECY----QVPTVY 657	
Db 1030 LTNRQSSLGGQQTT-----TATAFNMLSGKPSVAKPNDGSIVVYLPDGSPVTV 1082	
Qy 658 QNALSGGAPYFAAELP-----PGNLP----- 679	
Db 1083 QN-----YFIWNVPLRKSRGGFPILLGSPEDMDLBELIQDLSRLQRRSLRHSRQLE 1134	
Qy 680 -----EPAPFTVEDNRTYKGFWMNPLAERGKTMNLYFOAMSSVKEBTKTQCVRI 727	
Db 1135 VPRPYTAARFSILSPAVFHPGNQKQYGFDPNRLGLECHRYLFVLAV--LQKNEPT--- 1187	
Qy 728 ATKAATEEPEVI--PDPAKOTDRYVVKIAGTSAGLVFILLVVVY-VIVTKSKLAKKRK 784	
Db 1188 -FAASPSDPLQDNPDPQPLIVDGBGLIVVGPVAVVFLICITIAILYKPKPSKRK 1246	
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Qy 845 NHSATAESESSLIDLVPRYCEGTSSYQT-QQL-HAIRVADLQHINLMKTSDFYGFKEE 902	
Db 1271 -----EMRRI-----NFQTPGMLSHPIPDTMAEMERLKANDSLKLSQE 1311	
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Db 1312 YESIDGQQTWEHSSLEANKPKNHYANVAYDHSKVLQPLEGGMSDINANV----- 1367	
Qy 963 YRDGYORPSHYIATQGPVHETVYDFWRMIVWQSACIVMNTLVBNGRVCKYKYNPD-DT 1021	
Db 1368 --DGTRRNQAYATQZPLPTEFQDFPWRMIVYQRSATVMMTRLEXRSRVCDCQWVNRTG 1425	
Qy 1022 EVYGPERKVTCVEMPLAEYVVRTFLERGYNIEEVKQHFTGWPDGHVPUYHATGILSF 1081	
Db 1426 ETYGPFLQVTLIDTMELATECYTRFLSHKNGSSEKEVRHRQFTANPDHGPEYPTPLAF 1485	
Qy 1082 IRRVQLSNPPSAGAIPVWHCSAGAGRTGCVYIDIMLDMAREGVYDINYCKALRSRRIN 1141	
Db 1486 LRRVKTICNPPAGPVVHCSAGVGRGCFIVDAMLERIRTEKTVQVGHHTLMRSQRNY 1545	
Qy 1142 MVQTEQYXIPFHDAILEACLGETALPVCEFFKAAYFDMIRIDSQNTNSHLDKEFQTQTLNSV 1201	
Db 1546 MVQTEQYQSFTHEALIEAVGGNTVEPARSLTYIOKLAQVEPGHHTVGMLEFKLAS- 1604	
Qy 1202 TPLQABEDCSTACLPRNHDKNRFMMLPPDECLPLITIDG-ESSNYINALMDSYRQPA 1260	
Db 1605 -SKAHTSRFTITASLPCNKEKNRVLNLYPVESSRVCQTPVGECCSYDYNASF3TRQK 1663	
Qy 1261 AFIVTOYPLPNTVKDFWRLVYDGCCTSIYMLNEVDL--SOQCPQTMPEEGMLRYGP1QVE 1318	
Db 1664 AYATGPLAETEDWRALENNSTIVMLTKRMRMGRECKHQTPAERYQYFVFD 1723	
Qy 1319 CMSCSMDCDVCINRIPICNLTRPQEY-LMVQQFQYLVGASHREYVPGSKRSFLKL1QVE 1377	
Db 1724 PMA---EYNMQYIIREFKVTDARDQCSRTRQFQFTDW-PEQGAKPSGEQFIDFGQVR 1779	
Qy 1378 KWQEEEEGEERTI- THCLNGGGRSMFCALGIVEMVRONVUDVYHAKTILRNSKPNM 1436	
Db 1780 KTKEQF---GQDAPISVHCSAGVGRGTVFITSIVLIERMVEGVDDIFQTVKLVRPAM 1837	

Qy	1437 VEAPEOYRCYDVALEYLES 1456	Db	702 PQNLHSEGTTSTSVQLSWOPPVLAERNGVITKTYLIRDINV--FLLPMEMHLIVPADTSM 759
Db	1838 VQTDEYQFCPQQAALEYLG 1857		
RESULT 14			
Db	D54669	Qy	548 NIWNNTTHYEMHILHGFTTIOFFIRASTVRGFGPATAINVTNTNISRPLSPDYEGVDAASL-- 605
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor	N; Alternate names: MPRP delta type D; Protein tyrosine phosphatase, receptor type delta, splice form A	Db	760 TLTG-----LKSDDTYDVKAHTSQRGP----YSPSVQRTLPP---VQSMPFA 802
N; Contains: protein tyrosine phosphatase (house mouse)	C; Species: Mus musculus (house mouse)	Qy	606 ---NETATTIVLIR-- PAQAKGAPISAYQI---VVEQLHHRTRKR-- EAGAMEC 650
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	R; Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.	Db	803 KNFHVKAVMKTISVLLSWEPTENYPALISKFFNMGRNVIEVTRGRATQKLIVNLKPERK 862
C; ID: D54682; Asp689	Mol; Cell. Biol. 13, 5513-5523, 1993	Qy	651 YQVPVYQNALSGGAPYYFAEELPPG----NLPE---- 680
A; Title: MPRP delta, a putative murine homolog of HPTP delta, is expressed in specialized	A; Reference number: A54689; MUID:93360986; PMID:83555637	Db	863 YSFVLTNRGNSAGLQHRYTAKTAPDVLRTKPAFIGTKNLQDMITVQLPDVANEKGY 922
A; Accession: D54689	A; Status: preliminary	Qy	681 -----P 681
A; Residues: 1-1691 <MI2>	A; Molecule type: mRNA	Db	923 YIIIVPLKKSRSRKPTIKPWFNPPLAPRKGYNIYQAMSSVEKETKTQCYRIATAAATEPEVIP 982
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A; Experimental source: brain	A; Residues: 1-1691 <MI2>	Db	983 TEFTLGDDKHGGFTNKQLQSGQFY-VFVFLAVMDHAESK---MYATSPYSPDPVSMDL 1037
A; Note: sequence inconsistent with nucleotide translation	A; Note: sequence inconsistent with nucleotide translation (NCBIN:137486, NCBIP:136537)	Qy	742 DPAKOTDRVVKIAGISAGLU--VFLLLLIVIVKSKL-ACKRKDANGINTROBMTHMV 798
A; Accession: A54689	A; Status: preliminary	Db	1038 DPQPDTDEEGLIWVGPVLAVNPICIVIAILYKRAESESRSKSSLUPNSKEVPSH-- 1095
A; Molecule type: mRNA	A; Residues: 1-398 799-1691 <MI2>	Qy	799 NAMDRSYAQDQSLTAEDPUSLTMDQHNFSPRLPNNDPLVPTAVLDENTISATAECSRLLDV 858
A; Experimental source: brain	A; Status: preliminary	Db	1096 -----PHTDPVBLRRNN----- 1107
A; Note: sequence inconsistent with nucleotide translation	A; Note: sequence inconsistent with nucleotide translation from NCBI backbone (NCBIN:136522, NCBIP:136524)	Qy	859 PRYLCRGTESPYQTGQL--HPAIRVADLQLQHINLMKTSDSYGKKEYESFPPEGOSASMDV 916
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology	C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology	Db	1108 -----FOTPGMASHPPPILEADHIERLKLANDDNLKSEQEYESIDPGQQTFTWHEH 1156
C; Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrolysis	C; Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrolysis	Qy	917 AKRDQNRKAKRGNIAIDHSRVLQVEDPSSDIDYANYIDIWLYRDYQRPSHYIAT 976
F; i: 92-95/Domain; immunoglobulin homology <IM3>	F; i: 14-186/Domain; fibronectin type III repeat homology <FN3A>	Db	1117 SNLEVNPKNRYANVIAIDHSRVLSSALEGIPGSDYYNANYI----DGYRKONAYIAT 1210
F; i: 1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>	F; i: 449-1671/Domain: protein-tyrosine-phosphatase homology <PTP>	Qy	977 QGPVHETYYDFWRNWVWOSACTVMNLIVEVERKCYKWPD-DTEVYGFDFKVTCVME 1035
F; i: 1333/Active site: Cys (phosphocysteine intermediate) #status predicted	F; i: 1623/Active site: substrate: Cys (phosphocysteine intermediate) #status predicted	Db	1211 QGSLEPETFDFWRNW-BEATVMTMLEERSRKCDQWPSRGTEFHGLVQTLLDTV 1269
F; i: 1629/Binding site: Cys (phosphocysteine intermediate) #status predicted	F; i: 1629/Binding site: substrate phosphate (Arg) #status predicted	Qy	1036 PIAEYVPTFTLERGYMBIREVKQFHFGWPDHGVPVATHGLISFIRRVKLSNPSAGP 1095
Query Match	Score 1452.5; DB 1; Length 1691;	Db	1270 ELT-YCVTFALYNNGSSEKRYTRQFQFTAWPDHGVPHEPTPLFLFRVKTCPDACP 1328
Best Local Similarity 28.7%; Pred. No. 4e-99;	Matches 414; Conservative 205; Mismatches 466; Indels 359; Gaps 42;	Qy	1096 IIVHCAGAGRGTGCYIVIDIMDMAERGVDFLYNCVKALRSRIRNVMQTEBQVIFHIDA 1155
Db	420 SWQQPPVEKONGITTEYSKRYAAYDGEDDKPHEIGNSDDTTKYLLEOLEKNTHEY--RTT 477	Db	1329 MVYHCASAGVRTGTPCIVIDAMLERIKHETVDTIYGHVTLMRAQRNYMVTQDQYFIFHIDA 1388
Qy	253 SFLRQEVTRKIDQDLVYRQVOSERSGVSFAQLVREPRPIAPPOLIGV---GPTYLLI 309	Qy	1156 ILEACLCGETAIPVCEFKAYFOMIRIDSQTSNSSLDEFQUNSVTROLAQDCSIAL 1215
Db	361 SYRLQGLKNSLYPFRLSATSPQGLGAST-AEISARTMKPSAPPQDISCTSPPSTSILV 419	Db	1389 LLEAVTCRNTIEPARNLVAYIQKLTQBTGENTVGMELSFKRIAS--SKAHTSRFISANL 1446
Qy	3110 QLNANSIICDGPIIILK-EVEYRMTSGSMWTEHAV----NAPTYKMLHDPTDEYEIRVL 363	Qy	1216 PRNHDKNRFMDMLPPDRCLPPLITDG-ESSNYINAALMDSYRQPAAFIVTQYPLPNVK 1274
Db	420 SWQQPPVEKONGITTEYSKRYAAYDGEDDKPHEIGNSDDTTKYLLEOLEKNTHEY--RTT 477	Db	1447 PCNKKFKNLNVNMPYESCRLVQLOPIRGVGSVDYINASPLDGTQQQKAVIATQGPLAETE 1506
Qy	364 LTRCEGGCLGPGLPLITTKCACPMTPTKTLKABIQARRIAYDWS-----LG 413	Qy	1275 DFWRLVYDYGCTSILMVNEBVDL--SQGPQYWBEGMURYGP-QVBCMCNSCSMCDVIRI 1332
Db	478 VTAHTDVGPPESLSVLIRTDDEYDPSGPKPRKVEAVNATAKVWSRSEPVNQHQGIRG 537	Qy	1507 DFWRMLWBNHNTIVMLTKLREMREKCHQWPAERSARYQFVDPMA--BYNMPQYI 1563
Qy	414 YNITRCHTFNVTCTHYFRHNES-----RADCLDM----- 444	Db	1333 FRICNLTRPQEGLMVOQFOYLGWSHREBPGSKRSFLKLQVEMKNOBECEGEGRGTI 1392
Db	538 YQV-----HYVMMENGEPKSAMLKDVMLAQDPMIISGLQPPETSLSLTIVAXT 585	Qy	1564 LRKEPKVTDARDQERTVROQFTDW--PEQVPSGEGFDFIGQVHKTQFGQ-DGP-SV 1621
Qy	445 -----DPKAPOHVNNLPPPYTNVSLSKMLMTNPE----- 473	Db	1393 HCLNGGGSGMFCAGIIVVEMKRNQNTVDEHAVKTLRNSKPNMVEAPEQYRICYDVLE 1452
Db	586 TKGDGARSXPKLVSTTGSVPGKPLVNH---TQMNTZLQWHPPVDTFGLGQYRLKFG 641	Qy	1622 HCSAGVGRGTVFVFTLSIVLERYEYVTDIQTQVKMLRTQRPMVQTRDQYQFCYRAALE 1681
Qy	474 RK-----ESEETIQTD----- 492	Db	1453 YLES 1456
Db	642 RKMDEPLTLEFSEKEDHTATDIHKGASYVFRSLARNKVGFEEMYKVISVEEEIFPFG 701	Qy	493 PVSLQGTSENKFNLKFLWKEPL--EPNGITQYBVSSYRSFDPAVPVAG--PPQTVS 547

Search completed: June 1, 2005, 13:56:28
Job time : 51.7393 secs

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Page 1

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DR	MGD; NCBI:103210; Ptpx.	Qy	1DDIQVLSYPCDKSPHFLRGDVEYNAQONATEFOCIATGRDAVNKLWLRNGEDIPVA 240
DR	InterPro; IPR003961; FN_III.	Db	1DDIQVLSYPCDKSPHFLRGDVEYNAQONATEFOCIATGRDAVNKLWLRNGEDIPVA 240
DR	InterPro; IPR003599; FN_III-like.	Qy	241 QTKNINHRRFAASFRQEVKTDQDLYRCVQTSERSGSVSNPAQ1LIVREPRPIAPPQLL 300
DR	InterPro; IPR007110; 19-like.	Db	241 QTKNINHRRFAASFRQEVKTDQDLYRCVQTSERSGSVSNPAQ1LIVREPRPIAPPQLL 300
DR	InterPro; IPR000998; MAM.	Qy	301 GVGPTYLQNLANSITIGDGPILKEVXRTMSSWTETAVNAPTYKLWHLDPTEYEI 360
DR	InterPro; IPR000387; TYR_Phosphatase.	Db	301 GVGPTYLQNLANSITIGDGPILKEVXRTMSSWTETAVNAPTYKLWHLDPTEYEI 360
DR	Pfam; PF00041; Enz3; 2.	Qy	361 RVLURPGEGETGCPPLTRTKCAEPMRTPKTLKIAEIQARRIAVDWESLGYNTRCH 420
DR	Pfam; PF00047; Ig; 1.	Db	361 RVLURPGEGETGCPPLTRTKCAEPMRTPKTLKIAEIQARRIAVDWESLGYNTRCH 420
DR	Pfam; PF00629; MAM; 1.	Qy	421 TENVTCYHYFRGHNESRADCLMDPKAPQHVNLLPPYTIVSLKMILTNBEGRESEET 480
DR	Pfam; PF00102; Y_phosphatase; 2.	Db	421 TENVTCYHYFRGHNESRADCLMDPKAPQHVNLLPPYTIVSLKMILTNBEGRESEET 480
DR	PRINTS; PR00020; MAMPOMAIN.	Qy	481 IQTQDEDVPGPVYVKSLQGTSFENKLFILNWKPEPLNGITQYSSRSFDAPVVA 540
DR	PRINTS; PR00700; PRTPHPTASE.	Db	481 IQTQDEDVPGPVYVKSLQGTSFENKLFILNWKPEPLNGITQYSSRSFDAPVVA 540
DR	SMART; SM00060; FN3; 3.	Qy	541 GPPQTSNLANSTHVFMLHHPGTYOFFIRASTVKGFPATAINTNTNISAPSIPDYG 600
DR	SMART; SM00409; Ig; 1.	Db	541 GPPQTSNLANSTHVFMLHHPGTYOFFIRASTVKGFPATAINTNTNISAPSIPDYG 600
DR	SMART; SM00137; MAM; 1.	Qy	661 LSGGAPYFAAELPPGNLPEAPFTYKGFNWNPPLAKPGYNITYQAMSYVEKET 720
DR	SMART; SM00194; PTPC; 2.	Db	661 LSGGAPYFAAELPPGNLPEAPFTYKGFNWNPPLAKPGYNITYQAMSYVEKET 720
DR	PROSITE; PS00852; FN3; 4.	Qy	601 VDASINETATTITVLRPAQKAPISAYQIVVQEQLPHPTKREAGAMECYQVPTYQNA 660
DR	PROSITE; PS00740; Ig_LIKE; 1.	Db	601 VDASINETATTITVLRPAQKAPISAYQIVVQEQLPHPTKREAGAMECYQVPTYQNA 660
DR	PROSITE; PS00560; MAM; 2; 1.	Qy	721 KTQCVRATKAATTEPEVIPDPAKOTDRYVKAIGSAGILVPIILLYVIVTKSKLA 780
DR	PROSITE; PS00383; TYR_Phosphatase_2; 2.	Db	721 KTQCVRATKAATTEPEVIPDPAKOTDRYVKAIGSAGILVPIILLYVIVTKSKLA 780
DR	PROSITE; PS00555; TYR_Phosphatase_2; 2.	Qy	721 KTQCVRATKAATTEPEVIPDPAKOTDRYVKAIGSAGILVPIILLYVIVTKSKLA 780
KW	Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;	Db	721 KTQCVRATKAATTEPEVIPDPAKOTDRYVKAIGSAGILVPIILLYVIVTKSKLA 780
KW	Receptor; Repeat; Signal; Transmembrane.	Qy	781 KKRKDAMNTQEMTMNANDSADQSTHAEDPLSLTFMDQNFSPRLPDNDPLVPTA 840
FT	SIGNAL 1 25	Db	781 KKRKDAMNTQEMTMNANDSADQSTHAEDPLSLTFMDQNFSPRLPDNDPLVPTA 840
CHAIN	26 1457	Qy	841 VLDEHNSATESSRLIDPVRYLCGETESPYOTQGQHPAIRYADLLOHINLMKTSDSYGFK 900
FT	Receptor-type protein-tyrosine	Db	841 VLDEHNSATESSRLIDPVRYLCGETESPYOTQGQHPAIRYADLLOHINLMKTSDSYGFK 900
FT	phosphatase kappa.	Qy	901 EYESPFEGQASWIVAKDQNRAKRYGNITIADHSRVLIQPVEDDPSDYINANYIDI 960
FT	Extracellular (Potential).	Db	901 EYESPFEGQASWIVAKDQNRAKRYGNITIADHSRVLIQPVEDDPSDYINANYIDI 960
FT	Potential.	Qy	961 WLYRDGYQRPSHYIATQGPVHEBTYDFWRMWQEQSACTIVMTNLVBGRYKCYWPDD 1020
FT	Cytoplasmic (Potential).	Db	961 WLYRDGYQRPSHYIATQGPVHEBTYDFWRMWQEQSACTIVMTNLVBGRYKCYWPDD 1020
FT	MAM.	Qy	1021 TEVYGDFFKVTCYMEPIAEYVVRTFLERRGNEIREVKFHFTGMPDHGVYPHYATGLLS 1080
FT	Ig-like C2-type.	Db	1021 TEVYGDFFKVTCYMEPIAEYVVRTFLERRGNEIREVKFHFTGMPDHGVYPHYATGLLS 1080
FT	Ig-like	Qy	1 MDYAAAPAPAFVAFMILYWPWLGSALQSAGGCTSDGPGACDYHQDLDDFEWTHVS 60
FT	Fibronectin type-III 1.	Db	1 MDYAAAPAPAFVAFMILYWPWLGSALQSAGGCTSDGPGACDYHQDLDDFEWTHVS 60
FT	Fibronectin type-III 2.	Qy	1 FIRYKLSNPPSAGIPTVHCSAGAGRTGCYIVIDIMLDMAREGYDIDYNCVKALRSRR 1140
FT	Fibronectin type-III 3.	Db	1 FIRYKLSNPPSAGIPTVHCSAGAGRTGCYIVIDIMLDMAREGYDIDYNCVKALRSRR 1140
FT	Fibronectin type-III 4.	Qy	1141 NMVQTEQYIIFHDIALEACLGGETAIPIVCEFKAAFDMDIRISDSOPTSSHLKDEFQTLNS 1200
FT	Protein tyrosine phosphatase 1.	Db	1141 NMVQTEQYIIFHDIALEACLGGETAIPIVCEFKAAFDMDIRISDSOPTSSHLKDEFQTLNS 1200
FT	Protein tyrosine phosphatase 2.	Qy	61 AQEPHYLPPEMPOGSSYVVDSSNHDPEGKARLQOPTMKENDTHCIDEFSYLLYSQKGJNPG 120
FT	Phosphocysteine intermediate (By similarity).	Db	61 AQEPHYLPPEMPOGSSYVVDSSNHDPEGKARLQOPTMKENDTHCIDEFSYLLYSQKGJNPG 120
FT	Phosphocysteine intermediate (By similarity).	Qy	SEQUENCE 1457 AA; 164185 MW; 19DB99B7ECB8605 CRC64;
SQ		Db	
Query Match 100.0%; Score 7809; DB 1; Length 1457;			
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;			
Matches 1457; Conservative 0;			
1 MDYAAAPAPAFVAFMILYWPWLGSALQSAGGCTSDGPGACDYHQDLDDFEWTHVS 60			
1 MDYAAAPAPAFVAFMILYWPWLGSALQSAGGCTSDGPGACDYHQDLDDFEWTHVS 60			
Qy 61 AQEPHYLPPEMPOGSSYVVDSSNHDPEGKARLQOPTMKENDTHCIDEFSYLLYSQKGJNPG 120			
Db 61 AQEPHYLPPEMPOGSSYVVDSSNHDPEGKARLQOPTMKENDTHCIDEFSYLLYSQKGJNPG 120			

Qy	1201 VTPRLOAEDCSIACIPLRNHDKNREMDMLPPDRCLPFLITIDGESSIONYINAAALMDSYROPA	1260	DR PROSITE; PS00740; MAM_1; 1.
Db	1201 VTPRLOAEDCSIACIPLRNHDKNREMDMLPPDRCLPFLITIDGESSIONYINAAALMDSYROPA	1260	DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
Db	1261 AFIVTQYPPLNTVKDFWRLYDYGCTTSIVMLNEVDSLQCGCPQYNNPEEGMLRYGP1QVECM	1320	DR PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
Db	1261 AFIVTQYPPLNTVKDFWRLYDYGCTTSIVMLNEVDSLQCGCPQYNNPEEGMLRYGP1QVECM	1320	DR PROSITE; PS50055; TYR PHOSPHATASE_PTP; 2.
Db	SEQUENCE 1440 AA;	162271 MW;	KW Glycoprotein, Hydrolase, Receptor
Qy	1321 SCSMDCDVIRIFRICNLTRPQEGLMVOQFOQLGWASHREVPSSKRSPLKLILQVEKQ	1380	DR SEQUENCE 1440 AA; CRC64;
Db	1321 SCSMDCDVIRIFRICNLTRPQEGLMVOQFOQLGWASHREVPSSKRSPLKLILQVEKQ	1380	Query Match 97.2%; Score 752.5; DB 2; Length 1440;
Db	Best Local Similarity 97.5%; Pred. No. 0;	Matches 1421; Conservative 12; Mismatches 6; Indels 19; Gaps 3;	DR
Qy	1 MD-VAAAALPAFYALWLYLPWPLIGSALQFSAGGCTFDGPGAODYHDLDDFEWVH 59	60 SAQSFHLPPEMPOGSYMWDSNHDPGERKARLQLOPTMKENDTHCIDFSYLLYSQKGQNLNP 119	DR
Db	1 MDTRAAAALPAFYALWLYLPWPLIGSAAQQSAGGCTFDGPGAODYHDLDDFEWVH 60	61 SAQSFHLPPEMPOGSYMWDSNHDPGERKARLQLOPTMKENDTHCIDFSYLLYSQKGQNLNP 120	DR
Qy	60 SAQSFHLPPEMPOGSYMWDSNHDPGERKARLQLOPTMKENDTHCIDFSYLLYSQKGQNLNP 119	120 GTLNILVRNKGPLANPIWNVGTGTTGRDILRAELAVSTFWPNFQVPAEVSGRSRGYI 179	DR
Db	61 SAQSFHLPPEMPOGSYMWDSNHDPGERKARLQLOPTMKENDTHCIDFSYLLYSQKGQNLNP 120	121 GTLNILVRNKGPLANPIWNVGTGTTGRDILRAELAVSTFWPNFQVPAEVSGRSRGYI 180	DR
Qy	180 ADDIQVLSYPCDKSPHFRLGDVBNAGQNAFOCIATGRDAVHKWLQRNGEDIPV 239	180 ADDIQVLSYPCDKSPHFRLGDVBNAGQNAFOCIATGRDAVHKWLQRNGEDIPV 239	DR
Db	181 ADDIQVLSYPCDKSPHFRLGDVBNAGQNAFOCIATGRDAVHKWLQRNGEDIPV 240	181 ADDIQVLSYPCDKSPHFRLGDVBNAGQNAFOCIATGRDAVHKWLQRNGEDIPV 240	DR
Qy	240 AQTQMINHREAFASFRQLQEVTKTDQDLYRCVTQSERGSCVSNPAQOLIVREPPTIAPPOL 299	241 AQTQMINHREAFASFRQLQEVTKTDQDLYRCVTQSERGSCVSNPAQOLIVREPPTIAPPOL 300	DR
Db	241 AQTQMINHREAFASFRQLQEVTKTDQDLYRCVTQSERGSCVSNPAQOLIVREPPTIAPPOL 300	300 LGVGFTYLLIQLNANSIIGDGPILKEVYRMTSGSWETHANAPTYKLWHLDDTEYE 359	DR
Qy	300 LGVGFTYLLIQLNANSIIGDGPILKEVYRMTSGSWETHANAPTYKLWHLDDTEYE 359	301 LGVGFTYLLIQLNANSIIGDGPILKEVYRMTSGSWETHANAPTYKLWHLDDTEYE 360	DR
Db	301 LGVGFTYLLIQLNANSIIGDGPILKEVYRMTSGSWETHANAPTYKLWHLDDTEYE 360	360 IRVLILTRPSEGTTGPGLPPLITRKYCAEPMRTPKTLKAEPMRTPKTLKAEIQTARRIAVDEWSLGYNITRC 419	DR
Qy	361 IRVLILTRPSEGTTGPGLPPLITRKYCAEPMRTPKTLKAEPMRTPKTLKAEIQTARRIAVDEWSLGYNITRC 420	361 IRVLILTRPSEGTTGPGLPPLITRKYCAEPMRTPKTLKAEPMRTPKTLKAEIQTARRIAVDEWSLGYNITRC 420	DR
Db	420 HTFNVTICHYFRGNESRADCLDMDPKAQPHVNHLPPYTNSLKMILTNPEGRKESE 479	421 HTFNVTICHYFRGNESRADCLDMDPKAQPHVNHLPPYTNSLKMILTNPEGRKESE 480	DR
Qy	421 HTFNVTICHYFRGNESRADCLDMDPKAQPHVNHLPPYTNSLKMILTNPEGRKESE 480	480 TLIQTEDVPGPVWPKSLQGTSFENKIFLNWKEPDLPNGLTITQEBISSIRSPDAPVY 539	DR
Db	480 TLIQTEDVPGPVWPKSLQGTSFENKIFLNWKEPDLPNGLTITQEBISSIRSPDAPVY 539	481 TLIQTEDVPGPVWPKSLQGTSFENKIFLNWKEPDLPNGLTITQEBISSIRSPDAPVY 540	DR
Qy	540 AGPPOTVSNLWNSTHVFVNHLHPCTYOFFIRASTVKFGFPATAINTVNTNISAPS LPDYE 599	541 AGPPOTVSNLWNSTHVFVNHLHPCTYOFFIRASTVKFGFPATAINTVNTNISAPS LPDYE 600	DR
Db	541 AGPPOTVSNLWNSTHVFVNHLHPCTYOFFIRASTVKFGFPATAINTVNTNISAPS LPDYE 600	600 GVDASLNETATTITVLLRPAQKAPISAQYQIVYELPHPRTKBAGAMECYQVPTVYON 659	DR
Qy	600 GVDASLNETATTITVLLRPAQKAPISAQYQIVYELPHPRTKBAGAMECYQVPTVYON 659	601 GVDASLNETATTITVLLRPAQKAPISAQYQIVYELPHPRTKBAGAMECYQVPTVYON 660	DR
Db	601 GVDASLNETATTITVLLRPAQKAPISAQYQIVYELPHPRTKBAGAMECYQVPTVYON 660	660 ALSGGAPYFAAELPPRNLLPEAPAPTFVNPLAPPKGNYTFQAMS SVEKE 719	DR
Qy	660 ALSGGAPYFAAELPPRNLLPEAPAPTFVNPLAPPKGNYTFQAMS SVEKE 719	661 AMGGGAPYFAAELPPRNLLPEAPAPTFVNPLAPPKGNYTFQAMS SVEKE 720	DR
Db	661 AMGGGAPYFAAELPPRNLLPEAPAPTFVNPLAPPKGNYTFQAMS SVEKE 720	720 TKTQCVR1ATKAATEEEPEV1PDEAKQFDRVVKAIGISAGILVFTILLVVVTVKSKL 779	DR
Qy	720 TKTQCVR1ATKAATEEEPEV1PDEAKQFDRVVKAIGISAGILVFTILLVVVTVKSKL 779	721 TKTQCVR1ATKAATEEEPEV1PDEAKQFDRVVKAIGISAGILVFTILLVVVTVKSKL 780	DR
Db	721 TKTQCVR1ATKAATEEEPEV1PDEAKQFDRVVKAIGISAGILVFTILLVVVTVKSKL 780	780 AKKRKDAMGNTROQMTHNMADRSYADQSTLHAEDPLSLTMDQHNFSPRLPNPLVPT 839	DR
Qy	780 AKKRKDAMGNTROQMTHNMADRSYADQSTLHAEDPLSLTMDQHNFSPRLPNPLVPT 839	781 AKKRKDAMGNTROQMTHNMADRSYADQSTLHAEDPLSLTMDQHNFSPRY----- 832	DR
Db	781 AKKRKDAMGNTROQMTHNMADRSYADQSTLHAEDPLSLTMDQHNFSPRY----- 832	840 AVLDNBNSATAESSLDPYRVCGETGESPYQGQLHPAIRVALDQLQHINLMKTSDSYGF 899	DR
Qy	840 AVLDNBNSATAESSLDPYRVCGETGESPYQGQLHPAIRVALDQLQHINLMKTSDSYGF 899	841 AVLDNBNSATAESSLDPYRVCGETGESPYQGQLHPAIRVALDQLQHINLMKTSDSYGF 888	DR
Db	841 AVLDNBNSATAESSLDPYRVCGETGESPYQGQLHPAIRVALDQLQHINLMKTSDSYGF 888	853 --- ENHSSTAESSRLLDPYRVCGETGESPYQGQLHPAIRVALDQLQHINLMKTSDSYGF 888	DR
Qy	853 --- ENHSSTAESSRLLDPYRVCGETGESPYQGQLHPAIRVALDQLQHINLMKTSDSYGF 888	900 KEEYESFFEGQASASWDVAKCDQNRKGYNIIAYDHSRVLQFEDDPSSDYINANYID 959	DR

Db	889	KBEYESPPFEGSASAWDVAKCDONRAQYGNIIADHSRVLQFEDPSSDYINANYI-	947	DR PRINTS; PR00700; PTYPHPHTASE.
Qy	960	IWLRYDGYQRPSHYIATQGPVTHETVYDFWRMIVWQEOQSACIYTWTNLIVEGRVKCYKWPD	1019	DR SMART; SN00060; EN3; 3.
Db	948	----DGYQRPSHYIATQGPVHETVDFWRMIVWQEOQSACIYTWTNLIVEGRVKCYKWPD	1002	DR SMART; SN00137; MAN; 1.
Db	1020	DTEVYKDPKUTCYEMBLAEVYVRTFTFLERGYNETREVKFHTCWPDHGVPHATGLL	1079	DR SMART; SN00194; PTBC; 2.
Qy	1003	DTEVYKDPKUTCYEMBLAEVYVRTFTFLERGYNETREVKFHTCWPDHGVPHATGLL	1062	DR PROSITE; PS00335; IG_LIKE; 1.
Db	1080	SPIRKYKLNSNPPSAGPVVHCSAGRTGCVIVIDMLDAEREGVVDIINCVKALRSRR	1139	DR PROSITE; PS0040; MAM; 1.
Qy	1063	SPIRKYKLNSNPPSAGPVVHCSAGRTGCVIVIDMLDAEREGVVDIINCVKALRSRR	1122	DR PROSITE; PS50060; MAM; 1.
Db	1140	INMVQEYQYIFTHDATEACIGETAIPVCEFKAAFYFMDMIRDISOTNSNSSLKDEFQTLN	1199	DR PROSITE; PS50083; TYR_PHOSPHATASE; 1; 2.
Db	1123	INMVQEYQYIFTHDATEACIGETAIPVCEFKAAFYFMDMIRDISOTNSNSSLKDEFQTLN	1182	DR PROSITE; PS50056; TYR_PHOSPHATASE; 2; 2.
Qy	1200	SVTPRLQADEDCSTACIPLRNHDKNRENDMLPPDRCPLFLITDGESSIONYINNALMSYRQP	1259	KW Glycoprotein; Hypothetical protein.
Db	1183	SVTPRLQADEDCSTACIPLRNHDKNRENDMLPPDRCPLFLITDGESSIONYINNALMSYRQP	1242	SEQUENCE 1440 AA; 16129 MW; 41BA5B4D6EC0359 CRC64;
Qy	1260	AIFIYTOYPLNTVKDFWRLVYDYGCTSIVMLNEVLSQGCGPOYWEEGMRLYGPQVEC	1319	Query Match 97.2%; Score 7589.5;
Db	1243	AIFIYTOYPLNTVKDFWRLVYDYGCTSIVMLNEVLSQGCGPOYWEEGMRLYGPQVEC	1302	Best Local Similarity 97.4%; Pred No. 0;
Qy	1320	MSCSMDCDVIINRIFRICNLTRFQEGYIMVOOFOYLGSASHREVPGSKRSFLKLILQVEKW	1379	Matches 1420; Conservative 12; Missmatches 7; Indels 19; Gaps 3;
Db	1303	MSCSMDCDVIINRIFRICNLTRFQEGYIMVOOFOYLGSASHREVPGSKRSFLKLILQVEKW	1362	Qy 1 MD-VAAAALPAFAVAVLWLYPWPLISALGQFSAGGCTFPDPGACDYHODLYDDPEWVH 59
Qy	1380	QEECEBEGGRITIHCLNGGSGMFCAIGIYBEMVKRQNYDVFHAKVTLRNSKPNMVEA	1439	Db 1 MDTAAALPAFAVAVLWLYPWPLISALGQFSAGGCTFPDPGACDYHODLYDDPEWVH 60
Db	1363	QEECEBEGGRITIHCLNGGSGMFCAIGIYBEMVKRQNYDVFHAKVTLRNSKPNMVEA	1422	Qy 60 SAQEPHYPPEMPQSYMMVDSNHDPEGEKARLQOPTMKENDTCIDFSVLYSSQKGQLNP 119
Qy	1440	PQYRFCDVAYLESS	1457	Db 61 SAQEPHYPPEMPQSYMMVDSNHDPEGEKARLQOPTMKENDTCIDFSVLYSSQKGQLNP 120
Db	1423	PQYRFCDVAYLESS	1440	Qy 120 GTLNILVRVNKGPLANPINVTGFTGRDWLRAELAVSTFWMPNEYQVTFEAEVSGRSRGYI 179
Qy	11	SEQUENCE FROM N.A. TISSUE:Endometrium carcinoma cell line;		Db 121 GTLNILVRVNKGPLANPINVTGFTGRDWLRAELAVSTFWMPNEYQVTFEAEVSGRSRGYI 180
RESLT	3			Qy 180 AIDDIOQLSYPCDKSPHFLRLGDVENAGONATFQCIATGRDAVINKLWLRNNGEDIPV 239
Q68DT8	Q68DT8	PRELIMINARY;	PTT; 1440 AA.	Db 181 AIDDIOQLSYPCDKSPHFLRLGDVENAGONATFQCIATGRDAVINKLWLRNNGEDIPV 240
ID	Q68DT8			Qy 240 AQTKNINHRPFAASRQLQEVTKTDDLYRCYQTSBERGSYNSNPALIVREPRPPIAPPOL
AC	Q68DT8			Db 241 AQTKNINHRPFAASRQLQEVTKTDDLYRCYQTSBERGSYNSNPALIVREPRPPIAPPOL 300
DT	25-OCT-2004	(TRINBLre).	28, Created)	Qy 300 LGVGPTTYLLQLNANSIIGDGPILLKEVYRMTSSWTEHAVNAPTYKUWHLDPPTEYE 359
DT	25-OCT-2004	(TRINBLre).	28, Last sequence update)	Db 301 LGVGPTTYLLQLNANSIIGDGPILLKEVYRMTSSWTEHAVNAPTYKUWHLDPPTEYE 360
DE	Hypothetical protein	DKFZp646C2268.		Qy 360 IRLVLTTRPGEGGTGLPGPPLITRTKCAEPMRTPKTPKTLIAEQARRIAWDWESLGNI TRC 419
GN	Name=DPZp646C2268;			Db 361 IRLVLTTRPGEGGTGLPGPPLITRTKCAEPMRTPKTPKTLIAEQARRIAWDWESLGNI TRC 420
OS	Homosapiens (Human).			Qy 420 HTENTVTCYHYFRGNESRADCLMDPDKPAQPHVNHLPPTVNVSLKMILTNPEGRKSEEE 479
OC	Bukarvif; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Db 421 HTENTVTCYHYFRGNESRADCLMDPDKPAQPHVNHLPPTVNVSLKMILTNPEGRKSEEE 480
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.			Qy 480 TIIQTDDBDVPDPVPVLSQGTSFENKLFWKPELEPGNLTQYEVYSSIRSFDPAVPV 539
OX	NCBI_TaxID=9606;			Db 481 TIIQTDDBDVFCPVPVLSQGTSFENKLFWKPELEPGNLTQYEVYSSIRSFDPAVPV 540
RN				Qy 540 AGPOTVSNLWNSTHVFMHLHPGTTYOFFIRASTVKGFGPATAINVTNISAPSPLDYE 599
RP				Db 541 AGPOTVSNLWNSTHVFMHLHPGTTYOFFIRASTVKGFGPATAINVTNISAPSPLDYE 600
RC				Qy 600 GVDASLNETATTITVLLRPAOKGAPISAYQIVVWLPHRTKREAGAMECYQVPVTTYQN 659
RG				Db 601 GVDASLNETATTITVLLRPAOKGAPISAYQIVVWLPHRTKREAGAMECYQVPVTTYQN 660
RA	Ottenweller B., Obermaier B., Deutscherenbaur S., Schaiapp A.,			Qy 660 ALSGGAPYYFAELPGNLPPAPFTVGDNFTYKGTVNPPLAPRKGNNIQAMSSVYEKE 719
RA	Neves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,			Db 661 AMSGGAPYYFAELPGNLPPAPFTVGDNFTYKGTVNPPLAPRKGNNIQAMSSVYEKE 720
RL	EMBL; CR74927; CAH18132.1; -			Qy 720 TKTOCYRIATAAATREPEVTPDPAKOTDRVVKIAGISAGILVFLILLVVIVVKSKL 779
DR	InterPro; IPR003361; FN_III_1.			Db 721 TKTQCYRIATAAATREPEVTPDPAKOTDRVVKIAGISAGILVFLILLVVIVVKSKL 780
DR	InterPro; IPR003597; FN_III_1-like.			Qy 780 AKKRKADAMGNTROEMTMVNAMDRSYADOSTIHAEDPLSLTFMDOHNFSPLNPDPLVPT 839
DR	InterPro; IPR003599; Ig_1.			DR PRINTS; PR00020; MAMDOMAIN.
DR	InterPro; IPR007110; Ig_1-like.			DR PRINTS; PR00020; MAMDOMAIN.
DR	InterPro; IPR000998; MAM.			DR PRINTS; PR00020; MAMDOMAIN.
DR	InterPro; IPR003595; PTBC motif.			DR PRINTS; PR00020; MAMDOMAIN.
DR	InterPro; IPR003387; TYR_Phasphatase.			DR PRINTS; PR00020; MAMDOMAIN.
DR	InterPro; IPR003242; Tyr_PP.			DR PRINTS; PR00020; MAMDOMAIN.
DR	Pfam; PF00041; En3; 2.			DR PRINTS; PR00020; MAMDOMAIN.
DR	Pfam; PF00629; MAM; 1.			DR PRINTS; PR00020; MAMDOMAIN.
DR	Pfam; PF00102; Y_phosphatase; 2.			DR PRINTS; PR00020; MAMDOMAIN.

Db	781	AKKRDAMGNTROEMTHMMNAMDRSYADQSTLHABDPLSITFMDQHNFSPRY-----	832	
Qy	840	AVIDENHSAPESSLLDVPRYLCEGTESPYQTGQLHPAIRVALILQHNLMKTSDSYGP	899	"Molecular cloning and chromosomal localization of a human gene homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine phosphatase."
Db	833	---ENHSATAESESSRLDVPRYLCEGTESPYQTGQLHPAIRVALILQHNLMKTSDSYGP	888	Gene 186:77-82 (1997).
Qy	900	KEEYSSFFEGOSASNDVAKDQNRAKRNQNTIAYDHSRVTLQPVEDPSSDYINANYID	959	-!- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis.
Db	889	KEEYSSFFEGOSASNDVAKDQNRAKRNQNTIAYDHSRVTLQPVEDPSSDYINANYI-	947	Forms complexes with beta-catenin and gamma-catenin/plakophilin. Beta-catenin may be a substrate for the catalytic activity of PIP- kappa.
Qy	960	IWLRYDGYQRFQSHYIATGGPVHETTYDFWVMMWQEQSACTIVMTNLVEGRVRCYKYWD	1019	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate; Type I membrane protein; at adherens junctions.
Db	948	----DGYQRFQSHYIATGGPVHETTYDFWVMMWQEQSACTIVMTNLVEGRVRCYKYWD	1002	-!- SUBCELLULAR LOCATION: Type I membrane protein; at adherens junctions.
Qy	1020	DTEVYGDGFKTCVMEPLAKEYVIRFTTLERRGYNEIREVKQFHFGWPHQGVPHATGL	1079	-!- TISSUE-SPECIFICITY: High levels in lung, brain and colon; less in liver, pancreas, stomach, kidney, placenta and mammary carcinoma.
Db	1003	DTEVYGDGFKVTCVMEPLAKEYVIRFTTLERRGYNEIREVKQFHFGWPHQGVPHATGL	1062	CC -!- PTM: This protein undergoes proteolytic processing.
Qy	1080	SPIRERVKLSNPPSAGPIVWHCSAGAGRGCYIVIDMLMAEREQVTDYDGSNNYNAALMDSYRP	1139	CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.
Db	1063	SPIRERVKLSNPPSAGPIVWHCSAGAGRGCYIVIDMLMAEREQVTDYDGSNNYNAALMDSYRP	1122	CC -!- SIMILARITY: Contains 1 fibronectin type III domains.
Qy	1140	INMVOTEBOYTFIHDAILEACLGCTTAIPVCEFKAYAFMDIRISQTNSSHLKDEFQTLN	1199	CC -!- SIMILARITY: Contains 1 MAM domain.
Db	1123	INMVOTEBOYTFIHDAILEACLGCTTAIPVCEFKAYAFMDIRISQTNSSHLKDEFQTLN	1182	CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
Qy	1200	SVTPRLQAECSTACIPLPRHDKNRPMMDLPDRCLPFLITDGSNNYNAALMDSYRP	1259	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	1183	SVTPRLQAECSTACIPLPRHDKNRPMMDLPDRCLPFLITDGSNNYNAALMDSYRP	1242	CC -!- PTM: This protein undergoes proteolytic processing.
Qy	1260	AAFIVTQYPLPNTVTKDFWRLVYDYGCTSIVMLNEVDSLSCQCPQTWPEBEMLRYGPIQVEC	1319	CC -!- GO: GO:0005001; C:integral to plasma membrane; TAS.
Db	1243	AAFIVTQYPLPNTVTKDFWRLVYDYGCTSIVMLNEVDSLSCQCPQTWPEBEMLRYGPIQVEC	1302	DR InterPro; IPRO03961; FN III.
Qy	1320	MSCSMDCDVINRIFRICNLTTRPQEGLYMTQFOYLGWASHREVPGSKRSFLKLTIQVEKW	1379	DR InterPro; IPRO08957; FN III-like.
Db	1303	MSCSMDCDVINRIFRICNLTTRPQEGLYMTQFOYLGWASHREVPGSKRSFLKLTIQVEKW	1362	DR InterPro; IPRO07110; Ig-like.
Qy	1380	QEECBEGEGRTIIHCLNGGRSGMCAIGIVVENVKRONVVDHFAVKTLRNSKPNNYEA	1439	DR InterPro; IPRO00938; MAM.
Db	1363	QEECBEGEGRTIIHCLNGGRSGMCAIGIVVENVKRONVVDHFAVKTLRNSKPNNYEA	1422	DR InterPro; IPRO00387; TYR phosphatase.
Qy	1440	PEQTRFCYDVALEYLESS 1457		DR InterPro; IPRO00242; Tyr_PP.
Db	1423	PEQTRFCYDVALEYLESS 1440		DR Pfam; PP00041; fns; 2.
			DR Pfam; PP00047; ig1; 1.	
			DR Pfam; PP00629; MAM; 1.	
			DR Pfam; PP00102; Y_phosphatase; 2.	
			DR PRINTS; PR00020; MAMDOMAIN.	
			DR PRINTS; PR00700; PRYDHPHTASE.	
			DR PROSITE; PS50853; FN3; 3.	
			DR PROSITE; PS50835; IG_LIKE; 1.	
			DR PROSITE; PS500740; MAM; 2; 1.	
			DR PROSITE; PS50160; MAM; 2; 1.	
			DR PROSITE; PS500383; TYR_PHOSPHATASE; 1; 2.	
			DR PROSITE; PS50056; TYR_PHOSPHATASE; 2; 2.	
			DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.	
			KW Glycoprotein Hydrolase; Immunoglobulin domain; Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.	
			FT SIGNAL 1 26 1439 Potential.	
			FT CHAIN 27 1439 Receptor type protein-tyrosine phosphatase kappa. Extracellular (Potential).	
			FT DOMAIN 27 752 Cytoplasmic (Potential).	
			FT TRANSMEM 753 774 MAM.	
RX	SEQUENCE FROM N.A.			
RX	Medline=8662345; PubMed=8627945; DOI=10.1074/jbc.271.28.16712;			
RA	Fuchs M., Mueller T., Lerch M., Ullrich A.;			
RT	"Association of human protein-tyrosine phosphatase kappa with members of the armadillo family";			
RL	J. Biol. Chem. 271:16712-16719 (1996).			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RA	Medline=9199372; PubMed=9047348; DOI=10.1016/S0378-1119(96)00684-1;			
RC	TISSUE=Foreskin;			
RX	Medline=9199372; PubMed=9047348; DOI=10.1016/S0378-1119(96)00684-1;			
RA	Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;			

FT	ACT_SITE	1082	1082	Phosphocysteine intermediate (By similarity).	Db	601	GVDASLNETATTITVLRLPAQAKGAPISAYQIVVEELPHRTKREAGAMECYQVPTYQN 660
FT	ACT_SITE	1376	1376	Phosphocysteine intermediate (By similarity).	Db	660	ALSGGAPYYFAEELPGNILEPAPPTVGDNRTYKFQWNPPPLAPRKGNYTFOAMSVEKE 719
FT	DISULPID SITE	216	270	Potential.	Db	661	AMSGGAPYYFAEELPGNILEPAPPTVGDNRTYQFQWNPPPLAPRKGNYTFOAMSVEKE 720
FT	CARBONYD SITE	641	644	Cleavage site (Probable).	Db	720	TKTQCVTRIATKAATTEPEVTPDPAKOTDRVKLAGISAGILVFLILLIVIVTVKSKL 779
FT	CARBONYD	101	101	N-linked (GLCNAC. . .) (Potential).	Db	721	TKTQCVTRIATK-AATTEPEVTPDPAKOTDRVKLAGISAGILVFLILLIVILTVKSKL 779
FT	CARBONYD	140	140	N-linked (GLCNAC. . .) (Potential).	Db	780	AKKRKDAMNTROEMTHMAMDSYADSTLHAEDPLSLTDMOHNSPRLPNPDPLVPT 839
FT	CARBONYD	211	211	N-linked (GLCNAC. . .) (Potential).	Db	780	AKKRKDAMNTROEMTHMAMDSYADSTLHAEDPLSLTDMOHNSPRLPNPDPLVPT 839
FT	CARBONYD	416	416	N-linked (GLCNAC. . .) (Potential).	Db	831	----- 831
FT	CARBONYD	424	424	N-linked (GLCNAC. . .) (Potential).	Db	840	AVLDIENHSAATESSSLLDVRYLCGTESPYQTGQLHPAIRVALDLOHINLMKTSDSYGF 899
FT	CARBONYD	436	436	N-linked (GLCNAC. . .) (Potential).	Db	832	----- 887
FT	CARBONYD	462	462	N-linked (GLCNAC. . .) (Potential).	Db	840	AVLDIENHSAATESSSLLDVRYLCGTESPYQTGQLHPAIRVALDLOHINLMKTSDSYGF 899
FT	CARBONYD	552	552	N-linked (GLCNAC. . .) (Potential).	Db	840	AVLDIENHSAATESSSLLDVRYLCGTESPYQTGQLHPAIRVALDLOHINLMKTSDSYGF 899
FT	CARBONYD	586	586	N-linked (GLCNAC. . .) (Potential).	Db	888	KEEYSSFFEGOSASWDVAKDQDNRAKNRGCNTIAUDHSRVTLOPVEDDPSDYINANVYD 946
FT	CARBONYD	590	590	N-linked (GLCNAC. . .) (Potential).	Db	900	KEEYSSFFEGOSASWDVAKDQDNRAKNRGCNTIAUDHSRVTLOPVEDDPSDYINANVYD 959
FT	CARBONYD	607	607	N-linked (GLCNAC. . .) (Potential).	Db	960	IWLTFDGYQRPShYTATQGPVHETYTDWRMIVQFQSACIYMTVNLVEGRVKCYKWPD 1019
FT	CARBONYD	690	690	N-linked (GLCNAC. . .) (Potential).	Db	947	-----DGYQRPShYTATQGPVHETYTDWRMIVQFQSACIYMTVNLVEGRVKCYKWPD 1001
FT	CONFLICT	9	9	L-> V (in Ref. 2).	Db	1002	DTEVYGDFKYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1079
FT	CONFLICT	158	158	S-> T (in Ref. 2).	Db	1002	DTEVYGDFKYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
FT	CONFLICT	284	284	A -> P (in Ref. 2).	Db	1002	DTEVYGDFKYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
FT	CONFLICT	422	422	T -> S (in Ref. 2).	Db	1002	DTEVYGDfkYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
FT	CONFLICT	672	674	AEL -> CRT (in Ref. 2).	Db	1002	DTEVYGDfkYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
FT	CONFLICT	715	715	S -> T (in Ref. 2).	Db	1002	DTEVYGDfkYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
FT	CONFLICT	732	732	A -> AA (in Ref. 2).	Db	1002	DTEVYGDfkYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
FT	CONFLICT	1366	1366	E -> K (in Ref. 2).	Db	1002	DTEVYGDfkYTCVENEPLA8YVVRFTLERGYNIREYQFHFTGPDEGVPTYATGLL 1061
SQ	SEQUENCE	1439	AA;	162087 MW: EED129AF7C9F4451 CRC64;	Qy	1080	SFIRVKLSNPPSAGIVWHCSAGAGRGTGCVIDIMLDMAEREGVYDLYNCVKALRSRR 1139
Qy	1	MD-VAADALPAVALWLYPWLLGSAGQFQAGGCTFDQDGACDYHQDLYDDDEWAVH 59	Db	1062	SFIRVKLSNPPSAGIVWHCSAGAGRGTGCVIDIMLDMAEREGVYDLYNCVKALRSRR 1121		
Db	1	MDTTAAALPAVALLWLYSPWLLGSAGQFQAGGCTFDQDGACDYHQDLYDDDEWAVH 60	Qy	1140	INMVQTEEQYIFIDHAILECLCGTAIPCEPKAYFDMIRIDQTNSSHLKDFFQTLN 1199		
Qy	60	SAQEPHYLLPPEMPQGSTYMDSSNHDFEGKARLQLPIMKENDTHC1DFSYLLSOKGLNP 119	Db	1122	INMVQTEEQYIFIDHAILECLCGTAIPCEPKAYFDMTRIDC7CTNSHLLKDFFQTLN 1181		
Db	61	SAQEPHYLLPPEMPQGSTYMDSSNHDFEGKARLQLPIMKENDTHC1DFSYLLSOKGLNP 120	Qy	1200	SVTPRIQAEDCSIALPNEIDKNRFDMLLPDRCFLPLITDGESENINYALMSYRQP 1259		
Qy	120	GTLNLYLVRNKQPLANTWNTGFTGRDWLRAELAVSTFWPNEXQVTFEAEVSGGRSGYI 179	Db	1182	SVTPRIQAEDCSIALPNEIDKNRFDMLLPDRCFLPLITDGESENINYALMSYRQP 1241		
Db	121	GTLNLYLVRNKQPLANTWNTGFTGRDWLRAELAVSTFWPNEXQVTFEAEVSGGRSGYI 180	Qy	1260	AAFIYTOYPLPNTVDFWRLVYDYGCTSYMLNEYDLSOQCPQWPEEGMLRYGP1QVEC 1319		
Qy	180	ADDIQVLSYPCDKSPHFLRQDVEVNGQATFOCTAGRDVANKLWORRNGDIPV 239	Db	1242	AAFIYTOYPLPNTVDFWRLVYDYGCTSYMLNEYDLSOQGPQWPEEGMLRYGP1QVEC 1301		
Db	181	ADDIQVLSYPCDKSPHFLRQDVEVNGQATFOCTAGRDVANKLWORRNGDIPV 240	Qy	1320	MSCSMDCDVINRFRICNLTRPOEGYLIVMQFQYLGWASHREVPSSKRSFLKLIIQVEKW 1379		
Qy	240	AQTKNNHRFAASFRQEVTKITDQDLYRCVTSQSERGSGVNFQALIVREPPIAPPQ 299	Db	1302	MSCSMDCDVINRFRICNLTRPOEGYLIVMQFQYLGWASHREVPSSKRSFLKLIIQVEKW 1361		
Db	241	AQTKNNHRFAASFRQEVTKITDQDLYRCVTSQSERGSGVNFQALIVREPPIAPPQ 300	Qy	1380	QBEECEGEGRITIHCINGGRSGMFCAIGIVVEMYKRQNVYDVFHAVKTLRNSKPNVNEA 1439		
Qy	300	LGVGPTYLQIQLNANSITGDGPITLKEYEYRTSGSMWTEHVNAPTYKLWHLDPTDEYE 359	Db	1362	QBEECEGEGRITIHCINGGRSGMFCAIGIVVEMYKRQNVYDVFHAVKTLRNSKPNVNEA 1424		
Db	301	LGVGPTYLQIQLNANSITGDGPITLKEYEYRTSGSMWTEHVNAPTYKLWHLDPTDEYE 360	Qy	1440	PEQYRFCDYALEYLESS 1457		
Qy	360	IRVLTTRCEGGTGLPDPPLIRTKCEPMRPTKIKAEQARRIAVDWEISLNITRC 419	Db	1422	PEQYRFCDYALEYLESS 1439		
Db	361	IRVLTTRCEGGTGLPDPPLIRTKCEPMRPTKIKAEQARRIAVDWEISLNITRC 420	Qy	RESULT 5			
Qy	420	HTFNVTICHTYHRGHNERADCLMDPRAQPVVNHLPYTNVSLKMLTNPEGRKSEE 479	Db	Q68FM4	PRELIMINARY;	PRT;	1496 AA.
Db	421	HTFNVTCYHFGHNSKADCLMDPRAQPVVNHLPYTNVSLKMLTNPEGRKSEE 480	AC	Q68FM4;			
Qy	480	TIIQTDPEVPGPVPKS1QGTSFENK1FLWKPLEPLNGITIOYEVSYSRSFDPAVP 539	DT	Q68FM4;			
Db	481	TIIQTDPEVPGPVPKS1QGTSFENK1FLWKPLEPLNGITQYSSRSFDPAVP 540	DT	25-OCT-2004 (T-REMBLRe.	28,		
Qy	540	AGBPQTUSNLWNSTHVMHLHPTGTTQFIRASTKCGPATINTNSAPS1DYE 599	DT	25-OCT-2004 (T-REMBLRe.	28,	Last sequence update)	
Db	541	AGBPQTUSNLWNSTHVMHLHPTGTTQFIRASTVKGFPATAINTNSAPS1DYE 600	DT	25-OCT-2004 (T-REMBLRe.	28,	Last annotation update)	
Qy	600	GVDASLNETATTITVLRLPAQAKGAPISAYQIVVEELPHRTKREAGAMECYQVPTYQN 659	DE	Name=Ptprm,			
			CN	Mus musculus (Mouse).			
			OS	Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
			OC	Murinae; Sciurognathi; Muridae; Murinae; Murinae; Murinae; Murinae;			
			OC	NCBI_TaxID=10930;			

[1]	SEQUENCE FROM N.A.	
RP	STRAIN=C57BL/6; TISSUE=Brain;	
RC	STRAIN=C57BL/6; TISSUE=Brain;	
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Feingold E.A., Grouse C.M., Shemmen J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Derge J.G., Schaefer C.M., Bhat N.K., Hsieh F., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.P., Zeisberg B., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Lognelli N.A., Usdin T.B., Yoshihii S., Carnivale P., Prange C., Bosak S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Soederman B.J., Lu X., Gobius R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Torchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.J., Marra M.A., Smailus D.E., Schnarch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;	
RA	Director MGC Project;	
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBBJ databases.	
DR	EMBL: BC079621; AAH79621; 1-.	
DR	InterPro: IPR003965; FN III; -.	
DR	InterPro: IPR008957; FN III-like.	
DR	InterPro: IPR008979; Gal_bind_like.	
DR	InterPro: IPR003594; Ig_.	
DR	InterPro: IPR007110; Ig-like.	
DR	InterPro: IPR000988; MAM.	
DR	InterPro: IPR003595; PTc-motif.	
DR	InterPro: IPR000243; Tyr_Phosphatase.	
DR	Pfam: PF00041; fn.; 3.	
DR	Pfam: PF00047; Ig; 1.	
DR	Pfam: PF00029; MAM; 1.	
DR	Pfam: PF010102; Y_phosphatase; 2.	
DR	PRINTS: PR00020; MAMDOMAIN.	
DR	SMART: SMART0024; PTc_PhtPhtASE.	
DR	SMART: SMART0060; FN3; 3.	
DR	SMART: SMART0127; MAM; 1.	
DR	SMART: SMART0194; PTc; 2.	
DR	SMART: SM00404; PTc motif; 2.	
DR	PROSITE: PS50835; TG_LIKE; 1.	
DR	PROSITE: PS00740; MAM; 1.	
DR	PROSITE: PS50060; MAM; 2.	
DR	PROSITE: PS00383; TYR_phosphatase_1; 2.	
DR	PROSITE: PS50056; TYR_phosphatase_2; 2.	
DR	Glycoprotein; PS50055; TYR_phosphatase_PTP; 2.	
SEQUENCE	1486 AA; 167143 MW; 3698D57AD522D01A CRC64;	
SQ	Query Match 61.8%; Score 4822.5; DB 2; Length 1486; Best Local Similarity 60.4%; Pred. No. 2.4e-317; Matches 896; Conservative 208; Mismatches 320; Indels 59; Gaps 9;	
Qy	22 LLGSLGQFAGGCTFDGGACDYHQDLYDDFEVHVSAAQEPHYLPPMEMQGQSYMVDS 81	
Db	14 LLTANGEPTSGGLDFEPYTCGQSQADEDDFNEVQNTTKEPSDPWMSGFLVN 73	
Qy	82 SNHDPGEKARQLQPLTMKENDTHCIDSYLLYSOKGLNPGTINLYVRNKGPANPWN 141	
Db	74 SGKPEGQRAHLLPQLVKMTHCIDSYLLYSOKGLNPGTINLYVRNKGPANPWN 133	
Qy	142 GFCDRDWLRAELIASTFWNEYQVIFEAEGSGGRGYIADDIQQLSPCDKSEPHLRIG 201	
Db	202 DVEYNAGQATPQCATGDAVANKLWLRQRNGEDIPVAQTQKNNHRRPALSFRQEVTK 261	
Qy	193 NVEYNAGQATPQCATGDAVANKLWLRQRNGEDIPVAQTQKNNHRRPALSFRQEVTK 252	
Db	262 TDQDLYRCVTSBRSGVNSPAOLIVREPRPRIAPQLLGQGPTYLQIQLANSITGDGP 321	
Qy	253 RDAGKYRCMCITEGGVGISNYAELVKEPPVPIAPQLASGATYLIWQNLANSINSQDGP 312	
Db	322 IILKEVEYMTSGSWTEHAVNAPYKLWHLDPDPEYEIRVLLTRPGEGGTCLPQGPPLIT 381	
Qy	313 IVARBEVXTASGSNDRQDVDSYTSYKIGHLDPPDEYEISVLLTRPGEGGTGSQGPALRT 372	
Db	382 RTKCAEPMRTPKTLKIAEIQARRIAWDWESLGNYNTCRCHFENVTICHYFHGNESRAD 440	
Qy	373 RTKCAEPMRGPKRLEVVETKSROLTIRWEFGYNTVRCHSYNLTWHGYQVGQEOYVREE 432	
Db	441 -CLDDMPKAPOHVWHLPPTPVNSLURMILTTNPEGGRESEBTIQDDBDVPGPVPVKSLOG 499	
Qy	433 VSWDDTDNSHPQHTITNLSPTVNTSVKLILLNPEGGKESQELTVQDDEDLPGAVPTESIQ 492	
Db	500 TSFENKIFLNWKPEPLEPNGLITOYEVSSYSSIRSFFPAPVAGPPQTVSNLWNSTHVMFH 559	
Qy	493 SAFFEKIFLQWRREPTQYGVITLVEITYKAVSSPFEDISNOSSERVSKLGNETHPLFQFG 552	
Db	560 LHPOTTYQFPIRASTVKGSGPATAINVTNINISAPLDPYGVDAISLINEATTITVLRLPA 619	
Qy	553 LYPTTYSSTIRASTAKGQGSPPATNOFTKISAPSPMPAYE-FETPLNOTDNTVYMLKPA 611	
Db	620 QARKGAPISAYQIVVBLPHRTKEAGAMECYQVPVTYONALSGGAPYFYAAELPPGNLNP 679	
Qy	612 QSRQAPVSYQIVVBEERPRTKTEILKCYPVINFQASILNSQYYFAAEFPADSLO 671	
Db	680 EPAPFTVGDNRITYKGFWNPPLAQPKGNYIQFQMSVKEKTKTOCVIATAA----- 732	
Qy	672 AAQPFITGDNKTQYNTWPLPKPSYRYYQAAANGETKIDCVRVAATIIVTQLT 731	
Db	733 -----ATREPEVIFPDPAKOTDRVVKIAGISAGILVYFILLLUVVIVTVKK 776	
Qy	732 TPYTRIAPAGDQGTQGAIVTPKPVPEPEQTDHTVKIAGTAGLIVFVILPQGVLMVK 791	
Db	777 SKLAKRKDAMGNTRQEMTHVMADMRSYADOSTHILHAEDPLSLTMDHNFSPR----- 830	
Qy	792 RKLAKRKRETMSSTRQEMTVMNSDKS-AEQGTMCD--AFSTMGTANLGRSYSSPS 848	
Db	831 -----LPN-----DPLYPTAVDENHSATAESESSLRUDVPRY-LCEGTESPYQTG 873	
Qy	849 SFTMKNTLSTSIVNSYTPDPFVTAIDLTDTHTMASQPTTYKCKREADVYQTG 908	
Db	874 QLHPAIRYADLLOHINLAKTSDFGKEEKEYESFPGQASWDVAKDQNRAKNRGNMIIA 933	
Qy	909 QLHPAIRYADLQHITOMKAEGYGFKEEYESFEGQSAFWDSACKDENRMKNRGNMIIA 968	
Db	934 YDHSRVILQVDPVQEDPSSDYTINANTIDIWLYRDGYORPHSHYATQGPVHETYDFFWRMWQ 993	
Qy	969 YDISRVRQMLQLEGDNNSDINGNTI-----DGTRHPNHTATQCPMQETYDFFWRMWQ 1024	
Db	994 EQSACIVMNTNLVEGRVYCKYMPDPTEVYGFKEVTCVEMEPALAYWVFTETLERRGYN 105	
Qy	1023 ENTASIIIVNTNLVEGRVYCKYMPDPTEVYGFKEVTCVEMEPALAYWVFTETLERRGYN 108	
Db	1054 EIREVKOPHTGPMDHGVPYHATGLLSFIRRVLUSNPPSAGPIVWCHSAGAGRTGCVIVI 111	
Qy	1083 EIRERQHTGPMDHGVPYHATGLLGFTROVKSKSPNPGPLVTHCSAGAGRTGCFIVI 114	
Db	1114 DIMDMAREGVYDINYCKALRSRINNVQTEQQYIFTHDAILEACLCGETAIPVCEFK 117	
Db	1143 DIMDMAREGVVDINYCVELRSRVRANNQTEQQVFTHDAILEACLCGDSITPASQVR 120	
Qy	1174 AAYFDIMRIDSCQTSNSHUKDEFQNTNSYSPRLPQDCSACLPRHDKNRFMDMLPPDRC 123	
Db	1203 SLYXPDMKSLDPOINSOKKEFRTRNMMTPTRLVEDDCSIALPRHDKNRFMDMLPPDRC 126	
Qy	1203 GFTCDRDWLRAELIASTFWNEYQVIFEAEGSGGRGYIADDIQQLSPCDKSEPHLRIG 201	

Qy	1234	LPLFLITIDGESSNYINAALMDSYRQPAAFVITYQQLPNTVKDFEWRLVYDYGCTSTVMLNE	1293	GO; GO:0005001; P:transmembrane receptor protein tyrosine pho.
Db	1263	LPLFLITIDGESSNYINAALMDSYRQPAAFVITYQQLPNTVKDFEWRLVYDYGCTSTVMLND	1322	DR; GO:0006470; P:protein amino acid dephosphorylation; TAS.
Db	1294	VDLSSQCPQTWPEEGMLRKPIQVECMSSGMDCDVIRNIFRICNLTTRPQEGYLMQQFV	1353	DR; InterPro; IPR03961; FN III-like.
Qy	1294	VDLSSQCPQTWPEEGMLRKPIQVECMSSGMDCDVIRNIFRICNLTTRPQEGYLMQQFV	1353	DR; InterPro; IPR08979; Gal_bind_like.
Db	1323	VDPQLCPQWPENGVRHPIQVEFVSADLEDD1ISRERIYNAASRPQDGHRMNVQFQ	1382	DR; InterPro; IPR00998; MAM.
Qy	1354	LGWASHREVPGSKRSKRSFLKLILQVERKQEWCBEGEGRITIHLCLNGGGSMSMFCATGIVVEM	1413	DR; InterPro; IPR00387; TYR_phosphatase.
Db	1383	LGWPMVRDTPSKRSFLKLILQVERKQEWCBEGEGRITIHLCLNGGGSMSMFCATGIVVEM	1442	DR; Pfam; PF00041; fn3; 3.
Qy	1414	VKRQNVVDVFHAVKTLRNASKPNMVAPEQYRFCYDVALLEYLES	1456	DR; Pfam; PF00047; Ig; 1.
Db	1443	LRHQRTVDVFHAVKTLRNASKPNMVDLDDYKFCYEVALLEYLNS	1485	DR; SMART; SM00137; MAM; 1.
RESULT 6				
	PTPMP_HUMAN	STANDARD;	PRT;	1452 AA.
	AC	P28827;	PTPMP_HUMAN	
	DT	01-DBC-1992	(Rel. 24, Created)	
	DT	01-DBC-1992	(Rel. 24, Last sequence update)	
	DT	25-OCT-2004	(Rel. 45, Last annotation update)	
	DE	Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)		
	(R-PTP-mu).	Name=PTPMP; Synonyms=PTPRL1;		
	GN	Homo sapiens [Human].		
	OS	Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	NCBI_TaxID	9606;		
	SEQUENCE FROM N.A.			
	MEDLINE	90008644;	PubMed-1655529;	DOI=10.1016/0014-5793(91)81241-Y;
	GBbbk	M.F.B.-G., van Etten I., Heteboer G., Suijkerbuijk R.,		
	RA	Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;		
	PT	"Cloning, expression and chromosomal localization of a new putative		
	receptor-like protein tyrosine phosphatase.";			
	FEBS Lett.	290:123-130(1991).		
	[2]	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.		
	RX	DOI=10.1074/jbc.272.44.27505;		
	Medline	90010572; PubMed-3346878; DOI=10.1074/jbc.272.44.27505;		
	PA	Hoffmann K.M., Tonks N.K., Barford D.;		
	"The crystal structure of domain 1 of receptor protein-tyrosine			
	RL	phosphatase mu";		
	RN	J. Biol. Chem. 272:27505-27508(1997).		
	-I-	FUNCT: May play a key role in signal transduction and growth control.		
	-I-	CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.		
	-I-	SUBCELLULAR LOCATION: Type I membrane protein.		
	-I-	SIMILARITY: Belongs to the protein-tyrosine phosphatase family.		
	CC	Receptor class 2B subfamily.		
	CC	-I- SIMILARITY: Contains 4 fibronectin type III domains.		
	CC	-I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.		
	CC	-I- SIMILARITY: Contains 1 MAM domain.		
	CC	-I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.		
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	CC	DR; X58288; C2A4126.1. - .		
	CC	PIR; S17667; S17669. - .		
	DR	PDB; 1RPM; X-ray; A; B=879-1156.		
	DR	Genew; HGNC; 9575; PTPRM.		
	CO	GO:0005887; C:integral to plasma membrane; TAS.		

FT	STRAND	964	971	QY	680	EPAPPTVGDNRTTYKGFWNPPLAPRKGYNYIQQANSVSEKETKTQCVRIATKAATEEPEV	
FT	HELIX	976	978	Db	672	AAQPPTIGDNTKTYNQWNTPLLPKSYRQFQQAASRANGTQKIDQVATKGAAFPKP--	
FT	HELIX	979	988	QY	740	IPDPKQTDREVVKAGISAGILVPLLLVVIVTKSKLAKERKDAMGNTROENTHMYN	
FT	STRAND	989	996	Db	730	VPEPKQTDTIVKLAGVAGILPFTIFLGUVLYMKCKLACKERKETMSSTROENTHMYN	
FT	STRAND	1001	1002	QY	730	VPEPKQTDTIVKLAGVAGILPFTIFLGUVLYMKCKLACKERKETMSSTROENTHMYN	
FT	TURN	1003	1004	Db	800	AMDRYADQSTLHADPLSLTFMDHNFSRPLNP-----IYPTAVL-DENH	
FT	STRAND	1005	1006	QY	800	AMDRYADQSTLHADPLSLTFMDHNFSRPLNP-----IYPTAVL-DENH	
FT	STRAND	1016	1019	Db	790	SMDKSYAEQQTNCD--AFSEMDTHNLNGRSVSSPSSFTMKTNTLSTSUPNSYYPDETH	
FT	TURN	1020	1021	QY	847	SATAESSRLIDVPRY-LCERTEESPOTGOLHPAIVRADLJLQHTNLMKTSDSYGPKEYES	
FT	STRAND	1022	1032	Db	847	TMAISDSSLVQSHTVKRREPADVPTQGOLHPAIVRADLJLQHTNLMKTSDSYGPKEYES	
FT	TURN	1033	1034	QY	906	FREGGOSASWDVAKQDQNRKQRYGENMIAAYDHSRVTYLQPVEDDPSSSDYINANYIDIWLYRD	
FT	STRAND	1035	1044	Db	907	FREGGOSASWDVAKQDQNRKQRYGENMIAAYDHSRVTYLQPVEDDPSSSDYINANYIDIWLYRD	
FT	TURN	1045	1046	QY	966	GYQRSHYIATQGPVHETVYDFWMWQBOSACIIVMVTLNLVEVRVKCCCKYWPDDETEVY	
FT	STRAND	1051	1058	Db	961	GYHRPHHYATQGPQETIYDFWMWHENTASIIIMVTLNLVEVRVKCCCKYWPDDETEVY	
FT	HELIX	1071	1083	QY	1026	DFKYTCVEMEPFLAXYVVRTFLERGRGNTIREVRCFHFTGWPDHGCVPHATGLLSFIRR	
FT	TURN	1086	1087	Db	1021	DIVKVLIEELLAVRIRTAVERGRGVHATGLLGDFVRLQV	
FT	STRAND	1091	1094	QY	1086	KLSNPNPSAGPPIVWHCSAGAGRGTGCVYIDIMLDMAEREQVDIYCNKALRSRRNMVQT	
FT	HELIX	1100	1118	Db	1081	KSKSPPSAGPPIVWHCSAGAGRGTGCVYIDIMLDMAEREQVDIYCNKALRSRRNMVQT	
FT	STRAND	1120	1121	QY	1146	EEQYTFIHDIALECLCGTAAIPVCFKAYFDMRIDQTNSSHLDDEPOTANSVTPL	
FT	HELIX	1123	1133	Db	1141	EEQYTFIHDIALECLCGTAAIPVCFKAYFDMRIDQTNSSHLDDEPOTANSVTPL	
FT	TURN	1135	1136	QY	1206	QAEDSIACLPRNHDKNRFMDMLPDRCLPFLITIDGESNYINAALMDSYRQPAFIFT	
FT	HELIX	1141	1155	Db	1201	RVEDSIALLPRNHBKRNCMDILEPDRCLPFLITIDGESNYINAALMDSYKQSAFIFT	
SQ	SEQUENCE	1452	AA:	163633	MW:	08175D3595A6C7E0	
SEQUENCE	1452	AA:	163633	MW:	08175D3595A6C7E0	CRC64;	
Query Match		61	6%;	Score	4812.5;	DB 1;	
Best Local Similarity		61.4%;	Pred. No.	1.3e-316;	Length	1452;	
Matches	891;	Conservative	20;	Mismatches	322;	Indels	29;
Matches	891;	Similarity	61.4%;	Gaps	9;		
QY	22	LIGSALQFSAAGGCTPDDGPGACDYHDLYDDFENWVHSAQEYPHLPPMPQGSYMYDVS	81	QY	1086	KLSNPNPSAGPPIVWHCSAGAGRGTGCVYIDIMLDMAEREQVDIYCNKALRSRRNMVQT	
Db	14	LLLTAAAGTTEFGSGCLFDEPYSTCGYSQSEDDFNWEQVNLTKPTSDPMPMSGSLMLVNA	73	Db	1081	KSKSPPSAGPPIVWHCSAGAGRGTGCVYIDIMLDMAEREQVDIYCNKALRSRRNMVQT	
QY	82	SNHDFGEKARQLQPLPMKENDTHCIDSYLLIYSSORGLNPNGLTLYVNGKPLANPINTT	141	QY	1146	EEQYTFIHDIALECLCGTAAIPVCFKAYFDMRIDQTNSSHLDDEPOTANSVTPL	
Db	74	SGRPGQRAHILLFOLKENDTHCIDFYFSSKNSNSPGLNIVYKVNGNGLPNIPINTS	133	Db	1141	EEQYTFIHDIALECLCGTAAIPVCFKAYFDMRIDQTNSSHLDDEPOTANSVTPL	
QY	142	GFTGRDWLRQELAYSTFWNMEYQVIFEAEGSGRSGYIAADDICQLSYPCDKSPKSFHFLRG	201	QY	1206	QAEDSIACLPRNHDKNRFMDMLPDRCLPFLITIDGESNYINAALMDSYRQPAFIFT	
Db	134	GDPTRTWNAELAISTFWNPFYQTVFEVITSGHQGLLAIDEVKVGLHCTRHFLR1Q	192	Db	1201	RVEDSIALLPRNHBKRNCMDILEPDRCLPFLITIDGESNYINAALMDSYKQSAFIFT	
QY	202	DVEINAGQONATFOCIATGRDAVANKLWLQRRNGDIPIVPOTKNNINHRRPAASPLQEVTK	261	QY	1266	QYPLPNTVKDFWRLVYDYGCTSIYMLNEYDLSQCPQYMEPGMLRYGPQVECMSCSMD	
Db	193	NVEINAGQONATFOCSAIGRTVAGRLWLQGDYRDAPLKIEKVTSSRRIASVNNTK	252	Db	1261	QHPLPNTVKDFWRLVYDTHCTSVMLNDYDPAOLCPQZPENGTHRGHQPLQVEFVSADLE	
QY	262	TQDQBLYRCTQBSERGSVNAQIIVREPPRPIAPPOLQGVPYTLQIOLANANSTIGDGP	321	QY	1326	CDVINRIPICNLTQPEGYMLVQFQYLGASHREVPESKRSRSPFLKLQIYQEWKECEES	
Db	253	RDAGKVRCMIRTEGGVGSINYAELVKEPVPIAPPQLASVGATYLWQIUNANSINGDP	312	Db	1321	EDIISRIPFVYNAAPQDQYRMVQFQFGLGPWMTDTPSKRSRSPFLKLQIYQEWKECEES	
QY	322	IIIKEVEYRMTSGSWTETHAVNAPTYKWLHLDPTEYEYRVLTRPGEGGTGLPGLPPLIT	381	QY	1386	GEGRTHIHLNGGSGMFCIAIGIVVEMYKRONTYDVHFKVTLRNSXENMVBAPEQYRF	
Db	313	IYAREVEYCTAQSWSNDRQFDSTSYKHLQIAEQRRAVDWESLGNITRCFTNTICHYFRGNESRAD-	440	Db	1381	GEQTVVHCLNGGSGSGFTCAISIVCEMRHQRTDVHFKVTLRNNKENVMDLQYKF	
QY	382	RTKCAEPMTPKTKLIAEQRRAVDWESLGNITRCFTNTICHYFRGNESRAD-	440	QY	1446	CYDVALEYLES 1456	
Db	373	RTKCADPMGRPKLEVVEKSRQITRIMEFFGNYVTRCSYNTLVHCYQVGGOBQVRE	432	Db	1441	CYEVAYLELNS 1451	
QY	441	-CLNDPKAPQHQVNHLPPTVNLKMITNPECRKESBTIIQDDEDPGPYBVKSICG	499	RESULT	7		
Db	433	VSWDTNSEPHQHTNTLSPNTVSKLIMNPECRKESBLIQDDEDPGAVENTESQ	492	PTPM_MOUSE			
QY	500	TSFENKIFLWKEPLEPNGLITOEVYSSSIRSDFDPAVPGAVPQTVSNLWNSTHVFPMH	559	ID_PTM_MOUSE			
Db	493	STFEEKIFLWKEPLEPNGLITOEVYSSSIRSDFDPAVPGAVPQTVSNLWNSTHVFPMH	552	AC	P28828;		
QY	560	LHPGTTYQPFIRASTVKGGPATAINVNTNISASLSDVEGDASLNETATTIVLRLP	619	DT	01-DEC-1992 (Rel. 24, Created)		
Db	553	LYPGTTYSPTFIRASTAKGFPATNOFTXISAKSMPATE-LETPLNQDNTVYVMLKPA	611	DT	01-DEC-1992 (Rel. 24, Last sequence update)		
QY	620	QAKGAPISYQVIVYEQLHPRHTKREAGABMCYQPVTVNLSGAPYFAAELPPGNIIP	679	DE	Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)		
Db	612	HSRGPVSTYQIVVEERRPRTKTTEIIUKCYPVPIHFFNASLINSQYFAAEPADSQ	671	DE	(R-PTP-mu).		
QY				GN	Name=PrPm;		
				OS	Mus		
				OC	Bukarzo; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
				OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.		
				RN	[1]		
				RP	SEQUENCE FROM N.A.		

RC TISSUE=Lung; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;
 RX MEDLINE=9008644; van Etten I., Hafboer G., Suijkerbuijk R.,
 RA Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;
 RT "Cloning expression and chromosomal localization of a new putative
 receptor-like protein tyrosine phosphatase.";
 RL PELS Lett. 290:123-130 (1991).
 -!- FUNCTION: May play a key role in signal transduction and growth
 control.
 CC CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 CC SUBCELLULAR LOCATION: Type I membrane protein.
 CC TISSUE SPECIFICITY: Most abundant in lung, less in brain and
 heart.
 CC SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 2B subfamily.
 CC SIMILARITY: Contains 4 fibronectin type III domains.
 CC SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC SIMILARITY: Contains 1 MAM domain.
 CC SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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 or send an email to license@isb-sib.ch).

DR EMBL; X58287; CPA41225.1; - .
 DR PIR; S17670; S17670.
 DR HSSP; P28827; 1RPM.
 DR MGDB; 102694; Ptpm.
 DR Interpro; IPR003961; FN_III.
 DR Interpro; IPR008957; FN_III-like.
 DR Interpro; IPR008979; Cal_bind_like.
 DR Interpro; IPR003599; Ig.
 DR Interpro; IPR007110; Ig-like.
 DR Interpro; IPR000998; MAM.
 DR Interpro; IPR000387; TYR_phosphatase.
 DR Interpro; IPR000242; Tyr_PP.
 PFam; PF00041; fn3; 3.
 DR PFam; PF00047; Ig; 1.
 PFam; PF00629; MAM; 1.
 DR PFam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00020; MANDOMA_IN.
 DR PRINTS; PR00700; PTYPPHPTASE.
 SMART; SM00066; PN3; 3.
 SMART; SM00409; Ig; 1.
 SMART; SM00137; MAM; 1.
 SMART; SM00194; PTPC; 2.
 PROSITE; PS50852; FN3; 3.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR PROSITE; PS50740; MAM; 1; 1.
 DR PROSITE; PS50060; MAM; 2; 1.
 DR PROSITE; PS50038; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.
 Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;
 Receptor; Repeat; Signal; Transmembrane.
 SIGNAL 1 20
 CHAIN 21 , 1452 Receptor-type protein-tyrosine
 phosphatase mu. Extracellular (Potential).
 FT DOMAIN 21 742 Potential.
 FT TRANSMEM 743 764 Cytoplasmic (Potential).
 FT DOMAIN 765 1452 MAM.
 FT DOMAIN 22 184 Ig-like C2-type.
 FT DOMAIN 186 277 Fibronectin type-III 1.
 FT DOMAIN 281 371 Fibronectin type-III 2.
 FT DOMAIN 482 379 Fibronectin type-III 3.
 FT DOMAIN 589 671 Fibronectin type-III 4.
 FT DOMAIN 923 1153 Protein-tyrosine phosphatase 1.

FT DOMAIN ACT_SITE 1223 1447 Protein-tyrosine phosphatase 2.
 FT ACT_SITE 1095 1095 Phosphocysteine intermediate (By similarity).
 FT ACT_SITE 1339 1389 Phosphocysteine intermediate (By similarity).
 FT DISULFID 206 260 Potential.
 FT CARBOHYD 72 72 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 92 92 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 131 131 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 249 249 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 406 406 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 414 414 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 454 454 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 534 534 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 598 598 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 651 651 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 1452 AA; 161594 MW; F99D0FC6792C2CF1E CRC44;

Query Match 61.4%; Score 4793.5; DB 1; Length 1452;
 Best Local Similarity 61.3%; Pred. No. 2.4e-315;
 Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

Qy 22 LLGSAGQFSAGGCTDDGACDYPHQDLYDDFEVWVSAQEPHYPFLPEMPMQGSTMVDS 81
 Db 14 ILLITAGETSGGCDEFEPYSTCGSQADEDDFDWQDVNLTKPSPDPMNSGSPMLVN 73

Qy 82 SNHDDPGKEKARQLQPLTMKENDTHCIDSFLSYLSOKGLNPGLTUNLVVRNKGSPLANDPTWN 141
 Db 74 SGKPSQRHLPLPKNDTHCDPHYPSKSNSAAGLUNVYKVNNGPLGNLWN 133

Qy 142 GFTGDRWLRELAIVSTFWNEKQVLFEEAVSGGRGKXIAADDIQLTSYPCDKSPFHRLG 201
 Db 134 GDPTRTWHRAELAISTEWPNFQVTFEV-VTSGHQCYLALDEVKVLGHPCTRTPFLRIQ 192

Qy 202 DVEYNAGQNTAEQCLATGRDAVHNKLWLRPNNEDPVAQTKNMRHREASFRQJQVTK 261
 Db 193 NVEVNGQFATFOCAIGRTVAGDILWLQGDVRAPLKIKTVTSRRFATSPNVNRTK 252

Qy 262 TDQDLYRCVTCYOTSERSGGVSNPAQJLVRERPRPIAPPQLLGPTYLQIOLNANSITGDGP 321
 Db 253 RDAGYKRCMTCGEGVGSYNAELVVKKEPPVPIAPQLASGATLWQIOLNANSINGDP 312

Qy 322 LILKEVBYANTSGSWTEHANAPYKWLDPDEXEYIIVLTLRPGEGGTGLPQPPLT 381
 Db 313 IVAREVEYCTPASGSNDROPVDTSTYKIGHLDPDEYEISVLLTPGEGGTGSPGPALRT 372

Qy 382 RTKCACPPMRPTKLIKAEGARRIAVDWESLGYNTRCHTPTNVTCTHYFRGNNEBRAD- 440
 Db 373 RTKCADPMRPRKLEVEVKSQRTIRWEPEFGSYNTTRCHSYNLTHYQVGGQQEVRE 432

Qy 441 -CLMDPDKPAPOHVNHLPPTVNSLKMILTNPEGRKESEETIQTBDVGPVTPVRSLOG 499
 Db 433 VSWDDTDNSHPOHTINTLSPVTKLILNPEGGKESQELTVQDDBLGAVPVPSIQ 492

Qy 500 LHPGTYQFFTRASTVKGFPATANVNTNISAPSLPDYEGVADSLNETATTITVLLRP 559
 Db 493 SAFEXKIFLQREPQTYGVITLYETYKAVSSFPEIDLSNQSRSVSKLNETHFLFFG 679

Qy 560 LHPGTYQFFTRASTVKGFPATANVNTNISAPSLPDYEGVADSLNETATTITVLLRP 619
 Db 553 LYPTGTYSFTRASAKGFSPATNOFTKISAPMPAYE-FETPINQDNTVYMLKPA 611

Qy 620 QAKGAPISAYOIVVVKLPHRKTKRAGAMECYQVPTVQNALSGGAPYYFAELPPGNLP 679
 Db 612 QSRGAPSVTQVIVVEERPRKTCTEILCKPVIFQNSILSQYFAEFPADSLQ 671

Qy 680 EPAPTYGDNRTYKGFWNPPLAPRKGYNYIQAAMSVEKETKTOVRIATAATREPEV 739
 Db 672 AAQPFITGDNRTYQWNTPLPHSYRITYQAAARANGEKIDCVRATVKGAVTPRP-- 729

Qy 740 IPDPAQQTDRVVKLAGISAGILVFLILLVVIVKSKLAKGRKDAMGNTRQEIMTHMVN 799

Qy	311	LNANSTIGDPILKKEVYRMTSGSWTEHAVNAPTYKLWHDIDPTEYEIRVLLTRPGEG	370		Db	1308	QVDKXQBEYNGGEGRTVIGLNGGSRSGTCIAISVCMLRHQRTVDVFHAKTLRNKP	1367
Db	240	LNANSTINGDPVAREYCTASGSNDRQPDSTSKIGLDIDPTEYEISVLLTRPGEG	299		Qy	1435	NMVEPEQRFCYDVALEYLES	1456
Qy	371	GTGLPGPPLITRTRKCAEPMRTPKLUKIAEIQARRIAVWDWLGYNTINTRCHTFNTTICHY	430		Db	1368	NMVDDLDQKFCYEVALEYLNS	1389
Db	300	GTGSPGKALRTRKCADPMRGRKLEVEFVSKRQITISWEPGYNTRCHSYNLYVHYCY	359					
Qy	431	FRGHNSRAD--CLMDPKAPQHVNTHLPPTINNSKMLLTNPESRKESSETIQTDEV	488	RESULT 9				
Db	360	QVGQGEQREEVSDWTDENSHPOHTITNLSPYTNSVTKLNMPEGRKESQELIVQTDEDL	419	Q6Y148	PRELIMINARY;	PRT;	1434 AA.	
Qy	489	PGPVPKSLQGTSFENKFLAWKPLEPLNGLITQEVYSYSSJRSFPDPAVPAGPPQTVSN	548	ID Q6Y148;				
Db	420	PGAVPTEISIQSSTPFEEKFLQREPOTQYGTIVLITYRAVSSFPEDISLNQSQRVK	479	AC DT	05-JUL-2004	(TREMBLER.	27, Created)	
Db	549	LWNSTHVMFLMLHPGTTYOFFIRASTKGFGPATAINVTTNISAPSPLDYEGVDASLN	608	DT	05-JUL-2004	(TREMBLER.	27, Last sequence update)	
Qy	480	LGNETHLFFGPGTYSFTRASTAKGFPSAPSMATE-LETPLNQT	538	DE		Receptor tyrosine phosphatase.		
Db		Gallus gallus (Chicken)		OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
Qy	609	ATTITVLRLPAAKGAPISAYQIVVVEOLHPIRTRAGAMECYQDVTFYQNALSGAPPY	668	OC				
Db	539	DNTVTWMLKPAHSRGAVPSVQIVVVEERPRETKTTEILKCPYPHTQNASSLNSQQY	598	OX				
Qy	669	FAAELPQNLBPPAPFTVGDARTYKGFWNPNPLAPRKGNTYFQAMSVEKETKTQCVTA	728	RN	[1]	SEQUENCE FROM N.A.		
Db	599	FAAEFPADSLQQAQPFTGDNKTYINGWTNTPFLPKYSYRIFQASRANGESETKIDCVQA	658	RP				
Qy	729	TKAATTEPEVTPDPAKQTDRVYKLAGISAGILVFTILLVIVIVYKSKLAKKRKDAMG	788	RA		Aerne B.; Stoker A.; Ish-Horowicz D.;		
Db	659	TKGAAATKRP--VPEPEQKTDHVKVIAQVAGILVFTIVKLYMKRKLAKKERKETS	716	RA	Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases.			
Qy	789	NTRQEMTHMVIDMNRDSTADQSTLHAEPISLTEMDOQHNEFSRPLNP-----L	836	DR				
Db	717	STRQEMTMVNNMSMDKSYAEQGNCDE--AFSFMDTNLNGRSVSSSPSFTMKTNTLSTS	773	DR				
Qy	837	VPTAVL-DENHHAATABSRSLLDVPRY-LCEGTBESPYQTGQLPATRVDLQHINLMKTS	894	DR				
Db	774	VPNYYXPEDETTMASDSSLVIQSHTYKKRREPADVPTQGQHPAIRVDLQHTQMCKA	833	DR				
Qy	895	DSYGFKEEYESFFEGOSASWYAKDORAKNRYGNTIAYDHSRVLTQPVYDDESSDYN	954	DR				
Db	834	EGYGFKEEYESFFEGQCAPWDAKKGRENMRKNGNTIAYDHSRVLTQGTDNTSDYN	893	DR				
Qy	955	ANYIDIMWYRDQYQPSHXYINTQGPWHETVDFWRMWYQEQSACTIMTIVLVEVGRKCY	1014	DR				
Db	894	GNYI-----DGYTHREPNHYIAQGPMQBTIDYFWRAVWHENTASLIMTIVLVEVGRKCC	947	DR				
Qy	1015	KWPDDTEEVGDPKVTCVEMBIALEYVTRFTFLERGYNEREVQPHFTGWPDRHGVYH	1074	DR				
Db	948	KWPDDTEEVYDQKIVLTELLEAYVTRTFAVERGVWHEIREPQHFTGWPDRHGVYH	1007	DR				
Qy	1075	ATGLLSFRRVKLNSPPAGIYVHCSAGAGRTGCYIVIDIMDMAEREGYDLYNCVKA	1134	DR				
Db	1068	ATGLLGFVRQVGKSPPAGIYVHCSAGAGRTGCYIVIDIMDMAEREGYDLYNCVRA	1067	DR				
Qy	1135	LSPSRINMQTQEQQYIETHDALEFACUGETAIPIVCFKAAYPDMRIDSQTSQNSHILKDE	1194	DR				
Db		1128	PRQLQABDCSTACLPNHRDNKRFMMLPPRCLPLITIDGESSNYINALMD	1254	DR			
Qy		FOTLNSVTPRQLQABDCSTACLPNHRDNKRFMMLPPRCLPLITIDGESSNYINALMD	1187	DR				
Db		1128	FPTLNSVTPRQLQABDCSTACLPNHRDNKRFMMLPPRCLPLITIDGESSNYINALMD	1187	DR			
Qy	1255	SYROPAAFIVTOPLPNVTKDFNRLVYDGGTSIVMLNEYDLSQGCPQYWPBEGMLRYGP	1314	DR				
Db	1188	1QVBCMSCSMDDCIVMLFRICNULTRQEGQYLMVQOQYLGFLASHREVPGSKRSELKLL	1374	DR				
Qy	1315	1QVBCMSCSMDDCIVMLFRICNULTRQEGQYLMVQOQYLGFLASHREVPGSKRSELKLL	1374	DR				
Db	1248	1QVFBSVSDLEBDIISRFRTINAARPQDGYRMVQOFQFLGPMYRDPVSKRSFUKLR	1307	DR				
Qy	1375	QVEKWQEECEEGEGRTIHLNGGRRSGMFCAIGIVVEMVRQNVVDFHAKTLRNKP	1434	DR				

Query Match Score 59.9%; Best Local Similarity 60.7%; Pred. No. 2.5e-303; Mismatches 871; Conservative 214; Mismatches 313; Indels 36; Gaps 13; Sq 32 AGCTT - DDPGACDQHDLYDDFFWVHSAQEPPHLLPPMPOGSGYMVDSSHNDGEK 89

Db 24 SAGCTTFFEDDLNQCEVSQGDDDFGWELVSYMMMPHTADLPHGSYLMVASQHAAGQR 83

Qy 90 ARLQLPTMKENDTHCIDFDSYLYSOKGLNPCTLNLYVRVNGKPLANPiWVNTGFTGRDWL 149

FT	SIGNAL	1	18	Potential.	985	YDFWMAMWQEQSAC1VMVN1LVEGRVKCYKWPDDTEVYGFCKTCVEMEPLABYVRT	1044
FT	CHAIN	19	1436	receptor protein tyrosine phosphatase	960	YDFWMAMWQEQSAC1VMVN1LVEGRVKCYKWPDDTEVYGFCKTCVEMEPLABYVRT	1019
FT	SEQUENCE	1436 AA;	161092 MW:	C05B86FFTA9412D9 CRC64;	Db	FTLERGGNREIREVQFHFTGWPDPGVPYHATGLLSFIRVKLNPPSAGIVVCSAGA	1104
FT	Query Match	59.1%	Score 4619;	DB 2; Length 1436;	Qy	1045 FTLERGGNREIREVQFHFTGWPDPGVPYHATGLLSFIRVKLNPPSAGIVVCSAGA	1104
SQ	Best Local Similarity	60.4%;	Pred. No. 1.6e-303;	Indels 36; Gaps 12;	Db	1020 FALERGYSARHEVQFHFTAWPEGVPHATGLIAFIREVKASTPPDAGIVICSGT	1079
SQ	Matches 866;	Conservative 203;	Mismatches 329;	Db	1105 GRTGCVYIDIMLDAEREGNDIYNCVKALRSRSPINMQTQEQQYIFHDIALECLGE	1164	
Qy	3.2 AGGCTFD---DGPAGDYHQDLYDDEFWHVAQEPHYPMPQSYMDSSNHDPGE	88	Db	1080 GRTGCVYIDIMLDAEREGNDIYNCVKLCSREVNMIGTEEQYIFHDIALECLGE	1139		
Db	24 AGGCTFEASDPAVPCESQAYDDFQEWQRIHPGTRAPADLPGSYLWNTSCHAPGQ	83	Qy	1165 TAIPVCEFKAYFDMRIDQTSNSSLKDEFQTNISVTPLQAECISIACLPRNEDKNRF	1224		
Qy	89 KARQLQPTMKENDTHCIDSFLVSYOKGKNGPTLN1LTVRYNKGLPANPWNVTGETGRDW	148	Db	1140 TTIPVSEPKATYKEMRIDQSNSSQLEEFQTLNSVTPLDVETCSIALUPRNEDKNRF	1199		
Db	84 RAHVIFOSLSENDTHCQFSTFLYSLRGSPEITLGYVVRNGGLQSAVNMIGSHGRQW	143	Qy	1225 MDMLPPDRCLPFLITIDGESNNYTAALMDSYRQAAFTVQYLPNTVDFWRLVYDYG	1284		
Qy	149 LRAELAVSTFWPNKEYQVFEAEVSGGRSGYIAIDDIQVLSPCPDKSPHFLRGLDYEVNAG	208	Db	1200 MDVLPPDRCLPFLISTGDGSRNNYNAALITYSYTRAAFIYLHPLQSTTPDFWRLVYDYG	1259		
Db	144 HQAELAVSTFWPNKEYQVFEAEVSGGRSGYIAIDDIQVLSPCPAKHPSLRLGDEVNAG	203	Qy	1285 CTSTM1MLNEVDLSQG--CPOQWPPBEGMFLRYGP1QVECMSCSMDCDV1NFRICNLTRP	1341		
Qy	209 QNAFOCIATGDAVHNKLWLRNRGDIYPAQTKNINHRRFAASPLQEVTKTODLYR	268	Db	1260 CTSTM1MLNQNQSNSAWPCLQYWPGRQOGLMVEFMGSTADDVLVAVFVRONISRL	1319		
Db	204 QNAFSQCMAGRAAEARFLQFLORQGALVPAAGVRHISHRELATPLAAVSRAEODLYR	263	Qy	1342 QEGYLMVQDQOYLGVASHREVPYGRSRSPKLLQEKWAQSECEBEGRTITHCLGGGR	1401		
Qy	269 CTVOSBERGSVNSNAQOLVREPREPPTAAPOLIGVGPYLLIQLNANSIIGDGPILKEV	328	Db	1320 QEGHJLVRHQQFLRSLAYRTPDSKAFKHLIAFYDKWQ-AESESDGRTYVHCLGGGR	1377		
Db	264 CVSQAAPRAGVNSFAELVKEPPTIAPQQLLRAGTPLIQLQNTNSIIGDGPVKEIE	323	Qy	1402 GMFCAGIIVYVMEVKVQNVYDVFHAYKTLRNSKPVNNEAPBQYRFCDVALEYLE	1455		
Qy	329 YRMTSGSWTEHAVNAPYKLMHLDPOTEEYEVRLIITRPGEGGTGLPGPPLJITRKCAEP	388	Db	1378 GTFCACATVLEMIRCNLVDFFAAKTLRNYKPNVNETMDQHYFCYDVALYLE	1431		
Db	324 YRMARGPVAEVAVSLQGYKLUWHLDPOTEEYEVSLVLTTRPGDGTRGPPLJSRKAEP	383					
					RESULT 11		
					Q92850	PRELIMINARY;	
					ID	PRT;	1436 AA.
					AC	Q92850;	
					DT	Q92850;	(TREMBLrel. 02, Created)
					DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)
					DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)
					RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.	
					DR	U6289; AAB07074.1;	-.
					HSSP	P28827; IRPM.	
					DR	GO:00164020; C:membrane; IEA.	
					DR	GO:00167878; F:hydroxylase activity; IEA.	
					DR	GO:0004725; F:protein tyrosine phosphatase activity; IEA.	
					DR	GO:0004872; F:receptor activity; IEA.	
					DR	GO:0006470; P:protein amino acid dephosphorylation; IEA.	
					DR	Pfam; PE00041; fn3; 3.	
					DR	PFam; PE00623; MAM; 1.	
					DR	SMART; SM00499; IG; 1.	
					DR	SMART; SM00137; MAM; 1.	
					DR	SMART; SM00194; PTPC; 2.	
					DR	PRINTS; PRO0020; MANDOMAIN.	
					DR	PROSITE; PS50853; FN3; 3.	
					DR	PROSITE; PS00740; MAM; 1.	
					DR	PROSITE; PS50060; MAM; 2; 1.	
					DR	PROSITE; PS00383; TVR; PHOSPHATASE_1; 2.	
					DR	PROSITE; PS50056; TVR; PHOSPHATASE_2; 2.	
					DR	PROSITE; PS50055; TPTP; 2.	
					KW	Glycoprotein; Hydrolase; Receptor.	

QY	1436 AA;	161108 MW;	8F15D034058A809 CRC64;	
Query Match	59.0%	Score 4610;	DB 2; Length 1436;	
Best Local Similarity	60.3%; Pred. No. 6.4e-303;	Mismatches 203;	Indels 331; Gaps 12;	
Matches 865;	Conservative			
Db	32 AGGCTFD--DGGACDYDHDLYDFEWVHVSAAQEPHYLPEMFGSTMVVDSSNNHDPE 88			
Db	24 AAGCTTFFEEASDPAVCEYSSAQYDDFQEWCRHGTARADPHGLMVNTSOHAQG 83			
Qy	89 KARLQLPTMKENDTHCIDFSELLYSSQKGKLNPGTUNILVRVKNGPLANP1WNVGFTGRDW 148			
Db	84 RAHVTFQSLSENDTHCVCQSYSTFLISRGDHSPTGCVVNRGPGSAAWNMGSHGROW 143			
Qy	149 LRAELAVSTWPNEYQVIFPAEVSGGRSGCYIAIDDIQVLSPCDKSPHEFRLGDEVNAG 208			
Db	144 HOAEELAVSTWPNEYQVLFALISPDRRGEMGLDILLSSYPCAKAPHSRQLGDEVNAG 203			
Qy	209 QNAQFQCIATGARDHAVHNKWLQRANGEDLPVACTKINNERRFAASFRLOBVTKTDQDLYR 268			
Db	204 QNAQFQCMAGRAAFAERFLQORSGALVPAAGYHISHRFLATPLAAVSAEQLYL 263			
Qy	269 CTVOSERGSGSVSNPAQLTIVREPPRPIAPPOLLGGCGPTYLIJOLANSITLGDPGTLKEVE 328			
Db	264 CVSQAPRGAVGSNFABLIVLEPPIAPIAQQLRAGPTYLQINTNSTIGDPVTKRLIE 323			
Qy	329 YRMTSGSWTEATHNAPTYKLWHLDPDTEYEIRIVULTRGEETGTLGPPLPLRTKCAEP 388			
Db	324 YRMARGPWAEVHAASLQTYKLWHLDPDTEYEISVYLTRGTCRGPPLSRTKCAEP 383			
Qy	389 MRTPTKLKIAEQIQRRIAVDWEISGYNTRCHTPNVTICHYPRG--HNSRADCLMDP 446			
Db	384 MRAPKGLAFEAQIQRQLTQWPELGYNTRCHTYVLSCHYTGLGSSHNOTIRECVTEQ 443			
Qy	447 KAPOHVNHILPPPTNVSLKMLNTNPEGRKSEETLIOTEDVPGPVPKSLCTSSENKI 506			
Db	444 GVSXTTAKNLPLVANVHVLVLTNPREGKRGKETFQTDDBDVPSGIAAESLTTPLEDMI 503			
Qy	507 FLWKKEPLEPNGLITQXEVSYSSRSRSDPAPVYAGPQTWSNLNSTHVFNMHLHPGTY 566			
Db	504 FLKWEPEQPNGLITQXEVSYOESSDPAVNTEGPRTTISKURNETYHFSNLHHPGTY 563			
Qy	567 OFFIRASTYKGFGPATAINVTTNISAPS1PDYEVDA5LINE7ATITVLRPAQAKGAPI 626			
Db	564 LFSTYRATIGKGFQAALETTTINISAPS-F-DYADMPSLGESENTITVLLRPQGRGAPI 622			
Qy	627 SAYQIVVEQOLHPRHTKREAGAMECXQVPTVYONALSGGAPPYFAAELPPGNLPEPAPTY 686			
Db	623 SVQIVVEBARRLREQGQDFPVPVLFEARLARGVHYFAELLASSLPMAMPFTV 682			
Qy	687 GDNRTYKGFWMNPPLAPRKGYNIIQAMSSVEKETKTQCVIATKAATEEPEVIPDPAKQ 746			
Db	683 GDNQTYRGFWNPPLPEPKAYLIVFQAASHLKGETRLNC1R1ARKAACKESKRPL-EVQR 741			
Qy	747 TDRVYKIGISA-GILVFLILLVVIVKRSKLAKKRDKADMGRTOENTHYNAMDSEY 805			
Db	742 SEEMGLLIGCAGGLAVLILGAITIVRKGFQKEYSFPEG-----WDAFKKKOKVK 905			
Qy	806 ADOSTLHARDPLSLTFMDOHNFSPRLNDPPLVPTAVDENSAATESSRL-DVPRVLC 864			
Db	801 TDQSTLQEDBRLGISMFDTHGYSTR-----GDORSGGTAESSLGSSPRPG 849			
Qy	865 GTESPQYQFCQLHPAIRVADLQHINLMKTSDSYCFKEEYSSPFEGQSSAWDVAKKDQNR 924			
Db	850 RKGSPYHTSQCQLHPAIRVADLQHINOMKTAEGTGFQKEYSFPEG----WDAFKKKOKVK 905			
Qy	925 KNRYGNITIAYDHSSVILQVIPDEDDPSDTYNTANTIDIWLYRGCYQRFPSHYIATGPHVHTV 984			
Db	906 GSROEPMPPAYDHRVKLHPMLGDNDIANYI-----DGTHRSNFIATGQPKPMV 959			
Qy	985 YDFWFRMVMQEOQSACIVMTNLVEGRVCKCYKWPDDTEVYGDPRVTCYMEPLAEXYVRT 1044			
Db	960 YDFWFRMVMQOBHCSS1VMTKLVEGRVCKCYKWPDDTEVYGDPRVTCYMEPLAEXYVRT 1019			

PRINTS; PRO0020; MAMDOMAIN.	
DR PRINTS; PRO0070; PTYPHPHTASE.	
DR SMART; SN00060; FN3; 3.	
SMART; SN00409; IG1; 1.	
SMART; SN00137; MAM; 1.	
SMART; SN01194; PTPC; 2.	
PROSITE; PS50553; FN3; 2.	
PROSITE; PS00740; MAM; 1; 1.	
PROSITE; PS00660; MAM; 2; 1.	
PROSITE; PS50060; MAM; 2; 1.	
PROSITE; PS00383; TYR PHOSPHATASE; 1; 2.	
PROSITE; PS50056; TYR PHOSPHATASE; 2; 2.	
PROSITE; PS50055; TYR PHOSPHATASE; PTP; 2.	
Glycoprotein; Hydrolase; Receptor.	
SEQUENCE 1439 AA; 161655 MW; 99E8B6D14D7C965D CRC64;	
Query Match 58.9%; Score 4602.5; DB 2; Length 1439;	
Best Local Similarity 60.3%; Pred. No. 2.1e-302;	
Matches 865; Conservative 206; Mismatches 330; Indels 33; Gaps 13;	
Qy 32 AGGTGFD--DGPAGACDYHQDLYDDPEWVHSAQOEPHLPPEMPQGSYVYDSSNHDPE 88	
Db 24 AAGCTTEEASDPAVPCEYSQSYQYDDPQEWEQVRHPCSTRADPLGQSYLMNTSQHAQGQ 83	
Qy 89 KARLQDPTMENDTHCIDSFLSYSLQSRGNGFTNLILVRNKGPLANPWNVTGPTGRDW 148	
Db 84 RAHVIFQSLSENNDTHCQSYFLYSRSGHSPGTGLGVYVVRNGGLPGSAVNMTGSHGRQW 143	
Qy 149 LRAELAVSTFWPNYEQVIFEAEVSGGRSGYTAIDDIQVLQSYPCDKSDPSHFLRLGDEVNAG 208	
Db 144 HOAEALAVSTFWPNYEQVLFLEAISPPRRGMGLDDILLSYPCAPAHPSRLGDVBVNAG 203	
Qy 209 QNATPQCIATGRDAVNKLWLRQRNGEDIPYAQTKNNINHRFAASFRQLQEVTKTDOLYR 268	
Db 204 QNASFQCMAGRAAAEAFLLQROSSALVPAAGVRHSERFLATEPLAAVSRAQDLYR 263	
Qy 269 CTVTQSBERGSYNSNAQJLVRSPRPTAPPOLGVGPTYLITQKLIKEVE 328	
Db 264 CVSQARPGAGYSNFAELIVKEPPPTAPAPQQLRAGPTYLIQLNNTSIIQDGPIVTKIE 323	
Qy 329 YRMTCGSSWTEATHVNPATPYKLWHLDPDTYEIRVLTRPGEGGTGLPGPPLITRTKCAEP 388	
Db 324 YRMARCPWAEYHAWSLQTYKLWHLDDTDEYEISV-LSRPDGGTERGPGPPLISRTKCAEP 382	
Qy 389 MRTPTKLKARIQARRIAWDWESLGNNTTRCHTFNTVTCYHYFRG--HNESRADCLMDP 446	RESULT 13
Db 383 MRAPKGIAFAEQARQALONEPLG3TNVTRCHTYTSLCITYHTLGGSNQNTIRECVKTEQ 442	ID 035564 PRELIMINARY; PRT; 1436 AA.
Qy 447 KAOPHQVHNHLPPTYNSNFAQJLVRSPRPTAPPOLGVGPTYLITQKLIKEVE 506	AC 035564; DT 01-JAN-1998 (TREMBLrel. 05, Created)
Db 443 GVSRYTNIKLNLYPRYNTHVRLWLNPGKEKEVTFQTDEDVPGTAEEAESTTPELDI 502	DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
Qy 507 FLNKWKRPLEPGLLITQYEVSSYSSIRSFDPAVPGAPQPTVSNLNSTHVFEMHHLHPGTY 566	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db 503 FLKWKWERFQEPGLITQYEVSSYSSIRSFDPAVPGAPQPTVSNLNSTHVFEMHHLHPGTY	DB Ftp-1.
Qy 567 OFFIRASTVKFGFGPATANTTNISAPSPLPDEYGVDAISNETATTITVLLRPAQAKGAPI 626	GN Name=Ptprn; Synonyms=ftp-1;
Db 563 LFSVRAARTGKGFQQAALTEITNNISAPSFDYADMPSLGESENTITVLLRPAQGRGAPI 621	OS Mus musculus (Mouse).
Qy 627 SAYQIVVEQPHRTKREAGAMECYQPVYPTVNTTQGGAQPFYAAALPQNLPEPAPFTV 686	OC Bokermannia; Metazoa; Chordata; Vertebrata; Euteleostomi;
Db 622 SVQIVVVEERARRLRLREBPGGODCFPVLTEFAALLARGLVHFGAELAASSLPEAMPFTV 681	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10909;
Qy 687 GDNRTYKGWMNPPLAPRKGYNTFOAMSVEKEETKTOQVRIATAAATEEESEVIPDPAKQ 746	RN [1] RT phosphatase from murine fetal liver.
Db 682 GDNOTYRGFMNPPLPEPKAYLIYFQASHLKGETRNLCKIRAKACEKSRPL-EVSKR 740	RL Gene 194:241-247(1997).
DR HSSP; P28827; IPRM.	DR DR
DR MGI; MGI:1322151; PePrU.	DR DR
DR GO; GO:0005615; C:extracellular space; TAS.	DR DR
DR GO; GO:0016021; C:integral to membrane; TAS.	DR DR
DR InterPro; IPR001962; F1III subd.	DR DR
DR InterPro; IPR008957; F1III-like.	DR DR
Qy 747 TDRVVKTAGISA-GILVFLILLVVVTKSKLAKKRKDAMNTQFQEMTMVNMANDSY 805	Qy 747 DR
Db 741 SEEMLGLIGCIGCHGLAVLIGAIIVTRIGKPKVNTMK-TATVNVQEKTHMMSAVDSRF 799	DR DR
Qy 806 ADQSTLAEEDPLSLTMNDQHNFSESPRLNDPLPVTAIDENISATASSRLL-DVPEYLC 864	Qy 806 DR

InterPro; IPR008979; Gal_bind_like.	Db	683 GDNQTYRGFWNPPLPEPKAYLIVFQAAFLKGETRLNCIRAKACKESKRPL-EVSQR 741
DR InterPro; IPR003599; Ig.	Db	747 TDRYVKGAGSA-GILFELLLVVIVTIVKSKLAKKKRDKDAMGTRQENTHMYNMADRSY 805
DR InterPro; IPR007110; Ig-like.	Db	742 SEEMGLIGTCAGGGAVLILLGAIVIIRKGKPVNMTK-ATVNRQEKTHMMSSAVDRSF 800
InterPro; IPR000387; TYR_phosphatase.	Db	806 ADQSTLHAEDPLSLTEQDQHNSSPRLPNDPLVPTAVALDENHSATEASSRL-DVPRYLCE 864
Pfam; PF00041; fn3.	Db	801 TDQSTLQEDERLGLSFMDA.PGYSR-----GDORSGGTEASSLGGSPRRPCG 849
Pfam; PF00629; MAM_1.	Db	865 GTESPYQTGOLHPAVRDLQHNLMMTKSDSYGKEBEYESFPFGCOSASWDVAKKDQNRA 924
Pfam; PF0102; Y_phosphatase; 2.	Db	850 RKGSFVHTGOLHPAVRDLQHNLMMTKSDSYGKEBEYESFPFG-----WDATKCKDKLK 905
PRINTS; PR0004; FATTYPEPTII.	Db	806 KNRTGNTIAITDHSSRVLQFEDDSYDYNANYIDWLYTRDGYORPSHYTATQCPVHETV 984
PRINTS; PR00020; MANDOMAIN.	Db	906 GGROEPVSAVDHRHKLHPMLADADTSANTY-----DGTHRSHNPIATQGPKPEMI 959
PRINTS; PR00700; PRTPYPHPTASE.	Db	985 YDFWMRMWQEQSACTVMMTNLVEYGRVKCYKYPDPDTTEVYGFKVTCYMEPLAEYYVRT 1044
SMART; SM00060; FN3; 3.	Db	960 YDFWMRMWQEQSACTVMMTNLVEYGRVKCYKYPDPDTTEVYGFKVTCYMEPLAEYYVRT 1019
SMART; SM00049; IG_1.	Db	1045 FTLLRGYNBIREYKQFHTGWPDHGVPHATGLISFIRRKCLSNPPSGIVVHCSAGA 1104
SMART; SM00137; MAM_1.	Db	1020 FALERGYSARHEVYQFHETAWPEHGVPHATGLAFIRRKASTPDAGPVITHCSAGT 1079
SMART; SM00194; PFFC; 2.	Db	1105 GRTGTYIVTDIMLDMAREGVDYDNYCVALSRSPINQYTEEOTIFDAILEACLGCE 1164
PROSITE; PS50053; FN3; 3.	Db	1080 GRTGTYIVTDIMLDMABEGVVDYDNYCVALSRSPINQYTEEOTIFDAILEACLGCE 1129
PROSITE; PS50060; MAM_2; 1.	Db	1165 TAIPCEPKAAYFDMIRIDSQTQNSHLKDEFQTLNSVTPRQEDCSSTACLPNHDKNRF 1224
PROSITE; PS50056; TYR_Phosphatase_1; 2.	Db	1140 TTIPNEFATYRMRNIRDQNSQLREFOTLNNSVTPDVECSSTALLPRDKNRS 1199
PROSITE; PS50056; TYR_Phosphatase_2; 2.	Db	1225 MDVLPDPDCFLPFLITIDGESSNNYINAALMDSYROPAAFIVTOYPLPNTYKDFWRLVYDYG 1284
PROSITE; PS50055; TYR_Phosphatase_PTP; 2.	Db	1200 MDVLPDPDCFLPFLISSDGDPNNNTINAALTDSYTRSAAFVTLHPQSTTPDFWRLVYDYG 1259
Glycoprotein_Hydrolase.	Db	1285 CTSIVMLNEVDLSG---CPOYMPFEGMFLRYGPQVECMSMSDODVINRIFRCNLTRP 1341
SEQUENCE 1436 AA; 161157 MW;	Db	1260 CTSIVMLNOLQNSNSAWPLQYNPBPGRQGYLMEVFVSGTANBDLVSFRVFRQVNSSRL 1319
SQ	32 AGGCTFDGFG---ACDYHQDLYDDFEWVHVAQSEPHYLPPPEMPOGSTMVVDSSNNHDPGE 88	QY 89 KARLOLPTKENDTHCIDPSYSLXJSOKGKLNPGTILNLYVNGKPLANPWNVTGFTGRW 148
Best Local Similarity 60.0% ; Pred. No. 4..9e-302;	Db	84 RAHHTFQTLSENDTHCVOSFYSLPSYRSGHSPGTGLGVYRNGGPIGLSAWNMTGCSRGRQW 143
Matches 861; Conservative 208; Mismatches 330; Indels 36; Gaps 12;	Db	149 LRAELAVSTFWPEQVIFIPEAVEGGSGSIAIDDIQVSYPCDKSPHFLRLGDPVEVAG 208
Db	24 AAGCTFEASDPVVCBFSQAQYDDEQFWBVRIGHGTRPEDLPHGAYLMVNAQSQAHQ 83	Db 144 HOAELAVSTFWPEQVOLFEALISPDKHGKGYGLDDILLESYPCAKAHESRSLGDEVVAG 203
Qy	32 AGGCTFDGFG---ACDYHQDLYDDFEWVHVAQSEPHYLPPPEMPOGSTMVVDSSNNHDPGE 88	Qy 209 QNATFOCIATGRDAVNKLWLQRENGEDPVACTKNNINHRRFAASFRICQEVTKTQDQLYR 268
Db	84 RAHHTFQTLSENDTHCVOSFYSLPSYRSGHSPGTGLGVYRNGGPIGLSAWNMTGCSRGRQW 143	Db 204 QNASFQCMAGRAEAHHFLQROGVLPVAAGTRHISRRFLATPLASVGSEQDXR 263
Qy	149 LRAELAVSTFWPEQVIFIPEAVEGGSGSIAIDDIQVSYPCDKSPHFLRLGDPVEVAG 208	Qy 269 CYTOSERGGSGVSNEPQLIVTREPREPIAPDQGLGCGPTVLLQMANSTIGDGPILKEV 328
Db	144 HOAELAVSTFWPEQVOLFEALISPDKHGKGYGLDDILLESYPCAKAHESRSLGDEVVAG 203	Db 264 CVSQALPRGAVSVNPALELTKEPEPTTAPQOLLRAGPTVLLQNTNSTIGDGPILKEV 323
Qy	209 QNATFOCIATGRDAVNKLWLQRENGEDPVACTKNNINHRRFAASFRICQEVTKTQDQLYR 268	Qy 329 YRMTESGSWTETHAVNAPTYKLWHDPTDYEIRVLLTRGEGTGLGPBPLTRTKCAEP 388
Db	204 QNASFQCMAGRAEAHHFLQROGVLPVAAGTRHISRRFLATPLASVGSEQDXR 263	Db 324 YMRARGPWWAEHAVNLQTYKLWHDPTDYEISVLTRGDDGTGRGPPLISTKCAEP 383
Qy	269 CYTOSERGGSGVSNEPQLIVTREPREPIAPDQGLGCGPTVLLQMANSTIGDGPILKEV 328	Qy 389 MRTPKTLKTAEIQARRIAYDWESIGNTTRCHTFENVTCYHRG- -HNESTRADCLDNDP 446
Db	264 CVSQALPRGAVSVNPALELTKEPEPTTAPQOLLRAGPTVLLQNTNSTIGDGPILKEV 323	Db 384 TRAPKGLAFAEIQARQLTQWEPGYNTRCHTYAVSLCYRTLGGSHINTQIRECVKNER 443
Qy	329 YRMTESGSWTETHAVNAPTYKLWHDPTDYEIRVLLTRGEGTGLGPBPLTRTKCAEP 388	Qy 447 KAPQHVVNHLPPYNTVSLMILNTPEGKESSETLIQTEDVDPGPVYKSLQGTSFENKI 506
Db	324 YMRARGPWWAEHAVNLQTYKLWHDPTDYEISVLTRGDDGTGRGPPLISTKCAEP 383	Db 444 GASRYTIKWLPPFENHIVRLTNPBEGRECEGKEYFQTBDVPGCIAEASLTTPLEMI 503
Qy	507 FLANKBPLBEPNGLITQYEVSYSSTSRSFDADPVYAGPPQTVNSLWNHFMHLHPGTTY 566	Qy 507 FLANKBPLBEPNGLITQYEVSYSSTSRSFDADPVYAGPPQTVNSLWNHFMHLHPGTTY 566
Db	504 FLRKEEPQEPNGLITQYEVSYSLESSDADVNGPRTTISKURNETVHFNSLHPGTTY 563	Db 504 FLRKEEPQEPNGLITQYEVSYSLESSDADVNGPRTTISKURNETVHFNSLHPGTTY 563
Qy	567 OFFIRASTYKGFGPATATWNTNISAPSPLYDYESVTDASLINEATTITVLLRPAQAKGAPI 626	Db 567 OFFIRASTYKGFGPATATWNTNISAPSPLYDYESVTDASLINEATTITVLLRPAQAKGAPI 626
Db	564 LFSVARTSKGFGQALBTNTNISAPS-DYADMPSPGESENTITVLLRPAQGRGAPI 622	Db 564 LFSVARTSKGFGQALBTNTNISAPS-DYADMPSPGESENTITVLLRPAQGRGAPI 622
Qy	627 SAYQIVQEQLHPRHTKREGAMECYQVPTYQNALSGGPAPYFRAELPPGNLDEPAPTY 686	Db 627 SAYQIVQEQLHPRHTKREGAMECYQVPTYQNALSGGPAPYFRAELPPGNLDEPAPTY 686
Db	623 SVYQVVEERPRRLRERRGAQDFSVPLTFETALRGVHGAELAASSLLEAMPPTV 682	Db 623 SVYQVVEERPRRLRERRGAQDFSVPLTFETALRGVHGAELAASSLLEAMPPTV 682
Qy	687 GDNRTYKGFWNPPLAPRKGYNITYQAMSSVEKETKTCVRIATAEHEPEVTPDAKQ 746	Db 687 GDNRTYKGFWNPPLAPRKGYNITYQAMSSVEKETKTCVRIATAEHEPEVTPDAKQ 746

DR	MGD; MGI:1321151; PtPRU.	Qy	627 SAYOTIVVEOLPHRHTKREAGAMECYQVPVITYONVALSGGAPYFAELPPCNLPEFAPFTV 686
DR	GO; GO:0005615; C:extracellular space; TAS.	Db	623 SYYQVVBVEBPRURREGAQDCSVPLFETALARGLYHFGELAASSLLEMPFTV 682
DR	GO; GO:0016021; C:intercellular space; membrane; TAS.	Qy	687 GDNPTYKGFWNPPLAPRKSYNNIQFOAMSSVEKETKTQCVYIATAAATPEPEVIFDPAKQ 746
DR	InterPro; IPR003962; FnIII subd.	Db	683 GDNCQYRGFWNPPLPEPKAYLIVQQASHLKGETRLNCIRIARACKESKRPL-EVSQR 741
DR	InterPro; IPR003961; FN III-like.	Qy	747 TDRVVKAGISA-GILVFLILLVVIVKSKLAKKRDAMGNTRQEMTHVNAMDRSY 805
DR	InterPro; IPR008979; Ga1_bind_like.	Db	742 SEEMLIGLICAGAVLILGAIIVIIRKGKVWMTK-ATVNRQEKTHMMSAVDRSF 800
DR	InterPro; IPR003599; Ig.	Qy	806 ADOSTLHAEDPLSLTFMDOHNFSPRLNDPLVPTAVLDENHSATAESESSL-DVRYLCE 864
DR	IPR007110; Ig-like.	Db	801 TDQSTLQEDERLGLISFMADPGYSPR-----GDQSGGYTEASSLGGSPRRPCG 849
DR	IPR000998; MAM.	Qy	865 GTESSPYQTGOLHPAIRVADLLQHINLMKTSDSYGKTFKEEYESFFEGOSASNDVAKDQNRA 924
DR	IPR000387; TYR_phosphatase.	Db	850 RKGSTSYHTGOLHPAIRVADLLQHINQMKTAEGYGTQBYESFFEG----WDATKXDKLK 905
DR	PF00041; fn3; 3.	Qy	925 KNRVGNITAYDHSRVTLQPVEDPSSDYNANYIDIWLYRDGYQPSHYTATQGVHETV 984
PFam;	Pfam; PF00629; MAM; 1.	Db	906 GGRQEPVSAYSDRHVKLHPMLADPDADYISANYI-----DGYHRSHNHFATOGPKPEMI 959
DR	Pfam; PF00102; Y_phosphatase; 2.	Qy	985 YDFWMWNVWQFOQSACTVMVTNLVEGRVKCYKWPDDTEVYGFKVTCVEMPLAYXVVRT 1044
DR	PRINTS; PR00014; FNTYPEII.	Db	960 YDFWMWNVWQCASTVMTKLVGRVKCSRYWPPSDMGIKITLVKTETLAYVVRT 1019
DR	PRINTS; PR00020; MANDOMAIN.	Qy	1045 FTLEBRGNEIREVKYQFHETGWPDIQPVYHATGLSFIIRRVKLSNPPSAGIVVHCSAGA 1104
DR	PRINTS; PR00000; PRTPHPTASE.	Db	1020 FALERGYSARHEVQFHFTAWPERGVYHATGLAFIRRVKASTPPDAGPVICSGAT 1079
SMART;	SMART; SM000409; TG; 1.	Qy	1105 GRTGCVIVIDIMDAEREGVVDYINCKVAKLRSRINMVQEYQIFHDIALECLGE 1164
SMART;	SMART; SM00137; MAM; 1.	Db	1080 GRTGCVIVLDVMDLMAECGVVDYINCKVTLCSRRVNMQITEQYIFHDIALECLGE 1139
DR	SMART; SM00194; PTPC; 2.	Qy	1165 TAIPYCEPKAYFDMIRIDSQTSNSHLKDEQFTLNSVTPLQAEQDCSIACLPRNHDKNRF 1224
DR	PROSITE; PS50083; FN3; 3.	Db	1140 TRPINEFRATYRENRIDQNSNQSLREFEQTLMNSVTPDQDVETSIALLPRNDKNS 1199
DR	PROSITE; PS50060; MAN_2; 1.	Qy	1225 MDMLIPDRCLPLFLITIDGESSNYINAAALMDSYROPAFAFIVTOYPLPNPTVKDFWRLLVYDYG 1284
DR	PROSITE; PS50033; TYR_phosphatase_1;	Db	1200 MDVLIPDRCLPLFLISSDGDPPNNYINAAALTDSYTREAAFTVLHP-LQSTTPDWRLLVYDYG 1259
DR	PROSITE; PS50056; TYR_phosphatase_2;	Qy	1285 CTSIMLNEVDLSQG---CPOQWPGEGMLRYGPQIVECMCSMDVNPRLRICMLTRP 1341
DR	PROSITE; PS50055; TYR_phosphatase_2P.	Db	1260 CTSIMLNLQINOSNSAWPCLOYWPGRQYGLMEVTFVSCTANEDLVSRRFRVONSSRL 1319
KW	Glycoprotein; Hydrolase; Receptor.	Qy	1342 QEGYLMVQQFOYLGWASHREVPGSRSFLKLQWQEBCEGGRITIHCLNGGRS 1401
SEQUENCE	SEQUENCE 1436 AA; 161199 MW; EFAAES2C6903F02 CRC64;	Db	1320 QBGHLLVRHFQLRNSAYRDTDPSKAFLHLAETDKWQ - AESGDGRTVYHCLNGGRS 1377
Qy	Score 4591; DB 2; Length 1436;	Qy	1402 GMFCALGIVYEMVKRQNVDVFHVYKTLRNSKPNVVAPEOYRFYCDALEYLES 1456
Matches	859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;	Db	1378 GTFCACTAVLEMIRCHSLVDVFAAKTLRNYKPNNVETMDYHFCYDVALEYLA 1432
Qy	32 AGGCTFDGPG---ACTDHYDOLYDDEFWHVAQEPHYLPPPEMPOGSYMMVDSNHHDPGE 88	Qy	RESULT 15
Db	24 AAGCTTFFEARSDPVVCPFSQAQYDDQWEQVRHPTCTRTPDLPHGAYLMNASOHTPGQ 83	PTPT_MOUSE	STANDARD
Qy	89 KARLQLEPTMKENDTHCDPSYLISQKLNQGTINLILVRYNGKPLANPIWNTGFTGRW 148	ID	PTPT_MOUSE
Db	84 RAHIIFLTSSENDTHCVCQESTFLYSNDGHSPTLGYVVRNGGPGSAVNMITGSHGRW 143	AC	Q99MB0; Q99MB1; Q99MB2; Q9JIZ1; Q9JIZ2; Q9JLPO;
Qy	149 LRAELAYSTFWPNNEYQVTFEAEVSGGRSGYIAIDDIOQLVSYPCDKSPHFLRLGDEVNAG 208	DT	10-OCT-2003 (Rel. 42, Created)
Db	144 HOAELAYSTFWNEQFVLFEEAISPKDGYTQDILFVQDLYEVNAG 203	DT	10-OCT-2003 (Rel. 44, Last sequence update)
Qy	209 QNATFOCATGERDAVINKLWLORRNGEDIPVQTKNINHRRFAASPLQEVTKTDDLYR 268	DB	05-JUL-2004 (Rel. 44, Last annotation update)
Db	204 QNASFQCNAGAAAEAHFFLORQGTVLPAAGVRHLSHREFLATPLASVGRSEBDLYR 263	DE	Receptor-type protein-tirosine phosphatase T precursor (EC 3.1.3.48)
Qy	269 CTTQSERGCVSNFAQIIVREPRPRPAPQOLVGVTYLIQIANSIIGGPILKEE 328	DE	(R-PtP-T) (RPTPrho) (mRPTPrho) (mRPTPrn)
Db	264 CVSQAPRAGVSNAELVKEPEPTLAPPOLLRAGPTYLQLQNTNSIIGGPIVRKIE 323	DE	Name = Pptpr1;
Qy	329 YRMISGSSTETHAVNAPYKWLHDPTDEYEYRVLILTRGBEGTGLPGPLPLTRKCAEP 388	OS	Mus musculus (Mouse)
Db	324 YMARGPWAETVAVNLQTYKLWHDPTDEYEYSVLLTRPGCGTGRGPPLISRYKCAEP 383	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Qy	389 MRTPKTLKIAETOARRIAVADWESLGNTNTTRCHTFNTCYHYFRG--HNESRADCLMDP 446	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Db	384 TRAPKGFLFAETQARQTLQWPELGTNTVTRCHAYVSLCYRTLGSSHNQFIRECVYMR 443	OC	NCBI_TaxID=10090;
Qy	447 KAFQHVNHLIPYPTVNSKMLTNPEKRESSETIQTDEDVPGPVPVKSLOGTSENKI 506	RN	[1]
Db	444 GASRYTAKNLPLPFRNTIHWRLTNTPEGRKEGVFTQDVEDPGGIAAESLTFTPLEDMI 503		
Qy	507 FLWKWKEPBPGNGLITQYEVSSYTSRSPPAVPGPQTVSNLWNSTPHVFMHLHGTY 566		
Db	504 FLKWEERPBPGNLITQYEVSSYTSRSPPAVPGPQTVSNLWNSTPHVFMHLHGTY 563		
Qy	567 QFPIRASVKGFGPATAINVTNNISAPPLDYEVGVDASLNETATTIVLRLPAAQKCAPI 626		
Db	564 LFSVTRARTSKGFGQAAALTBTINISAPS-DYADMPSPLGESSENTIVLRLPAAQKCAPI 622		

/FTID=vsp 007805.
 R -> RHPAETVGGATLGRAASPGM (in isoform
 2).
 /FTID=vsp 007806.
 Missing (in Ref. 1).
 R -> P (in Ref. 1).
 GGCFS -> RGYF (in Ref. 1).
 A -> T (in Ref. 4; AAF82401).
 A -> T (in Ref. 4; AAF82401).
 FT CONFLICT 254 254
 FT CONFLICT 266 266
 FT CONFLICT 602 602
 FT CONFLICT 822 822
 FT CONFLICT 825 825
 FT CONFLICT 844 845
 FT CONFLICT 1016 1016
 FT CONFLICT 1049 1049
 FT CONFLICT 1050 1050
 FT CONFLICT 1076 1076
 FT CONFLICT 1103 1103
 FT CONFLICT 1259 1259
 FT CONFLICT 1266 1266
 FT CONFLICT 1269 1269
 FT CONFLICT 1454 AA; 163012 MW; C604647B423F8A8 CRC64;
 SQ SEQUENCE

Query Match, Score 4579, DB 1, Length 1454;
 Best Local Similarity 57.8%; Pred. No. 8 3e-301;
 Matches 841; Conservative 239; Mismatches 333; Indels 42; Gaps 8;

21 PLLGSAIGQFSAAGCTFDGPGACDYHQDL-YDDFEWVHVSQAQEPHYLPPPEQSYMVY 79
 22 PPLPGACQASAGGCSDFEYHSNCGTSVALTGTWQEQNTWEKMLDPAVPTSEMMV 81
 Qy 80 DSSNHDEGEKARLOLPTMKENDTHC1DFSTLILYSQKGLNPTGLNLIVRNGPFLANPIN 139
 82 NSSGRASGKQAHILLPTKEKNDTHC1DFHYFFSSRDRSPGALNYYKVNGPQGNPVNN 141
 Qy 140 VTFGFTGRDWLRWLRALAVSTFWPHFYQTVFTEAVFSGGRSGSYTAIDDIOQLSYCDKSYPHEFLR 199
 Db 142 VSGVITTEGVWRAELA1STFWPHFYQTVFESTLSLGKGPYIADVDEVRLAFCRKAFHFLR 201
 Qy 200 LGDVEVNAQONATFOCATTGRDAVNKLWLORRNGEDIPVQTKNINHRFAASPLQEV 259
 Db 202 LQNEVYKVNQONATFOCAGKWSQHDWLWLQWNGDTHALMVTYVNRHRSATSVADT 261
 Qy 260 TKTQDQLKRCVTOQSERSGSVNSFAQLIVRERPRPIAPPOLQVGPTYLQJLNANSIGD 319
 Db 262 SQRISKYRCVTRSDGSSGVNSYAEVKEPTPTAPPELLAVGATYLWIKPNANSIGD 321
 Qy 320 GPILKEVEYRTNTSGSMTEHVAAPTYKLWHLDPDTYEYTRVLUTRGEGGTGLGPPL 379
 Db 322 GPILKEVEYRTNTSGSMTEHVAAPTYKLWHLDPDTYEYTRVLUTRGEGGTGLGPPL 381
 Qy 380 ITRTKCAEPMRPTKTLKIAETOARRAIVDWESLGNTNTRCHTENTYCHYFRGINRESA 439
 Db 382 ITRTKCAEPMRPTKTLKIAETOARRAIVDWESLGNTNTRCHTENTYCHYFRGINRESA 439
 Qy 440 DCLMDPDKAQPQHVNHLRPYTNSLKMINTBGRKESSEBLIQDVEDPGPVPKSLQG 499
 Db 440 EABEVQIOTSSHTYLRGIRPFMTIRLRLLSNPEGRMESEELVQTBEDPGAVPLES1QG 499
 Qy 500 TSPENKIFLANKBPELEPNGLTQYEVSSSFRSFDPAVPGPPQVNLSNTHRFVMH 559
 Db 500 GPPEEKYIQLWPPNETNGVLTLYENYKAVSLSLSDAISLSSQGRVFKRNETHFLFG 559
 Qy 560 LHPGTTYCOFFIRASTVKGFPATAINTNTNISAPSPLPDYEGYDASLNETATTITYLLRPA 619
 Db 560 LYPTTGSTFTKASTAKGFPVVTTRATKISAPSMEYD-ADTPNEDTDTYMLRPA 618
 Qy 620 QAKGAPISAYQIVVEQHPPRTKREAGAMECYQVQPYTQNALSGGARYFAAELPGNLP 679
 Db 619 QERGAPSVYQLVVKERLQSKERRAADIIECPSVPYRNASNLDLHYFAELKESNLNP 678
 Qy 680 EPAPFTYGDNRITYKGFMNPPPLAPRKGYNNYFQAMSSVKEKTXTCVRIATAATEBEPV 739

Search completed: June 1, 2005, 13:55:00
 Job time : 177.044 secs

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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:31:52 ; Search time 145.589 Seconds
(without alignments)

Title: US-09-887-669-2

Perfect score: 7709

Sequence: 1 MDTTAAALPAFLILLSP.....EAPEQYRFYCVDALLELESS 1439

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16D0e04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	7692	99.8	1439	2	AAR63632		Aarj3632 Human rec
2	7688	99.7	1439	2	ADJ68478		Adj58478 Human hea
3	7656	99.3	1440	2	AYV2991		Aayv2991 Human pro
4	7656	99.3	1440	8	ADI23886		Adi23886 Human PTP
5	7571	98.2	1457	5	ABB57308		Abb57308 Mouse isc
6	7524	97.6	1457	2	AAR63633		Aarj3633 Murine re
7	7474	93.1	1407	2	AAR63631		Aamj9159 Murine re
8	4818	62.5	1452	4	AAM79159		Aamj9159 Human pro
9	4807	62.4	1452	8	ADJ80761		Adj580761 Human pro
10	4806	62.3	1452	6	ABR58229		Abrj58229 Human can
11	4784	62.1	1452	7	ADJ68277		Adj58277 Human hea
12	4777	62.0	1455	4	AAM80143		Aamj80143 Human pro
13	4602	59.5	1436	7	ADB79775		Adb79775 Rat Reptor
14	4586	59.5	1436	2	AAW41361		Aaw41361 Receptor
15	4577	59.4	1462	5	ABB97521		Abb97521 Novel hum
16	4564	59.2	1463	6	ABJ37035		Abj37035 Human bre
17	4564	59.2	1463	7	ADB75519		Adb75519 Prostate
18	4554	59.2	1520	5	ABJ05584		Abj05584 Breast ca
19	4555	59.1	1499	4	AAM25768		Aamj25768 Human pro
20	4374	56.7	1442	7	ADJ68999		Adj58999 Human hea
21	4287	55.6	1430	2	AAW49907		Aaw49907 Human pan
22	2493	32.3	623	4	AAM25675		Aamj25675 Human pro
23	2210	28.7	815	4	AAM25875		Aamj25875 Human pro
24	1529	19.8	1501	2	AAR72858		Aar72858 Rat recep
25	1513	19.6	1254	8	ADN02662		Adn02662 Liver dis

ALIGNMENTS

RESULT 1
AAR3632 standard; protein; 1439 AA.
ID AAR3632;
XX AAR3632;

AC XX DT 21-OCT-2004 (revised)
DT 25-MAR-2003 (revised)
DT 26-OCT-1995 (first entry)
XX DB Human receptor-type protein tyrosine phosphatase (RPTP) kappa.
XX KW Receptor-type protein tyrosine phosphatase protein; cellular signal; RPTase-kappa, protease.

XX OS Homo sapiens.
OS Unidentified.
XX FH Key Domain FT Domain FT Domain FT Domain
Location/Qualifiers
/label = Ig-like domain
/label = alpha helical transmembrane domain
207 .277
755 .774

XX WO9424161-A1.
XX PD 27-OCT-1994.
XX PP 20-APR-1994;
XX PR 21-APR-1993;
PR 01-JUL-1993;
PR 01-JUL-1993;
XX PA (UYNY-) UNIV NEW YORK MEDICAL CENT.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX PI Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;
XX DR WP; 1994-341769/42.
DR N-PSDB; AAQ72913.
XX PT Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)
protein and DNA - useful to identify cpds which bind to RPTP-k and
modulate enzymatic activity. Also inhibition of type II RPTP homo:phobic
binding (Eng).
XX PT Claim 4; Fig 15; 144pp; English.

The novel receptor-type protein tyrosine phosphatase protein or glycoprotein is termed RPTP kappa (also known as RPTase-kappa). Human breast cancer cell line SK-BR-3 was examined by PCR using primers B correspond to conserved sequences within the PTP catalytic domains shared by all identified PTPases. Several known PTPases were revealed together with some novel members of the PTPase family. One novel sequence, designated MCP7 (Mammary carcinoma-derived PTPase clone 7) was highly represented in all 121 clones examined. The MCP7 PCR fragment was used to screen a SK-BR-3 cDNA library. The results are AA07213 and its deduced AA sequence AARc3632. The AA sequence displays the structural organisation of a type II transmembrane PTPase. The N-terminal hydrophobic stretch of 20-6 AAs is typical of signals peptides. A second region consisting of hydrophobic residues (see FT) is predicted to be a single alpha-helical transmembrane domain. It is followed by a short region of mainly basic residues characteristic of a transfer stop sequence. The amino-terminal portion of the putative extracellular domain contains a sequence motif, a so-called MAM domain, spanning a region of about 100 residues. This motif is followed by one possible Ig-like domain (see FT). (Updated on 25-MAR-2003 to correct PN field.)

Revised record issued on 21-OCT-2004 : Correction to Feature table key

Query Match	Score	DB 2;	Length	1439;
Best Local Similarity	99.9%;	Pred.	No. 0;	
Matches 1437; Conservative	1;	Mismatches	1;	Indels
Qy	1	MDTTAAALAPAVALLLSPWPLGSAQGOSAGGTFTDGPAGCDYHQDLYDDFEWVTV	60	
Db	1	MDTTAAALAPAVALLLSPWPLGSAQGOSAGGTFTDGPAGCDYHQDLYDDFEWVTV	60	
Qy	61	SAQEPHILPPENPOGSWMIIVOSSDHDPGEKARLQLPMTMKENDTHCIDSFLYLYSQGLNP	120	
Db	61	SAQEPHILPPENPOGSWMIIVOSSDHDPGEKARLQLPMTMKENDTHCIDSFLYLYSQGLNP	120	
Qy	121	GTLNLYLVRNKGPLANPIWNTGFTGRDWLRAELAVSTFWNEYQVTFEAEGSGRSGYI	180	
Db	121	GTLNLYLVRNKGPLANPIWNTGFTGRDWLRAELAVSTFWNEYQVTFEAEGSGRSGYI	180	
Qy	181	AIDDIQVLSYPCDKSPHFLRGDVEVNGONATFOCITGRDAVINKLWLORNGEDIPIV	240	
Db	181	AIDDIQVLSYPCDKSPHFLRGDVEVNGONATFOCITGRDAVINKLWLORNGEDIPIV	240	
Qy	241	AOTKINHRRFASTLQLQVTKDQIIRCUTQSERSGSVNAQFLIREPREPRAPPQI	300	
Db	241	AOTKINHRRFASTLQLQVTKDQIIRCUTQSERSGSVNAQFLIREPREPRAPPQI	300	
Qy	301	LGVGPTYLQIQLNANSITGDGPITLKEVEYRMTSGSWEVTHAVNAPTYKLWHDPPDTEYB	360	
Db	301	LGVGPTYLQIQLNANSITGDGPITLKEVEYRMTSGSWEVTHAVNAPTYKLWHDPPDTEYB	360	
Qy	361	IRVLTLTRPEGEETGLPGPPLTRTKCAEPMRTPKTLKIAEQARIAWDLSGNITRC	420	
Db	361	IRVLTLTRPEGEETGLPGPPLTRTKCAEPMRTPKTLKIAEQARIAWDLSGNITRC	420	
Qy	421	HFPNTICHYFRGHNSKADCLMDPKAQPQVNHLPKPNVSLTMIDPEGRKESE	480	
Db	421	HFPNTICHYFRGHNSKADCLMDPKAQPQVNHLPKPNVSLTMIDPEGRKESE	480	
Qy	481	TIIQTDEDPVGPPVVKSLQGTSEPNKLFLANKEPLDENGITQYEISYSSRSFDPAVV	540	
Db	481	TIIQTDEDPVGPPVVKSLQGTSEPNKLFLANKEPLDENGITQYEISYSSRSFDPAVV	540	
Qy	541	AGBPQTVSNLNSTHAYMHJHPGTYCFFTRASTYKFGPATAINVTNISAPTLPDYE	600	
Db	541	AGBPQTVSNLNSTHAYMHJHPGTYCFFTRASTYKFGPATAINVTNISAPTLPDYE	600	
Qy	601	GVDAISLNENATTITVLLRPAQKAPISAQYQVVEELHPHRTKREAGMECYQVPTVYQ	660	
Db	601	GVDAISLNENATTITVLLRPAQKAPISAQYQVVEELHPHRTKREAGMECYQVPTVYQ	660	
Qy	661	AMSGGAPYYFAABLPPGNLPEPAPFTVGDNRTYQGFNNPPLAPRKGINIYFOAMSSVKE	720	

CC	Db	661	AMSGGAPYYFAABLPPGNLPEPAPFTVGDNRTYQGFNNPPLAPRKGINIYFOAMSSVKE	720
CC	Qy	721	TKTQCVTRIATAKATEBPEVTPDPAQTDVVKIAGISAGILVFLILLVVLLVTKSKLA	780
CC	Db	721	TKTQCVTRIATAKATEBPEVTPDPAQTDVVKIAGISAGILVFLILLVVLLVTKSKLA	780
CC	Qy	781	KKRKDAMGNTQEMTHVMNAMDTSYADQSTLHADPLSITFMDONFSPYENHSATAES	840
CC	Db	781	KKRKDAMGNTQEMTHVMNAMDTSYADQSTLHADPLSITFMDONFSPYENHSATAES	840
CC	Qy	841	SRLUDPVRYLCEGETSPYQTGQLHPAIRYADLQLQINLAKTSDFGKBEYESFPEGOSA	900
CC	Db	841	SRLUDPVRLCBGTRBSPYQTGQLHPAIRYADLQLQINLAKTSDFGKBEYESFPEGOSA	900
CC	Qy	901	SWDVAKKDQNRAQKNGYNTIAYDHRVILQVEDPSSDYINANTIDGQYRPSHVIATQG	960
CC	Db	901	SWDVAKKDQNRAQKNGYNTIAYDHRVILQVEDPSSDYINANTIDGQYRPSHVIATQG	960
CC	Qy	961	PVHEVYDFWRMINEQEQACIVMNTVLEVGRVICKYKYNDDTEVYGGDFKTYCVMEMPLA	1020
CC	Db	961	PVHEVYDFWRMINEQEQACIVMNTVLEVGRVICKYKYNDDTEVYGGDFKTYCVMEMPLA	1020
CC	Qy	1021	EYVDTFTLERRGNEIREYKQFHITGWPDHGVPTHATGLSPIRRVLKLSNPPSGAPIVV	1080
CC	Db	1021	EYVDTFTLERRGNEIREYKQFHITGWPDHGVPTHATGLSPIRRVLKLSNPPSGAPIVV	1080
CC	Qy	1081	HCSAGAGRIGTCYIVIDIMDMAERGVVDIYNCYRALSRRINMVQTEQYIIFIDAILE	1140
CC	Db	1081	HCSAGAGRIGTCYIVIDIMDMAERGVVDIYNCYRALSRRINMVQTEQYIIFIDAILE	1140
CC	Qy	1141	ACLGCTAAIPVCEFAAYFDMIRIDSQTNSSHLDKFOTLNSVTPLQEDCSIACLPRN	1200
CC	Db	1141	ACLGCTAAIPVCEFAAYFDMIRIDSQTNSSHLDKFOTLNSVTPLQEDCSIACLPRN	1200
CC	Qy	1201	HDKNRFMDMLPPDRCLPPLITDGESSNYINAALMSYROPAAFVTOYDPLPNTKDFWR	1260
CC	Db	1201	HDKNRFMDMLPPDRCLPPLITDGESSNYINAALMSYROPAAFVTOYDPLPNTKDFWR	1260
CC	Qy	1261	LYVDYGCSTSVMNLNDYLDLSQCGPQWPEEGMLRYGPQVCMSCSMDCDVINRIPICNL	1320
CC	Db	1261	LYVDYGCSTSVMNLNDYLDLSQCGPQWPEEGMLRYGPQVCMSCSMDCDVINRIPICNL	1320
CC	Qy	1321	TRPOEGYLMQCOFOYLGASHREVPGSKRSFLKLJLOVEKQOEYKEGEGRTIHLNLGG	1380
CC	Db	1321	TRPQEGYLMQCOFOYLGASHREVPGSKRSFLKLJLOVEKQOEYKEGEGRTIHLNLGG	1380
CC	Qy	1381	GRSGMFCAIGIVVYENVKRQNVYDVFHAVKTLRNSKPNMVAPEQYRFCYDVALEYLESS	1439
CC	Db	1381	GRSGMFCAIGIVVYENVKRQNVYDVFHAVKTLRNSKPNMVAPEQYRFCYDVALEYLESS	1439
XX	RESULT 2			
XX	ADJ66478			
XX	ID ADJ66478	standard; protein;	1439 AA.	
XX	DT 06-MAY-2004	(first entry)		
XX	DB Human heat mitochondrial protein as a therapeutic target	SeqID234.		
XX	AC ADJ66478;			
XX	KW Huntington's disease; osteoarthritis;			
XX	KW Leber's hereditary optic neuropathy; LHON;			
XX	KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;			
XX	KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;			
XX	KW neuroprotective; nootropic; anticonvulsant; antiarthritic;			
XX	KW osteopathic; ophthalmological; cytostatic.			
XX	OS Homo sapiens.			
XX	PN WO2003087768-A2.			
XX	PN			

XX	PD 23-OCT-2003.	Qy 421 HTPNVTICHYFRGNESKAACDCLMDPKAPQHVVNHLPPYNTVSLRMLTNTNPEGRKESEE 480
XX	PF 04-APR-2003: 2003NO-US010870.	Db 421 HTPNVTICHYFRGNESKAACDCLMDPKAPQHVVNHLPPYNTVSLRMLTNTNPEGRKESEE 480
XX	PR . 12-APR-2002; 2002US-037843P.	Qy 481 TIIQTEDVPGPVVKSLQGTSPEKIFLNWKEPIDLPNGITOYBISYSIERSPDAVPV 540
PR . 17-SEP-2002; 2002US-038987P.	Db 481 TIIQTEDVPGPVVKSLQGTSPEKIFLNWKEPIDLPNGITOYBISYSIERSPDAVPV 540	
PR 20-SEP-2002; 2002US-0412418P.	XX (MTO-) MITOKOR.	XX (BUCK-) BUCK INST AGE RES.
XX	PA (MTO-) MITOKOR.	PA (BUCK-) BUCK INST AGE RES.
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	Qy 541 AGPPOTVSNLWNSTHVFNMHLHPCTTYOFIRASTVKGGPATATNVTNISAPLPDV 600	
PI Warnock DE;	Db 541 AGPPOTVSNLWNSTHVFNMHLHPCTTYOFIRASTVKGGPATATNVTNISAPLPDV 600	
XX DR ; WPI: 2003-845169/78.	Qy 541 GVDSLNETATTITVLRPAQAKSAPIASYQIVVEELPHRTKREAGAMECYQVPTVQN 660	
PT Identifying a mitochondrial target for drug screening assays and for	Db 601 AMSGGAPYYFAAELPPGNLPEAPPFTVGDRNTRVQFWPLPKGNYTFQAMSVEKE 720	
PT treating diseases associated with altered mitochondrial function,	Db 601 AMSGGAPYYFAAELPPGNLPEAPPFTVGDRNTRVQFWPLPKGNYTFQAMSVEKE 720	
PT comprises detecting a modified polypeptide in a sample and correlating	Db 661 AMSGGAPYYFAAELPPGNLPEAPPFTVGDRNTRVQFWPLPKGNYTFQAMSVEKE 720	
PT with the disease.	Db 721 TKTOCVRATKAATEPEVTPDPAKQTDRVKLAGISAGLVFILLLVILTVKSKLA 780	
PS XX	PS SEQ ID NO 284; 180pp; English.	Db 721 TKTOCVRATKAATEPEVTPDPAKQTDRVKLAGISAGLVFILLLVILTVKSKLA 780
CC This invention relates to novel mitochondrial targets that can be used	Qy 781 KKRKDAMGNTROEMTHNMAMDYSYADQSTLHAEDPLSTEMDHOHNFSRPNHSAATES 840	
CC for therapeutic intervention in treating a disease associated with	Db 781 KKRKDAMGNTROEMTHNMAMDYSYADQSTLHAEDPLSTEMDHOHNFSRPNHSAATES 840	
CC altered mitochondrial function. Specifically, it refers to a method for	Db 841 SRLLDVPRVLCGETGSPYOTQOLHPAIRAVDLQHINLMKTSDSYGFKEYESPFEGQSA 900	
CC identifying proteins of the human heart mitochondrial proteome that are	Db 841 SRLLDVPRVLCGETGSPYOTQOLHPAIRAVDLQHINLMKTSDSYGFKEYESPFEGQSA 900	
CC useful for drug screening assays, as well as therapeutic targets. The	Qy 901 SWDYAKODNRAKNTGYNTIAYDSRVLQVEDPSSDYNANYIDGQRPSHIAATQG 960	
CC present invention describes a method for identifying such proteins that	Db 901 SWDYAKODNRAKNTGYNTIAYDSRVLQVEDPSSDYNANYIDGQRPSHIAATQG 960	
CC can be used in the treatment of various diseases associated with altered	Db 961 PVHETYDFWRMTIWOQSACIVMVNLVEYGRVYCKWPMDDTEVYGFKVTCVMEPLA 1020	
CC mitochondrial function including diabetes mellitus, Huntington's disease,	Db 961 PVHETYDFWRMTIWOQSACIVMVNLVEYGRVYCKWPMDDTEVYGFKVTCVMEPLA 1020	
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	Qy 1021 EYVTRTFILERGNEIREVKQFFTGWDHGVPYHATGLSFPIRVLSNPAGPIVV 1080	
CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy	Db 1021 EYVTRTFILERGNEIREVKQFFTGWDHGVPYHATGLSFPIRVLSNPAGPIVV 1080	
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	Qy 1141 ACLOCGETALPVCEPKAYFDMDIRISQTNSSHLKDEFQTLNSVTPRLQAFDCSTAICLPRN 1200	
CC compositions have neuroprotective, nootropic, antidiabetic,	Db 1141 ACLOCGETALPVCEPKAYFDMDIRISQTNSSHLKDEFQTLNSVTPRLQAFDCSTAICLPRN 1200	
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and	Qy 1201 HDKNRFMDMLPPDRCLPFLITIGBSNSYNAALMSDTRQPAAPIVTVQPLPNTVKDFVR 1240	
CC cytoskeletal activities. This polypeptide sequence is a human heart	Db 1201 HDKNRFMDMLPPDRCLPFLITIGBSNSYNAALMSDTRQPAAPIVTVQPLPNTVKDFVR 1240	
CC mitochondrial protein of the invention.	Db 1261 LVDYDGCTSIVMINEVDISQGPCKWPEGMRLYGPIOVECMCSMDCDVINRFRICNL 1320	
XX SQ Sequence 1439 AA;	Qy 1261 LVDYDGCTSIVMINEVDISQGPCKWPEGMRLYGPIOVECMCSMDCDVINRFRICNL 1320	
Best Local Similarity 99.7%; Score 7688; DB 7; Length 1439;	Db 1261 LVDYDGCTSIVMINEVDISQGPCKWPEGMRLYGPIOVECMCSMDCDVINRFRICNL 1320	
Matches 1436; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Qy 1321 TRPOQGYLMQQFOYLGWASHREVPGSKRSFLKLLOQVKWQREWKEGSRGRTIHLCLNG 1380	
Qy 1 MDTTAAALPAFAVALLISPWPLIGSACQFSAGSCTEDFGPAGCDYHODLYDDFEMVHV 60	Db 1321 TRPOQGYLMQQFOYLGWASHREVPGSKRSFLKLLOQVKWQREWKEGSRGRTIHLCLNG 1380	
Db 1 MDTTAAALPAFAVALLISPWPLIGSACQFSAGSCTEDFGPAGCDYHODLYDDFEMVHV 60	Qy 1381 GRSGMFCAGIVVEMVRQVWVDFHAVTKLRNSKPNNVAEPOYRCYDVALYLESS 1439	
Qy 61 SAQEPHYLPPEMPQSYMIVDSSDEDPGKARLQLOPTMKENDTHCIDFYLILYSQKGAMP 120	Db 1381 GRSGMFCAGIVVEMVRQVWVDFHAVTKLRNSKPNNVAEPOYRCYDVALYLESS 1439	
Db 61 SAQEPHYLPPEMPQSYMIVDSSDHDPGKARLQLOPTMKENDTHCIDFYLILYSQKGAMP 120	Qy 1381 GRSGMFCAGIVVEMVRQVWVDFHAVTKLRNSKPNNVAEPOYRCYDVALYLESS 1439	
Qy 121 GTLNILVLRVTKGPIANPIVNTGFTGRDVLRAELAVSTWPNEYQVIFPAEVSGRSGT 180	Db 1381 GRSGMFCAGIVVEMVRQVWVDFHAVTKLRNSKPNNVAEPOYRCYDVALYLESS 1439	
Db 121 GTLNILVLRVTKGPIANPIVNTGFTGRDVLRAELAVSTWPNEYQVIFPAEVSGRSGT 180	Qy 181 ADDIQVLSYPCDKSPHFLRQDVEVNAGONATFOCIATGRDAYHNLKWLQRNGEDIIV 240	
Qy 181 ADDIQVLSYPCDKSPHFLRQDVEVNAGONATFOCIATGRDAYHNLKWLQRNGEDIIV 240	Db 181 ADDIQVLSYPCDKSPHFLRQDVEVNAGONATFOCIATGRDAYHNLKWLQRNGEDIIV 240	
Qy 241 AQTQINHRFAASPRLQLQVTKDOLYRCTQSERGSGVSNFQOLIVEPRPPIAPPQ 300	Qy 241 AQTQINHRFAASPRLQLQVTKDOLYRCTQSERGSGVSNFQOLIVEPRPPIAPPQ 300	
Db 241 AQTQINHRFAASPRLQLQVTKDOLYRCTQSERGSGVSNFQOLIVEPRPPIAPPQ 300	Db 241 AQTQINHRFAASPRLQLQVTKDOLYRCTQSERGSGVSNFQOLIVEPRPPIAPPQ 300	
Qy 301 LGVGPYLLIQLNANSIIGGPILIKEVYRMTSWSWTHAANAPTYKLWHLDPDTE 360	Qy 301 LGVGPYLLIQLNANSIIGGPILIKEVYRMTSWSWTHAANAPTYKLWHLDPDTE 360	
Db 301 LGVGPYLLIQLNANSIIGGPILIKEVYRMTSWSWTHAANAPTYKLWHLDPDTE 360	Db 361 IRVLTTRPSEGCGTGLPGPLPLTRTKCAEPMRTPKTLKIAEIQARIAYWESLGYNITRC 420	
Qy 361 IRVLTTRPSEGCGTGLPGPLPLTRTKCAEPMRTPKTLKIAEIQARIAYWESLGYNITRC 420	Db 361 IRVLTTRPSEGCGTGLPGPLPLTRTKCAEPMRTPKTLKIAEIQARIAYWESLGYNITRC 420	

RESULT 3
AAV29591 standard; protein; 1440 AA.
ID AAV29591

XX	AAY29591;	481	TIIQTDEDVYEGPVPKSLQGTSFENKIFILNWKEPPLDPNGLITOYEISYSSIRSFPDAVPV	540
AC		541	AGPPOTVSNIWNSTHVTHMLHPGTYYQPIRASTVKGCPATAINTVNINISAPTLIDYE	600
XX	14-OCT-1999 (first entry)	541	AGPPOTVSNIWNSTHVTHMLHPGTYYQPIRASTVKGCPATAINTVNINISAPTLIDYE	600
DE	Human protein phosphatase k.	541	AGPPOTVSNIWNSTHVEMHLHPGTYYQPIRASTVKGCPATAINTVNINISAPTLIDYE	600
XX	Human; protein phosphatase k; HPTPK.	601	GVDA8LINEATTITVLRLPAQKAPISAYQIVVVELPHPRTRKEAGAMECYQVFTVYQN	660
OS	Homo sapiens.	601	GVDA8LINEATTITVLRLPAQKAPISAYQIVVVELPHPRTRKEAGAMECYQVFTVYQN	660
XX	KM OS KR98026246-A.	661	AMSGCAPIYFAAELEPGNLPPEPAPPTVGDNRTYQGFWNPLAPRKGNTYFOAMSVKE	720
PN		661	AMSGCAPIYFAAELEPGNLPPEPAPPTVGDNRTYQGFWNPLAPRKGNTYFOAMSVKE	720
XX	PD 15-JUL-1998.	721	TKTQCVRIAIK-ATTEPEVYLPDPAKOTDRVKAGISAGILVFLILLWVLLWIKSKL	779
XX	PF 08-OCT-1996;	721	TKTQCVRIAIK-ATTEPEVYLPDPAKOTDRVKAGISAGILVFLILLWVLLWIKSKL	780
XX	96KR-00044614.	780	AKRKDAMGNTRQENTHMYNAAMDREYADQSTLHAEDPLSTFMDOHNFSPRYENSAAE	839
PR	08-OCT-1996;	781	AKRKDAMGNTRQENTHMYNAAMDREYADQSTLHAEDPLSTFMDOHNFSPRYENSAAE	840
XX	96KR-00044614.	840	SSRLUDPVRLCEGTESPYOTGOLPAIRADLQHINLMTSDSYGKFKEYESFFEGQS	899
PA	(KOAD) KOREA ADV INST SCI & TECHNOLOGY.	841	SSRLUDPVRLCEGTESPYOTGOLPAIRADLQHINLMTSDSYGKFKEYESFFEGQS	900
XX	Hah HJ, Kil MC, Yang Y, Byun GH;	900	ASWDVAKDQONRAXYKGNLIAVDISRVILQPDSSPYDINANVYIDGKQRPSHYIATQ	959
PI	PI: 1999-335582/28.	901	ASWDVAKDQONRAXYKGNLIAVDISRVILQPDSSPYDINANVYIDGKQRPSHYIATQ	960
DR	N-PSDB; ANZ08539.	960	GPVHETTYDFWRMWIQEQSACIVMVTNLVEGRYRYCKWPDDETVYGDPKVTCMEPL	1019
XX	PT Human protein phosphatase, base sequence thereof and amino acid sequence thereof.	961	GPVHETTYDFWRMWIQEQSACIVMVTNLVEGRYRYCKWPDDETVYGDPKVTCMEPL	1020
PS	Disclosure; Fig 1a-d; 14pp; Korean.	1020	AEVYRTFTLERRGYNEIREVKOFFGMDHGVYHATGLLSFRRVKLSNPPSAGPIV	1079
XX	The present sequence represents human protein phosphatase k (HPTPK).	1021	AEVYRTFTLERRGYNEIREVKOFFGMDHGVYHATGLLSFRRVKLSNPPSAGPIV	1080
CC		1080	VHCSAGAGRGCYIIVIDIMDMAEBCGNDIINCXKAIRSRINNQTEQYIIFHDAIL	1139
XX	Sequence 1440 AA;	1081	VHCSAGAGRGCYIIVIDIMDMAEBCGNDIINCXKAIRSRINNQTEQYIIFHDAIL	1140
SQ	Query Match 99.3%; Score 7656.5; DB 2; Length 1440;	1140	EACLGCTA1PVCEPKAYEDMIRDMSQTNSSHLKDFEFQTLNSVPRLOADECSACLPR	1199
Best Local Similarity 99.4%; Pred. No. 0; Mismatches 3; Indels 5; Gaps 1;	Db	1141	EACLGCTA1PVCEPKAYEDMIRDMSQTNSSHLKDFEFQTLNSVPRLOADECSACLPR	1200
Matches 1431; Conservative 3; Mismatches 5; Indels 5; Gaps 1;	Db	1200	NHDKNRFMDMLPPDPCLPFLITIDGESESSNTINAALMDSTROPAAPTIVTOYPLPNTVKDFW	1259
Query 1 MDTAAALPAVALLLSPWPLGSAQGFSAGGCTFDGSPGACDYHQDLYDDFEWAVH 60	Db	1201	NHDKNRFMDMLPPDPCLPFLITIDGESESSNTINAALMDSTROPAAPTIVTOYPLPNTVKDFW	1260
Db 1 MDTAAARAVPAVALLLSPWPLGSAQGFSAGGCTFDGSPGACDYHQDLYDDFEWAVH 60	Db	1260	RLYDYGCTSIVMLNEVDIISOGCPQYWPEEGMLRGPQVCECMSMDCDVINRIFRICN	1319
Query 61 SAQEPHYPPEMPGSTMIVDSSDHDFGKEARLQLPTMKENDDTHC1DFSYLYSOKGLNP 120	Db	1261	RLYDYGCTSIVMLNEVDIISOGCPQYWPEEGMLRGPQVCECMSMDCDVINRIFRICN	1320
Db 61 SAQEPHYPPEMPGSTMIVDSSDHDFGKEARLQLPTMKENDDTHC1DFSYLYSOKGLNP 120	Db	1262	LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1379
Query 121 GTLNILYVRNKGPLANPIWNTGFTGRDWLRAELAYSTFWNEYQVIFEAEVSGGRSGYI 180	Db	1263	1320 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380
Db 121 GTLNILYVRNKGPLANPIWNTGFTGRDWLRAELAYSTFWNEYQVIFEAEVSGGRSGYI 180	Db	1321 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Query 181 ADDIQVLSYPCDKSPHFLRLQDVEVAGQNTFOCATGRDAVANKLWLRNGEDIPV 240	Db	1322 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Db 181 ADDIQVLSYPCDKSPHFLRLQDVEVAGQNTFOCATGRDAVANKLWLRNGEDIPV 240	Db	1323 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Query 241 ACTKNINRRFAASFRLOQVTKTDQDLRYCVTQSERGSIVSNAQIIVREPREPIAPPQL 300	Db	1324 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Db 241 ACTKNINRRFAASFRLOQVTKTDQDLRYCVTQSERGSIVSNAQIIVREPREPIAPPQL 300	Db	1325 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Query 361 IRLVLTTPGEGGTGLPGLPLPRTKCAPMRTPTKIAEQARRAVDWSLGNITRC 420	Db	1326 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Db 361 IRLVLTTPGEGGTGLPGLPLPRTKCAPMRTPTKIAEQARRAVDWSLGNITRC 420	Db	1327 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Query 421 HTFNVNTICHYHRGHNESKADCLDMDEKAQPHVNLHPYTNSLKMLTNPEGKESEE 480	Db	1328 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Db 421 HSFNVNTICHYHRGHNESKADCLDMDEKAQPHVNLHPYTNSLKMLTNPEGKESEE 480	Db	1329 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
Query 481 TIIQTDEDVYEGPVPKSLQGTSFENKIFILNWKEPPLDPNGLITOYEISYSSIRSFPDAVPV 540	Db	1330 LTRPQEGLYMQOFQYLGMASHREPGKSRSRSPKLIQLOVKWQEWKEGEGRTHCLNG	1380	
		RESULT 4		
		AD123886		
		ID AD123886 standard; protein: 1440 AA.		
		XX		
		XX DT 22-APR-2004 (first entry)		
		XX Human PTPrk protein SEQ ID NO:4.		

KW	antisense oligonucleotide; human;	Db	301	LGVGPTYLJQLNANSIIIGDGPILIKEKEYVRMTGGSWTETHAANAPTYKLWHLDPPDTEYE	360
KW	protein tyrosine phosphatase receptor type K; PTPRK; cytostatic;	Qy	361	IRVLLTRPSEGGETLPGPLIITRKCABEPMRTPKTLKABEQARRIAVDWEISLYNITRC	420
KW	antinflammatory; antidiabetic; antisense gene therapy; diabetes.	Db	361	IRVLLTRPSEGGETLPGPLIITRKCABEPMRTPKTLKABEQARRIAVDWEISLYNITRC	420
XX		Db	421	HTFNNTICHTYFRGNESKADCLMDPKAPQHVNHLPPYTNSLKMILTNPEGRKESEE	480
OS	Homo sapiens.	Db	421	HSFNNTICHTYFRGNESKADCLMDPKAPQHVNHLPPYTNSLKMILTNPEGRKESEE	480
PN	WO2004005312-A1.	Qy	481	TIIQDDEDVGPGPVKSLOGTSPEKNIFLNWKERPLDPNGSITQBISSYSSIRSFPDPAVPV	540
XX	15-JAN-2004.	Db	481	TIIQDDEDVGPGPVKSLOGTSPEKNIFLNWKERPLDPNGSITQBISSYSSIRSFPDPAVPV	540
XX	27-JUN-2003; 2003WO-US016237.	Qy	481	TIIQDDEDVGPGPVKSLOGTSPEKNIFLNWKERPLDPNGSITQBISSYSSIRSFPDPAVPV	540
PF	03-JUL-2002; 2002US-00189429.	Db	481	TIIQDDEDVGPGPVKSLOGTSPEKNIFLNWKERPLDPNGSITQBISSYSSIRSFPDPAVPV	540
PR	(ISTS-) ISIS PHARM INC.	Qy	541	AGPPQTVSNLWNSTHVPFHLPOTTYQFIRASTVKFGPATAINVTNNISATLDPYE	600
PA		Db	541	AGPPQTVSNLWNSTHVPFHLPOTTYQFIRASTVKFGPATAINVTNNISATLDPYE	600
XX		Qy	601	GVDASLNETATTITVLLRPAQKCAPISAYQIVVEELPHTRKREAGAMECYQPVTYON	660
PI	Cowser LM, Freier SM;	Db	601	GVDASLNETATTITVLLRPAQKCAPISAYQIVVEELPHTRKREAGAMECYQPVTYON	660
XX	WPI: 2004-083493/08.	Qy	661	AMSGCAPPYFAELPGNLPAPAPFTVGFMNPLAPRKGNFYFOAMSVKE	720
DR	N-PSDB; ADI23748.	Db	661	AMSGCAPPYFACTPGNLPAPAPFTVGFMNPLAPRKGNFYFOAMSVKE	720
XX	New antisense Oligonucleotide, having a sequence targeted to a nucleic acid encoding PTPRK, useful for preparing a composition for treating diabetes, inflammation or hyperproliferative disorder, e.g., cancer.	Qy	721	TKTQCVRIATK-ANTEPPVIPDPAKQDRTVTKAGISGIGLFLILLVVLVITYKSKL	779
PT		Db	721	TKTQCVRIATKAAATEEPEVIPDPAKQDRTVTKAGISGIGLFLILLVVLVITYKSKL	780
PT		Qy	780	AKGRKDAMNTROQMTHNMADRSYADOSTLHAEDPLSITFMDQHNFSPRYENHSATAE	839
CC		Db	780	AKGRKDAMNTROQMTHNMADRSYADOSTLHAEDPLSITFMDQHNFSPRYENHSATAE	839
CC		Qy	781	AKGRKDAMNTROQMTHNMADRSYADOSTLHAEDPLSITFMDQHNFSPRYENHSATAE	840
CC		Db	781	SSRLIDVPRLCETESPYQTGOLHPAIRVADLQHINLMKTSPSDYGFKBEYESFFEGQS	899
CC		Qy	840	SSRLIDVPRLCETESPYQTGOLHPAIRVADLQHINLMKTSPSDYGFKBEYESFFEGQS	899
CC		Db	840	SSRLIDVPRLCETESPYQTGOLHPAIRVADLQHINLMKTSPSDYGFKBEYESFFEGQS	899
CC		Qy	900	ASWDYAKDQNRAKRNKGNYNIIADYHSLRVLQPOYEDPSSDYYNAYDQYQRPHYIATQ	959
CC		Db	900	ASWDYAKDQNRAKRNKGNYNIIADYHSLRVLQPOYEDPSSDYYNAYDQYQRPHYIATQ	959
CC		Qy	960	GPVHETTYDFWRMIWQEASACTYNTNLIVEGRVCKYKWPDDTEVYGBFKUTCVCMEPL	1019
CC		Db	960	GPVHETTYDFWRMIWQEASACTYNTNLIVEGRVCKYKWPDDTEVYGBFKUTCVCMEPL	1019
CC		Qy	961	GPVHETTYDFWRMIWQEASACTYNTNLIVEGRVCKYKWPDDTEVYGBFKUTCVCMEPL	1020
CC		Db	961	GPVHETTYDFWRMIWQEASACTYNTNLIVEGRVCKYKWPDDTEVYGBFKUTCVCMEPL	1020
XX	Example 13; SEQ ID NO 4; 150pp; English.	Qy	1020	AEVYVRFETLTERGYNEIREVKOFHFTGMPDHGVPYHATGGLSPRIRYKLSNPPSAGPTV	1079
CC	The present invention describes an antisense oligonucleotide (I), having a sequence comprising 8-80 base pairs, targeted to a nucleic acid encoding protein tyrosine phosphatase receptor type K (PTPRK), that specifically hybridises with the nucleic acid encoding PTPRK and inhibits expression of PTPRK. Also described: (1) a composition comprising the compound and a carrier or diluent; (2) a method of treating an expression of PTPRK in cells or tissues; (3) a method of treating an animal having or suspected of having a disease or condition associated with PTPRK; and (4) a method for screening for an antisense compound. (I) has cytostatic, antiinflammatory and antidiabetic activities, and can be used in antisense gene therapy. The antisense oligonucleotide (I) can be used for preparing a composition for treating diabetes, inflammation or hyperproliferative disorder, e.g., cancer. The present sequence represents human PTPRK, which is used in an example from the present invention. The human PTPRK gene is located on chromosome 6, more specifically to 6q22.2-23.1.	Db	1021	AEVYVRFETLTERGYNEIREVKOFHFTGMPDHGVPYHATGGLSPRIRYKLSNPPSAGPTV	1080
CC	Sequence 1440 AA;	Qy	1080	VHCSAGAERTGCYIVIDMLDMAERGVUDIYNCVKALSRRRNMVQEEOYFPHIDAIL	1139
CC	Query Match 99.3%; Score 7656.5; DB 8; Length 1440;	Db	1081	VHCSAGAERTGCYIVIDMLDMAERGVUDIYNCVKALSRRRNMVQEEOYFPHIDAIL	1140
CC	Pred. No. 0; Mismatches 3; Indels 1; Gaps 1;	Qy	1140	EACLGETAIPVCEFKAAFDMDRIDSQTSNSHLKDEBFTLNSVTPRLOAEDCSIACLPR	1199
CC	Matches 1431; Conservative	Db	1141	EACLGETAIPVCEFKAAFDMDRIDSQTSNSHLKDEBFTLNSVTPRLOAEDCSIACLPR	1200
Qy	1 MDTAAAAPAFVALLISWPLIGSAQGSAGCTTDFGPGACDYHDLYDDFEWTH 60	Qy	1200	NHDKRFDMLPPDRCLPLITDGEESNYINALMDSYRQPAAFIVTOYPLPNYKDFW	1259
Db	1 MDTAAAAPAFVALLISWPLIGSAQGSAGCTTDFGPGACDYHDLYDDFEWTH 60	Db	1201	NHDKRFDMLPPDRCLPLITDGEESNYINALMDSYRQPAAFIVTOYPLPNYKDFW	1260
Qy	61 SAQEPHYPPEPMQGSMYTVSSDHDPGKARLQLOPTMKENDTHCIDFYLISQKGJNP 120	Qy	1260	RIVYDYGCTSIVMLNEVDSLQGCPQYWPEGMRYGPLOVCNSMSMCDVIRFRICN	1319
Db	61 SAQEPHYPPEPMQGSMYTVSSDHDPGKARLQLOPTMKENDTHCIDFYLISQKGJNP 120	Db	1261	RIVYDYGCTSIVMLNEVDSLQGCPQYWPEGMRYGPLOVCNSMSMCDVIRFRICN	1320
Qy	121 GTLNILVRYNKGLPLANPINNNTGFTGRDYLRAELAVSTWPNEYQVIFAEVSGGRSGYI 180	Qy	1320	LTRFQGYLMVQQFQYLGSHREVPGSKRSFLKLILQVEKNOBEWKEGEGRTHIHCING	1379
Db	121 GTLNILVRYNKGLPLANPINNNTGFTGRDYLRAELAVSTWPNEYQVIFAEVSGGRSGYI 180	Db	1321	LTRFQGYLMVQQFQYLGASHREVPGSKRSFLKLILQVEKNOBEWKEGEGRTHIHCING	1380
Qy	181 ADDIQVLSYPCDKSPHFRGDFEVNAGNATQCIATGRDAVHNKLWLQRANGEDIFV 240	Qy	1380	GGSGMFCAIGIVYEMVKRNQVYDVFHAVKTLRNSKPNMVAEQQYRECYDVAYEYLBS	1439
Db	181 ADDIQVLSYPCDKSPHFRGDFEVNAGNATQCIATGRDAVHNKLWLQRANGEDIFV 240	Db	1381	GGSGMFCAIGIVYEMVKRNQVYDVFHAVKTLRNSKPNMVAEQQYRECYDVAYEYLBS	1440
Qy	241 AQTKNINHRRFAASFRQLETTKTDOLYRCVTOSERGSVSNPQALIVEPPRPIAPQI 300	Qy			
Db	241 AQTKNINHRRFAASFRQLETTKTDOLYRCVTOSERGSVSNPQALIVEPPRPIAPQI 300	Qy			
Qy	301 LGVGPTYLJQLNANSIIIGDGPILIKEKEYVRMTGGSWTETHAANAPTYKLWHLDPPDTEYE 360	Qy			

Db	180	AIDDIQVLSYPCKDSKSPHPLRLGDVEVNAGONATPQCATGRDAVNKLWLQRNGEDIPV
Qy	241	AOTKININHRFAASFRLOEVTKDOLYRCYTOSERGSVSNFAQLTYREPPRIAPPOL
Db	240	AQTKININHRFAASFRLOEVTKDOLYRCYTOSERGSVSNFAQLTYREPPRIAPPOL
Qy	301	LGVPTYLQIQLQNLQNLNSIIIGDGPILKEVEYRMTSGSNTETHAVNAPTYKLWHDPTDEYE
Db	300	LGVPTYLQIQLQNLQNLNSIIIGDGPILKEVEYRMTSGSNTETHAVNAPTYKLWHDPTDEYE
Qy	361	IRVLTRPGEGGTGLPGPLITRKCAEPMRPKTLKAEIQARRIADWESLGYNITRC
Db	360	IRVLTRPGEGGTGLPGPLITRKCAEPMRPKTLKAEIQARRIADWESLGYNITRC
Qy	421	HTFNTVTCYHYFRGHNESSKACDCLMDPKAQHVNHLPPYTNSLKMILTNPEGRKSEEE
Db	420	HTFNTVTCYHYFRGHNESSRACDCLMDPKAQHVNHLPPYTNSLKMILTNPERKESSE
Qy	481	TIIQTDEDVPGPVVKSLQGTSPENKIFLNWKPLDPNGLIQTYBISYSSIRSDFPAVEY
Db	480	TIIQTDEDVPGPVVKSLQGTSPENKIFLNWKPLDPNGLIQTYBISYSSIRSDFPAVEY
Qy	541	AGPPQTYSNLWNLWSTHVNMLHJPGTTOFFIRASTVKGFPATAINVFTNISAFPLDPB
Db	540	AGPPQTYSNLWNLWSTHVNMLHJPGTTOFFIRASTVKGFPATAINVFTNISAFPLDPB
Qy	601	GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTRKEAGAMECYQWPVYTON
Db	600	GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTRKEAGAMECYQWPVYTON
Qy	661	AMSGAPYFAELPPGNLPEPAPPTGDNRTYQGFNNPLAPRGKNTYFOAMSSVEKE
Db	660	AMSGAPYFAELPPGNLPEPAPFTGDNRTYQGFNNPLAPRGKNTYFOAMSSVEKE
Qy	721	TKTQCVRATK-AATEEVPIPPAKQTDRVVKIAGSAGIVFLLLVIVLVIKKSKL
Db	720	TKTQCVRATKAAATEEVPIPPAKQTDRVVKIAGSAGIVFLLLVIVLVIKKSKL
Qy	780	AKKRKDAMGNTROEMTMVNAMDRSYADQSTLHAEDPLSITFMQHNFSPRY-----
Db	780	AKKRKDAMGNTROEMTMVNAMDRSYADQSTLHAEDPLSITFMQHNFSPRY-----
Qy	832	ENHSATASSRLIDPVRLCEGTESPYQONGQHPAIRVALDLQHINLMKTSDSYGF
Db	840	AVLDENSATASSRLIDPVRLCEGTESPYQONGQHPAIRVALDLQHINLMKTSDSYGF
Qy	888	KEEYESFPEGQSAWSWDVAKDQNRAKNYGNIAYDHSRVILQVEDDSSDINYANYI-
Db	900	KEEYESFPEGQSAWSWDVAKDQNRAKNYGNIAYDHSRVILQVEDDSSDINYANYI
Qy	947	- - -DGYORPHSHIATOGPVHETVYDFWERMTOEQSACIYMTNLVEGRVKCYKWPD
Db	960	IWJYRDGQRPSHIAQGPVHEVYDFWERMVHQEQSACTIWWVNLVEGRVKCYKWPD
Qy	1002	DTEVYGDPKUTCYBMEPLAEYYVTRPTFLERRGYNEIREVYQFHGTGPDHGVPYHATGIL
Db	1020	DTEVYGDPKUTCYBMEPLAEYYVTRPTFLERRGYNEIREVYQFHGTGPDHGVPYHATGIL
Qy	1062	SFIRRVLUSNPQGPAGTIVHCSAGAAGRIGCYIIVDILMDMAERGVUDIYNCVALRSRR
Db	1080	SFIRRVLUSNPQGPAGTIVHCSAGAAGRIGCYIIVDILMDMAERGVUDIYNCVALRSRR
Qy	1122	INNVQTEBOYFIHDAILEAACGCTTAIPCEFFAYFDMRISQTNSSHLDKFQTIN
Db	1140	INNVQTEBOYFIHDAILEAACGCTTAIPCEFFAYFDMRISQTNSSHLDKFQTIN
Qy	1182	SVPRLQAEDCSTACLPNHDKRFMMDLPPDRCLPFLITIDGESSNYNAALMDSYROP
Db	1200	SVPRLQAEDCSTACLPNHDKRFMMDLPPDRCLPFLITIDGESSNYNAALMDSYROP
Qy	1242	AAFIWVTCIPLPNVTKDFRVLVNGTFCQWPEEGMLYGPQVEC
Qy	5	RESULT
ID	ABB57308	standard; protein; 1457 AA.
AC	AC	ABB57308;
DT	07-MAR-2002	(first entry)
DE	Mouse ischaemic condition related protein sequence SEQ ID NO:862.	
XX	Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;	
XX	vasospastic ischaemia; ischaemic condition; ischaemic disease.	
XX	Mus musculus.	
XX	WO200188188-A2.	
XX	22-NOV-2001.	
PD	18-MAY-2001; 2001WO-JP004192.	
XX	PR 18-MAY-2000; 2000JP-00145977.	
XX	PA (UNIV-) UNIV NITHON SCHOOL JURIDICAL PERSON.	
XX	Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;	
XX	WPI; 2002-04.	
DR	N-PSDB; AB199774.	
XX	Examining the ischemic condition (e.g. occlusive ischaemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.	
PT	Claim 2: Page 2155-2161; 2690pp; English.	
XX	The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI199202 to ABI199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI199913 and ABI199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.	
XX	Sequence 1457 AA;	
Qy	Query Match 98.2%; Score 7571; DB 5; Length 1457;	
Db	Best Local Similarity 97.3%; Pred. No. 0; Mismatches 13; Indels 20; Gaps 4;	
Matches 1419; Conservative 13; MisMatches 6; Indels 20; Gaps 4;		
Qy	1 MDTTAAALPAFAVALLIISPWPLLGSAQGQPSAGGCTEDDGGPACDYQDLYDDPFWHV 60	
Db	1 MD-VAALPAFAVALLIISPWPLLGSAQGQPSAGGCTEDDGGPACDYQDLYDDPFWHV 59	
Qy	61 SAQEPHYPPEPMPOGSTMYVDDSDHDEPCKAROLQPKENDTHCIDSYLYSOKLN 120	
Db	60 SAQEPHYPPEPMPOGSTMYVDDSSHHDPCKAROLQPKENDTHCIDSYLYSOKLN 119	
Qy	121 GTINILIVRNKGPLANPWNWTGFTGRDWLRQBLAVSTFWNEYQVIFAEVSGGRGGYI 180	
Db	120 GTINILIVRNKGPLANPWNWTGFTGRDWLRQBLAVSTFWNEYQVIFAEVSGGRGGYI 179	
Qy	240 ADDIOVLSYPCKDSKSPHPLRLGDVEVNAGONATFOCIATGRDAVNKLWLQRNGEDIPV	

Page 8

360	IRVLLTRPREGGTGLPPPLITRKYCAEFRTPTKLKAEIQRRIAVDWEISGYNITRC	419
421	HTPNVTCIHYFRGNHESKAACLDDMPKAQHVYVNNHLPPTYNSLKMILTNPGRKESB	480
420	HTPNVTCIHYFRGNHESKAACLDDMPKAQ-	- 450
421	TIIQTDWVPGPVPKVSLQGTSPEENKIFLNWKELPDNGLITQYEISYSIRSFDPAVP	540
420	-----SPEHKIFLHWKEPLEPNGLITQYEVSYSIRSFDPAVP	489
421	AGPPQTVSNLWNSTHVMFHLPOTTYOFIRASTVKGPATAINTVNISAPTLPPDE	600
420	AGPPQTVSNLWNSTHVMFHLPOTTYOFIRASTVKGPATAINTVNISAPSLPPDE	549
421	GVDASLNETATTITVLRAQAQKAPISAYQIVVEELPHPRTRKEAGAMECYQVPTYQN	660
420	GVDASLNETATTITVLRAQAQKAPISAYQIVVEOLHPRTRKEAGAMECYQVPTYQN	609
421	TKHQCVRFATK-LATEEPVIPDAKOTDRVVKTAGISAGILVILLVVVLLVKKSL	779
420	TKHQCVRFATKAAATEPVIPDAKOTDRVVKAGISAGILVILLVVVLLVKKSL	729
421	AMGGAPAYFAAELPPGNLPEPAPFTVGDNRTYQFWMNPFLARKGYNLYQAMSSVKE	720
420	ALSGGAPYFAAELPPGNLPEPAPFTVGDNRTYQFWMNPFLARKGYNLYQAMSSVKE	669
421	721 TKHQCVRFATK-LATEEPVIPDAKOTDRVVKTAGISAGILVILLVVVLLVKKSL	779
420	721 TKHQCVRFATK-LATEEPVIPDAKOTDRVVKTAGISAGILVILLVVVLLVKKSL	729
421	XX	XX
420	XX	XX
421	03-FEB-2000; 2000US-00496914.	.
420	PR 27-APR-2000; 2000US-00560875.	.
421	PR 20-JUN-2000; 2000US-00598075.	.
420	PR 01-SEP-2000; 2000US-00620325.	.
421	PR 01-SEP-2000; 2000US-00654936.	.
420	PR 15-OCT-2000; 2000US-00663561.	.
421	PR 20-OCT-2000; 2000US-00693325.	.
420	PR 30-NOV-2000; 2000US-00728422.	.
421	XX	PA (HYSE-) HYSEQ INC.
420	XX	PA
421	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;	.
420	Xue AJ, Yang Y, Weijhman T, Goodrich R,	.
421	WPI: JP2001-476283/51.	.
420	XX	Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
421	XX	Claim 20; Page 4196-4199; 6221PP; English.
420	XX	The invention relates to polynucleotides (AAK51456-AAK53425) and the encoded polypeptides (AM78323-AM80302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or cytokine therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematoopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and anti-inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK5252), and 3666 (AM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
421	XX	Sequence 1452 AA;
420	XX	Query Match 62.5%; Score 4818; DB 4; Length 1452;
421	CC	: Best Local Similarity 60.8%; Pred. No. 0;
420	CC	Matches 890; Conservative 324; Mismatches 42; Gaps 8;
421	CC	: :
420	CC	Db 3 TUGTGTATLAGLIL-:-TAAGETPSGGCLFDEPYSTCGYSOSEGDENNEQVNTL 54
421	CC	QY 4 TAAALAPAVALLSPNPLGSQGFSAGGCTPDDGPGACDYQLYDDEFTHVSAQ 63
420	CC	QEWKEGBRTI1HCLNGGRSGMFCAGIVVEMVKRONVVDVFHAVKTLRNSKPNNVVA 1421
421	CC	QEECEGEGRTI1HCLNGGRSGMFCAGIVVEMVKRNQVVDVFHAVKTLRNSKPNNVVA 1389
420	CC	PEOYRFCDYDALEYLESS 1439
421	CC	PEOYRFCDYDALEYLESS 1407

acid molecules encoding PTPRM. The antisense compound can also be used as research tools and diagnostics. It can also be used as tools in different and/or combinatorial analyses to elucidate expression patterns of a portion or the entire complement of genes expressed within cells and tissues. The compound can also be used for treating diseases or conditions associated with PTPRM, preferably hyperproliferative disorder, for example cancer or metabolic disorders, for example diabetes. The compound can also be used as prophylaxis, for example to prevent or delay infection, inflammation or tumour formation. The present sequence is that of the human protein tyrosine phosphatase receptor type mu (PTPRM) which is related to the invention.

Sequence 1452 AA;

Query Match	62.4%	Score 4807;	DB 8;	Length 1452;	
Best Local Similarity	60.8%	Pred. No. 0;			
Matches	889;	Conservative	206;	Mismatches	326;
Db	5	TkpTSDPWNPGSMLVNAGRPQRARHLLPKQKENTHCTDHYFVSSKNSPPGGL	114	Qy	4 TAAALPAVALLLSPWPWLGSAGQFSAAGCYPDDGPGACDYHQDLVDFEVVHVSQ 63
Db	3	TLGCLATLAGLL-----TAGETSGGCGLEDEPSTCGYSQSEBDFNWEQVNTL 54	124	Qy	64 EPHYLPPENMQGSTMIVDSSDDHDPEGEKARQLQPLTMKENDOTHCTIDFSYLYSOKGLNPGTL 123
Db	55	NVYKVNNGPGLNPWTWNSCDPTTWNRALAIATSTWPFYQVIFEV-ITSGHQGYLAID 173	124	Qy	124 NIVLRVNGKPLANPWNVTCGFTGRDWLRKLAIASTFWPNPEYQVIFEAETGGGSGSYIAD 183
Db	1115	DQVLSYPCDPSKPHFLRQDGVEVNAQONAFQCIATGRDAVHNKLWLQRNRNGDIPVACT 243	184	Qy	184 DQVLSYPCDPSKPHFLRQDGVEVNAQONAFQCIATGRDAVHNKLWLQRNRNGDIPVACT 243
Db	174	EVKVLGHPCTRTPFLRQDNVEVAGQPAFQCSAIGRTVAGDRLWQJDVRAPIKEI 233	244	Qy	244 KNINHRFFAAASFRILQEVTKTDODLYRCYTOSERGSGVSNFAQLIVREPRPRIAPPQLIGV 303
Db	234	KVTSSRRPFAFNVNNTTRGDAGYCRCMTRTEGGVGSYIAELVKEPVPIAPPOLAVS 293	304	Qy	304 GPTLLIQNANSITIGDGTILKEVEYMTSGSWTETHVNAPTYKLNFLDPDTBEYERY 363
Db	294	GATYLWILQNLANSINGDGPVAREVEYCTAGSNSNDROPVDSYKIGHLDPTBEYESV 353	364	Qy	364 LLTRPGEGETGTGLPGSPPLTRTKCAEPMRPTKLIABQARRLAWDWEELGYNNTRCTFP 423
Db	354	LLTRPGEGETGTGSPGPALRPTKACADPMRSPRKLEVEVEKSQRTIRWEFGYNTRCSY 413	424	Qy	424 NYTICYYHFRGNESKAD--CLMDPKPAQHVVNHLPPPTVNSKMLTNPGRKESRET 481
Db	414	NLTWHYCYQGGQBVREVSMWTENSHQHTITNLSPTNVSKLILNPGRKESQSL 473	482	Qy	482 LIQDDEDVGPVPPVPSLQGTSPEKNFKLWKEPDLPNGITQVIBISYSSIRSPPAVVA 541
Db	474	IYQTEDEDLFGAVPTIESIQGSTFEKKIPLQREPTQTYGTTLYBITYKAVSSFPPEIDIS 533	542	Qy	542 GPPOTVSNWNSTHHVFMHLHPGTTYQFTRASTVKFGSPATAINVNTNISAPLDPDYEG 601
Db	534	NQSRVSKLGNETHFLFGGPGTYSFTRASTAKFGSPATNOFTKVISASMPAVE- 592	602	Qy	602 VDASLINEATTITVLLRPAQKAGPASATQIVYVEELHPRTKREGAEMCYQVPTVONA 661
Db	593	LETPLANQNTNTVWLMKPASHRGAVPSVYQIVWEERPRTKCTTEILCKYPVPHFQNA 652	652	Qy	652 MSGGAPYYFAELPPGPNLPPAPPTVGDRTYQGFWNPLAPRKGYNYIQANSVKEET 721
Db	653	SLLNSQYQYAEFPDSLQAQPPFTIGDQKTYQASRANGEET 712	722	Qy	722 KTQCVRIATKAATPEPEVLPDPAKOTDRVVKIAGISAGLIVFILLVLLVITYKSKLAK 781
Db	713	KIDCVQVATKGAA-TPKPVEPEKOTDHVKIAGIVAGILLFVIFGVLVNMKRLAK 771	782	Qy	782 KRKDAMGNTRQEMTHMVNAMDRSYADQSTLHAEDPLSITFMQHNFSPRY----- 831
Db	772	KRKETMSSSTRQEMTVMVNSMDKSYAEGTNCDE--AEPMDTINLNGRSVSSPSSFTMK 828	832	Qy	832 -----ENHSATAESSRLLDVPRY-LCEGTESPQYQTCOLHPAIRYADLQH 875
Db	829	TNTLSTSIVNSYYDEDEHTMASDTSLSVQSHTYKREPADVYQTCOLHPAIRYADLQH 888	829	Db	829 TNTLSTSIVNSYYDEDEHTMASDTSLSVQSHTYKREPADVYQTCOLHPAIRYADLQH 888
Db	876	INLMKTSDSYKGFKEYESPFEGQASWVAKDODRAKRNQNTIAYDHSRVLQPEVED 935	876	Qy	876 INLMKTSDSYKGFKEYESPFEGQASWVAKDODRAKRNQNTIAYDHSRVLQPEVED 935
Db	889	ITQNKCAEYGPKEEYESPFEGQASWVAKDODRAKRNQNTIAYDHSRVLQPEVED 948	889	Db	889 ITQNKCAEYGPKEEYESPFEGQASWVAKDODRAKRNQNTIAYDHSRVLQPEVED 948
Db	908	PSSDVTINANYIDYQFRPSHVIATQPVPHETVYDWRMMTWOEQSACTIVMTNLVEGRVKC 995	908	Qy	908 PSSDVTINANYIDYQFRPSHVIATQPVPHETVYDWRMMTWOEQSACTIVMTNLVEGRVKC 995
Db	949	TNSDVTINGVYIDYQFRPKVIATQPMQETYDWRMMVWHTENASIIYMTNLVEGRVKC 1008	949	Db	949 TNSDVTINGVYIDYQFRPKVIATQPMQETYDWRMMVWHTENASIIYMTNLVEGRVKC 1008
Qy	996	YKYNPDDTEEVYGFKVTCVMBPLAEEYVTRFTLBERRYNEIREVKQFHPTGWDHGVPY 1055	996	Qy	996 YKYNPDDTEEVYGFKVTCVMBPLAEEYVTRFTLBERRYNEIREVKQFHPTGWDHGVPY 1055
Db	1009	CKYWPDDTEIYKODIKVTLLETELIAEVIRTFAYEVIRTFAYEVIRTFAYEVIRTFAYEV 1068	1009	Db	1009 CKYWPDDTEIYKODIKVTLLETELIAEVIRTFAYEVIRTFAYEVIRTFAYEVIRTFAYEV 1068
Db	1056	HATLSPFIRRVLNSNPPSAGAPIVTHCSIGAGRTGTYVIDIMDMAREGVVDIYNCYK 1115	1056	Qy	1056 HATLSPFIRRVLNSNPPSAGAPIVTHCSIGAGRTGTYVIDIMDMAREGVVDIYNCYK 1115
Db	1069	HATGILGFYTRQTSKSPSAGLYVTHCSAGRTGCFIVYDIMALDMAREGVVDIYNCYR 1128	1069	Db	1069 HATGILGFYTRQTSKSPSAGLYVTHCSAGRTGCFIVYDIMALDMAREGVVDIYNCYR 1128
Qy	1116	ALRERRINNVQTEQYOFIHDALIEACLGETATPVCECTKAAYDMRIDSQTSNLSHLD 1175	1116	Qy	1116 ALRERRINNVQTEQYOFIHDALIEACLGETATPVCECTKAAYDMRIDSQTSNLSHLD 1175
Db	1129	BLRSBRVNNVQTEQYVFYHDALEACLGDTSPASQVRSLYDMNKLDPQTNSQIKE 1188	1129	Db	1129 BLRSBRVNNVQTEQYVFYHDALEACLGDTSPASQVRSLYDMNKLDPQTNSQIKE 1188
Qy	1176	EFQTLNSUTPRLQABDCSTAICLPRNHDKNRFDMDMLPPDRCLPFLITIDGBSSNNYNAALM 1235	1176	Qy	1176 EFQTLNSUTPRLQABDCSTAICLPRNHDKNRFDMDMLPPDRCLPFLITIDGBSSNNYNAALM 1235
Db	1189	EFRTLINMTPPTLRVBDCTSTALLPRNHEKQNRCMDILPPDRCLPFLITIDGBSSNNYNAALM 1248	1189	Db	1189 EFRTLINMTPPTLRVBDCTSTALLPRNHEKQNRCMDILPPDRCLPFLITIDGBSSNNYNAALM 1248
Qy	1236	DSTROPAAPITVQPLPNTVKDFWPLVTDYGCSTIVMINBNVDLSQGCPQYWPEBGMRLRYG 1295	1236	Qy	1236 DSTROPAAPITVQPLPNTVKDFWPLVTDYGCSTIVMINBNVDLSQGCPQYWPEBGMRLRYG 1295
Db	1249	DSYKQPSARTVQHPLPNTVKDFWRLVLDYHCTSVMLNDVDPAOLCPQYWPEENGVHRHG 1308	1249	Db	1249 DSYKQPSARTVQHPLPNTVKDFWRLVLDYHCTSVMLNDVDPAOLCPQYWPEENGVHRHG 1308
Qy	1296	PIQYECMSMCDVINDRIFCNTRPOEGYLMVQQFOLGWSHREYPTGSKRSKFLKL 1355	1296	Qy	1296 PIQYECMSMCDVINDRIFCNTRPOEGYLMVQQFOLGWSHREYPTGSKRSKFLKL 1355
Db	1309	PIQVFVSDLEBDSISFRITNAARPDPGIRNMVQDFLGWMHIRDTPVKRSKFLKL 1366	1309	Db	1309 PIQVFVSDLEBDSISFRITNAARPDPGIRNMVQDFLGWMHIRDTPVKRSKFLKL 1366
Qy	1356	LOVEKWOEWKECERGRTIHCINGGRSGMFCAIGTIVVMKRQVNQVVDVPHAVKTLRNSK 1415	1356	Qy	1356 LOVEKWOEWKECERGRTIHCINGGRSGMFCAIGTIVVMKRQVNQVVDVPHAVKTLRNSK 1415
Db	1369	RQDVKWQEYNGGEGGGPTVUHCLNGGGRSGCTFCATIVCEMLRHQRDTVDVFAVKTLRNSK 1428	1369	Db	1369 RQDVKWQEYNGGEGGGPTVUHCLNGGGRSGCTFCATIVCEMLRHQRDTVDVFAVKTLRNSK 1428
Qy	1416	PNVYVAPEBYRFCDVAEYLES 1438	1416	Qy	1416 PNVYVAPEBYRFCDVAEYLES 1438
Db	1429	PNVYDLDQKFCVYALEYLNS 1451	1429	Db	1429 PNVYDLDQKFCVYALEYLNS 1451

RESULT 10
ABR58629 standard; protein; 1452 AA.

XX DT 09-JUL-2003 (first entry)

AC ABR58622;

XX DE Human cancer related protein SEQ ID NO:286.
XX PN WO2003025138-A2.XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
XX Homo sapiens.

XX XX 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-US029560.

XX PR 17-SEP-2001; 2001US-0323469P.

XX PR 20-SEP-2001; 2001US-0323887P.

XX PR 13-NOV-2001; 2001US-050666P.

XX PR 08-FEB-2002; 2002US-0355145P.

XX PR 08-FEB-2002; 2002US-0355257P.

XX PR 12-APR-2002; 2002US-0372246P.

XX	(EOS-B-) EOS BIOTECHNOLOGY INC.	Qy	501	TSFENKIFLNKEPKLDPDNGITIQYRISYSSIRSFSFPAPVYAGPPQTUVNLWNSTHVFMH 560
PA		Db	493	STFERXIFLOWREPPQTYGVTLYETYKAVSSPPEIDEISNQSSRVSKGNETFLFFG 552
XX	Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;	Qy	561	LHPGTYQFTRASTYTKGFSPATAINTVNISAPLPDYGVADASLINEATTITVLRPA 620
PI	Zlotnik A;	Db	553	LYPGTYSFTRASTYAKGFSPATNQFTKIKSAPSMPAYS-LETPLNQNTONTVNLKPA 611
XX	WPI: 2003-354600/33.	Qy	621	QAKGAPIASYQIVVEBLPHPRTKRAGAMCYQVPTVYONAMSGGAPYYPAELPGNLP 680
PT	PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.	Db	612	HSRGPVSVQIVVEEERPRKTTEILKCPVPHFQASLNSQYYPAEPADSLSQ 671
XX	Claim 12; Page 750: 767pp; English.	Qy	681	EPAPPYVGDNRTYQGFNWNPPLAPRKGNTYFOAMSSVEKETKTOCVRIATAEPEV1 740
PS		Db	672	AAQPTIGDNTYQGNTWNTULLPYSKYRIVQAARANGETKIDCQVATGAA-TPKPV 730
XX	The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC7261 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABRS521 to ABRS709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies.	Qy	741	PDPAKOTDRVYKLAGISAGILVPIILLVVLLIVVKSKLAKRKDKAMGNTROEMTHMNA 800
CC		Db	731	PEPEKOTDHVYKLAGSYTAGILFVILGTVYVLMKCRKLARKRKEMTSSTRQEMTMVNS 790
CC		Qy	801	MDRSAQDSTLHAEDPLSLTMDQINFSPPY--7-----ENHS 835
CC		Db	791	MDKSAEQGTNCDE--AFESMDTINLNGRSVSSPSSFTMKMTNTLSTSVPNSYPPDEHT 847
CC		Qy	836	ATAESESSLJQVRYP-LCEGTEBSPYTGOLHPAIRYADLQHINLMMKTSDSYGFKEEYESF 894
CC		Db	848	MASDTSVLVQSHSYKREPADPVYFGQQLPAIRADLQHINLMMKTSDSYGFKEEYESF 907
CC		Qy	895	PEGQASMSWDYAKKDQNRKRYGNITAYDHSRSLVILQVEDPSSSYDINANYIDGQRPSH 954
CC		Db	908	FEQGQAPWDSAKKDNEMTRNMRGYGNITAYDHSRSLVILQTEDPNTNSDINGNYIDGTHRPNH 967
CC		Qy	955	YIATQOPVHETVYDFTWRMTWQBQSACIWMVNTNLVEGRVYKYPDDTEVYGDPRVTCV 1014
CC		Db	968	YIATQGPMQETTYDFTWMVHENTTAISIMVNTNLVEGRVYKYPDDTEVYKDIKVTLI 1027
CC		Qy	1015	EMEPABEVYVTRFTLERRGYNEIREVKOFTGWPDHGVYHATGLLSFIRRVLKSNPPS 1074
CC		Db	1028	ETELLAEBVTRFTAVERGHEIRETRQFHPTGPWHGPVPHATGLLGFQVKSKSPPS 1087
CC	Best Local Similarity 61.4%; Pred. No. 0; Mismatches 886; Conservative 206; Matches 886; Indels 318; Gaps 7;	Qy	1075	AGPIVYHCSAGAGRTGCYIVIDIMLDMAEREQVVDIYNCYKALRSRRINMVQTEQYIFI 1134
CC		Db	1088	AGPLVHCSAGAGRTGCFTIVIDIMLDMAEREQVVDIYNCYRELRSRRVNNMVQTEQYVFI 1147
CC		Qy	1135	HDAILEBACLGCTETAPVCEFAAYDMIRDSQTINSHLDEQFQTLNSVTPRLQEDCSI 1194
CC		Db	1148	HDAILEAFCLGCGDTSPSASQVRSLYDMNKLDPOTNSQIKEFRFLNMVTPRLQEDCSI 1207
CC		Qy	1195	ACLPRNHDKNRFMDMLPPDPCLFLITIDGESENNTINAALMDSYROPAAFITVQYPLNT 1254
CC		Db	1208	ALLPRAHENKRCMDLIPPDRLPFLITIDGESENNTINAALMDSYROPAAFITVQYPLNT 1267
CC		Qy	1255	VKDFWFLVYDYGCTSTMVNEVDLSQGCPQYKWPREGMLRYGPQVCECMSCSMDCDVINRI 1314
CC		Db	1268	VKDFWFLVYDHTCTSVMLNDVPAOLCPQWPGENGVRHRHGPQVEVSADLEDDISRI 1327
CC		Qy	1315	FRCINLUTRPGQYLWVQOFQYLGWASHREPGSKSFKLILQVEWQEENKEGERTII 1374
CC		Db	1328	FRIYNAARPQDGYRMWQFQFLGWPMDRTPEVSKSFKLIRQVNDKWBEYNGESEPTVV 1387
CC		Qy	1375	HCLNGGRSGMFCAIGIVVENVKRNQVVDYHAVTFLRNSKPNMVAPEQYRFCYDVALE 1434
CC		Db	1388	HCLNGGRSGMFCAISIVCENLRHQRFTDVDHAVTFLRNSKPNMVDLQYKPCYEVALE 1447
CC		Qy	1435	YLES 1438
CC		Db	1448	YLNS 1451
CC	RESULT 1.1 ADJ68277 standard; protein: 1452 aa. ID ADJ68277	Qy	442	-CLDMDPDRQHVNHLPPYTNVSLKMLLTNPREGRESEETIQTDEDVPGPVPYKSLQG 500
CC		Db	433	VSDTNTSHPQHTITNLSPTYNVSVKLIMNPEGRKESQELIVQTDBDLPGAVIPESIQG 492

Db 1189 EFTLANKVTPTLRVEDCSIALPRNHEBNRCDILPPDRCLPFLITIDGESSNYTNAALM 1248
 Qy 1236 DSYRDPANFITYQPLDNTVDFWRLVYDGCSTYMLNEVDLSQQCPQWPEEEMLRIG 1295
 Db 1249 DSYKQPSAIFTVQHLPNTVKDWRVLVDYHTCTSVMLNDVPAQICPQWPENSYHRIG 1308
 Qy 1296 PIQEBCMSCSMCBVINRIFCILNLRPQEGTYLMQFQTYLGSWASHREVEPGSKRSFLKL 1355
 Db 1309 PIQVEFYSADLEDSRISIPIFLYNAAPQDCHRMYQFQFLGWPMTDTPSKRSALLI 1368
 Qy 1356 LQVEKWOEWEKEGEGRITIHCUNGGRSGMFCAGIGIVEMYKRONYDVFHAVKTLRNSK 1415
 Db 1369 RQVDKHOEYENGEGRPTVHCUNGGRSGRTCAISITCVERLHQRTDVFHAVKTLRNSK 1428
 Qy 1416 PNMVTADEPQFRCIDVALEYLES 1438
 Db 1429 PNMVDLUDQKFCYEVALEYLNS 1451

RESULT 12
 AAM80143 standard; protein; 1455 AA.
 ID AAM80143 standard; protein; 1455 AA.
 AC AAM80143;
 DT 06-NOV-2001 (First entry)
 XX Human protein SEQ ID NO 3789.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 vaccine; peptide therapy; stem cell growth factor; haematoopoiesis;
 tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001IW0-US004098.
 PR 03-FEB-2000; 2000US-00496314.
 PR 20-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-0059875.
 PR 19-JUL-2000; 2000US-0062025.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-0069332.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Wang ZN;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Goodrich R,
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R,
 XX WPI: 2001-476283/51.
 DR N-PSDB, AAK53276.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

Claim 20: Page 437-438; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM8323-AAM80302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematoopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and

CC activitin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK5281), 2111 (AAK5282) and 3666 (AAW0020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

XX Sequence 1455 AA;

CC Query Match 62.0%; Score 4777.5; DB 4; Length 1455;

CC Best Local Similarity 60.4%; Pred. No. 0;

CC Matches 885; Conservative 207; Mismatches 330; Gaps 9;

CC SQ

Qy 4 TAAALPAVALLISSPWPPLIGSAGQSAGGCTPDGPACDYQDLYDFFEWTHVSAQ 63
 Db 3 TIGCTCATLALL-----TARGETPSGGCLDEPYSTCGSOSSEGDDFNWFOVNTL 54
 Qy 55 TKPTDPMWSGSFMIIVNASGRPQQEQRHILLPKQENDTHCIDPHYFVSSKSNSPPGLL 114
 Qy 124 NILVURWKGLANDPWNWTCGETGRWILRAFLAVSTFWPNFNEYQVTEAEVGGRSGRSYIAID 183
 Db 115 NVYVKVNNGPGLGNPWNISCDPTTWNRALIAISTFWPNFQVTEBV-ITSGHQCYQLAID 173
 Qy 184 DIQVISYPDCDKSPHFLRLGQDVBNQNQATFOCIAITGRDAVHNKWLQRNGED-PVAQT 243
 Db 174 EVKVLGHPCPTRPTPLRQVNEVNGQFQCSIGRTYAGDRLWLGQ3DVRDPLKEI 233
 Qy 244 KNINHRRFAASFRQEQVTKTDQLYRCVTOSERGGSVNSFAQLITREPRPRPIAPPOLLGV 303
 Db 234 KVTSRERFIAFSFVNNTTRDAGKRCMRTEGGGINSNTAELVKEPPVIAFPQLASV 293
 Qy 304 GPTYLQIQLNANSIIGDGPILLKEVBYRMTSGSMWETHANAPTYKLWHLDPDTBEYIRV 363
 Db 294 GATYLIQIQLNANSINGDGPVAREVBYCTASGSWNDROPVDSITSKIGHLDPTYEISV 353
 Qy 364 LLTRPCEGGTGTGLPGLPLTRPTKCAPMRPTKLPALRPTKCAPMGRPKLKEVVEKSRQITRWEPEVNTYRCHSY 423
 Db 354 LLTRPCEGGTGTSPGPALRPTKCAPMGRPKLKEVVEKSRQITRWEPEVNTYRCHSY 413
 Qy 424 NVTICICHYFRGHNESKAD--CLDMDPKAPKOHVNHLPPYTNVSLKMLTNPGRKESEET 481
 Db 414 NLTVHICQVQGQBOVREEVSWDTHNHSPTOTITLSPYTNVSVLILMNPFGRQSQEL 473
 Qy 482 LIQTEDDPGPVYVKSLQGTSRENKFLNKKKEPLDNGLITQYETSYSSIRSFDAPVVA 541
 Db 474 IVQTEIDLPGAVPTTSIQGSTPEECIFLQREPTOTGYGVTLYETTYKAVSFDPPIIDS 533
 Qy 542 GPPQTVSNLNSTHNFMLHLPGTQFFRASITKGFPTAINTVTTNISAPTLDYEG 601
 Db 534 NQSGRYSKLGKNETHLLFEGLYGPTTSFTTRASTKGFPPTAQTTKISAPSMPAYE-592
 Qy 602 VDASLINEATTITVLLRPAQKGAISAYQIVVBEIHPHRYKREAGAMECYQVPTTYQNA 661
 Db 593 LETPQNQTDNTVTVNLKPANSRGAPSYVQIVVEERPRRTKKTBLKCPVPHFQNA 652
 Qy 662 MSGGAPYYFRAABLPGNLPPAPAFYQGHNPNPLAPRKGYNNYFOAMSSEYKET 721
 Db 653 SLLNSOXYFAAEFPDSLQARQPFITGDNKTYNGWNTPLPPYKSTRYFOAASRANGET 712
 Qy 722 KTQCVRILATKATEPEVIPDPAKQDPRVKAIGASAGILVPLLLVLLVVKSKLAK 781
 Db 713 KIDCQVATKGA-TPKPVDPPEKQDHTVKIAQVAGIATLFLVFLGVYVMKRLKL 771
 Qy 782 KRKDANGNTROBMTHVNAMD--REYADOSTLHAEDPLSTEMD01FNSPYY----- 831
 CC 772 KRKEIMMSSTROBIDMIGELNGPRSYAEQGTKLATAFRS--FMDTANLNGRSVSPPSFT 829
 CC 832 -----ENHSATAESRSRJLUDVPRY-LCEGTEESPYOTGOLHPAIRYADLL 873
 CC 830 MKNTNLISTSVNPSYYDETMASITSSLYVOSHTYKREPADVPXTGOLHPAIRYADLL 889
 CC 874 QHINLMKTSDSYGFKEYESEFEGQSASWVAKDQNRKNGNTIAYDHISRVLQPVE 933

Db	890	QHITQMKCAESGYFKEEYSSFFEGQSAPWISAKDENRMCNRGNTIAVDHSRVRLQTE	949	PT diagnosing pain.
Qy	934	DDPSSPYINANITYDGYQRSPHYIATQGPVIETVYDEWRMWTQEQAICUVMNIVLVEGRV	993	XX Claim 1; Page 59-64; 334pp; English.
Db	950	GDTNSDTINGNYTDGYHRPHYIATQGPVIETVYDEWRMWTQEQAICUVMNIVLVEGRV	1009	CC The present invention relates to nucleotide sequences which are useful in the screening of compounds for the treatment of pain, or for the diagnosis of pain. The nucleotide sequences are up-regulated in the spinal cord in response to streptozocin-induced diabetes. The present sequence was used to illustrate the invention.
Qy	994	KCYKWPDPDEYGVDFKVTCVEMEPLAEXYVTRFTLERGYNEIREVKQDFHFTGPWDHGCV	1053	CC
Db	1010	KCCRTWPDPDIEYTKVTLTETELAAYIRTFAVEKRGVTHETRIGRHFPTWDHGCV	1069	CC
Qy	1054	PYHATGLLSPIRRVLSNPPSAGPIVWHSAGAGRTGCMYIVIDIMLDMAEREGRVYDYNIC	1113	CC
Db	1070	PYHATGLLGPRVQKSPPSAGPLVWHSAGAGRTGCFIVIDIMLDMAEREGRVYDYNIC	1129	CC
Qy	1114	VKALESRRRIVNQTEQQYIHDALCJGETALPVCEKAYFDMDRIDSQINSHL	1173	CC
Db	1130	VRELESRRVNMVQTEQQYIHDALCJGCDISVPASQVRSLYDMMNKLDPQTNSQI	1189	CC
Qy	1174	KDEFOTLNSTTPRLOADECSТАCLPRNHDKNRFMDMLPPDRCLPFLITDGEESNNYINA	1233	CC
Db	1190	KEEFYLNNWTPTRVEDCSТАLLPRNHBNRCDILPPRCLPFLITDGEESNNYINA	1249	CC
Qy	1234	LMDSYRQPAAFIYIQYPLPNTYKDFWRLYDYGCTSIVMLNEUDLSQGPOYMPPEGMER	1283	CC
Db	1250	LMDSYRKQPSAFIVTQHPLNTPVQDFWRLYDYGCTSIVMLNDPAQLCPOYWSENGVR	1309	CC
Qy	1294	YGPJOVCEMSMCDVNNIFRCLNLTRIQQEGTMVQOFOYLGWASHREVPGSKRFSIK	1353	CC
Db	1310	HGPJOVCEWPKQEWKGEBGRTRTHCLNGGSGMFCAIGIYEVMMVKRQNVDVFHAKTILRN	1369	CC
Qy	1354	LILLOVEKQWEWKGEBGRTRTHCLNGGSGMFCAIGIYEVMMVKRQNVDVFHAKTILRN	1413	CC
Db	1370	LIRQVDRKWWBQBYNGBGRTRVHCINGGSGTFCASIVYCEMLRHQRQTVDVFHAKTILRN	1429	CC
Qy	1414	SKPNNVVEAPQQYRFYCDALEYLES	1438	CC
Db	1430	NKPNMVLDLQDKFCYEVALEYLN	1454	CC
RESULT 13				
ADB79775				
ID	ADB79775	standard; protein; 1436 AA.		
XX				
AC	ADB79775;			
XX	04-DEC-2003	(first entry)		
XX	Rat	putative receptor tyrosine phosphatase, SEQ ID 15.		
XX	KW	Analgesic; pain; streptozocin-induced diabetes; rat.		
OS	Rattus norvegicus.			
XX	EP1279744-A2.			
XX	29-JAN-2003.			
XX	PF	26-JUL-2002; 2002EP-00255249.		
XX	PR	27-JUL-2001; 2001GB-00018354.		
XX	07-FEB-2002; 2002GB-00002910.			
XX	PA (WARN) WARNER LAMBERT CO.			
XX	Brooksbank RA, Dixon AK, Lee K, Pinnock RD;			
DR	WPI: 2003-395407-38.			
DR	N-PSDB; ADB79776.			
XX	Use of isolated gene sequences and encoded polypeptides that are up-regulated in the spinal cord in response to streptozocin-induced diabetes for screening compounds for the treatment of pain, or for			
Qy	265 PAIRVALDQLQHINLMKTSDSYSGPKKEYESFFEGQASWVDYKQDNRKRYGNIIAYDH	924		
Qy	748 DRVVKTAGISA-GIVLFILLVVLIVKKSKLAKKRDAMGNTROEMTHMYNAMDRSYA	806		
Db	743 EEMGLILGICAGGAVLILGATIVRKGPVNMTK-ATVNYRQBKTMMASAVDRSPT	801		
Qy	807 DQSTLHAEDPLSLSTMDQHNFSPRYENHs -ATABSRLLDVPRLCBESTESPVQTGQLH	864		
Db	802 DQSTLQEDRLGLSFMAGYSFRGDQSGGTTEASSLLGGSPRPCGRKGSPYHTGQLH	861		
Qy				

Db	862	PAVRADLQLINQMTAEGFKQDYESFPEG---WDAKKDKXLKGGRQEPEVSDR	917	XX	PR 24-MAY-1996; 96US-00652971.
Qy	925	SRVILQVEDPSSDVINANTIDGYORPHVATOPPHETVYDFWRMIVQEQSACIVMV	984	XX	(GETH) GENENTECH INC.
Db	918	HHVKLHPMLADEDADTISANYIDGYRSNHFIATQCPKEMIYDFWRMVQEQSACIVM	977	XX	Cheng J, Lasty LA;
Qy	985	TNLVEYGRKCYKWPDDTEVYGFKVTCMEPLAEYVTRFTLERGYNEIREVKQFH	1044	XX	WPI: 1998-018312/02.
Db	978	TKLVEYGRKCSRYWPDSDMGDIKITLVKTYLLEYVTRFTLERGYNSARHEVRQFH	1037	XX	DR DR-N-PSDB; AAV15004.
Qy	1045	FTGWPDPHGVPYTHATGLLSIRRVLKSNPSAGIVHCSAGAGRCCYIVIDIMDMAE	1104	XX	Receptor protein tyrosine phosphatase lambda polypeptide - potentially useful in treating paralytic diseases and preventing metastases.
Db	1038	FTAWPERGVPYTHATGLLAFTERVKAFTPDPAGIVTHCSACTGRTGCVYIVLDVMDMABC	1097	PS	Claim 6; Fig 1; 118PP; English.
Qy	1105	EGVVDIYNCKALRSRRINMVQTEBQYI FHDIALEAICCTAIPCEFKAAYDPMIRI	1164	XX	This sequence represents the mouse receptor protein tyrosine phosphatase (PTP) lambda polypeptide of the invention. PTP Lambda is: (i) mainly expressed in adult mammalian brain, lung and kidney; (ii) not expressed in adult liver; and (iii) can dephosphorylate phosphorylated tyrosine (pY) residues. The DNA sequence is used for screening DNA libraries, PTP Lambda, and also as a source of probes for isolating cDNA libraries. PTP Lambda is used to isolate the receptor's cognate ligand (potentially useful for treating paralytic diseases), and for preventing metastatic spread. PTP Lambda is also used as a molecular marker for particular tissues, as a reagent in an assay for identifying PTP (ant)agonists, and as a molecular weight marker in protein gels. The Ab is used in diagnosis, tissue-typing and purification of PTP lambda, also it may crosslink the receptor, resulting in its upregulation. PTP Lambda is a mediator of cell adhesion and may be involved in development of epithelial and neuronal structures (neuronal pathfinding)
Db	1098	EGVVDIYNCKVTKLCSRNVNMVQTEBQYI FHDIALEAICCTAIPVNEFRATYREMIRI	1157	XX	Claim 6; Fig 1; 118PP; English.
Qy	1165	DSQTNSSHLLKDEFOQTINSVTPQLAEDCSTACLPNHDKNRFMDMLPPDRCLPFLITIDG	1224	CC	Sequence 1436 AA;
Db	1158	DHQSNSSSQLREFQTINSVTPQLAEDCSTACLPNHDKNRFMDMLPPDRCLPFLISSG	1217	CC	Query Match 59.5%; Score 4586.5;
Qy	1225	ESSNYINAALMDSYROPAAFIVTQYPLPNTYDFWRLVYDGCTSIVMLNEVDSLQG--	1281	CC	Best Local Similarity 60.3%; Pred. No. 0;
Db	1218	DENNYINAALDTSYTRAFAFLVTLHPLQSTPDEFWRLVYDGCTSIVMLNQNSNSAWP	1277	CC	Matches 854; Conservative 213; Mismatches 331; Indels 19; Gaps 9;
Qy	1282	CQYWPEBGMLYGPYBCHCSMDDCIVNIFRICLNTRPQEGYLWVQOFQYLGWASH	1341	CC	Qy 33 AGGCTFDGPG---ACDYHDQDLYDEFEWVHSQAQSPHYLPPEMPGQSYYMVDSSHDPGC 89
Db	1278	CLQYWPEBGRQQYGLMEVYFSGTANEDLVSERVQNSRPLQEGHLVRFQFLRWSAY	1337	CC	Db 24 AAGCTFEAASDPVPPPEFSQAFQYDFDQWEQTRIHPTRTPELDPLPGAYLVMNASQHTPGQ 83
Qy	1342	REVPGSKRSFLKLILQVKEWKQEWKEGEGRTHCLNGGSRGMFCAGTAGIVEMYKRONV	1401	CC	Qy 90 KARLQOPTMKENDTHCIDFESYLLYSOKGLNPGTUNLTVRYNKGPLANPIWVNTGFGRDW 149
Db	1338	RQTPDSRAFLLAAEYDQWQE--SDGRTVHCINGGSGTFACATVLEMIRCHSL	1395	CC	Db 84 RAHITFQTLSENDTHCVQFSYFLYRDGHSPTGTVQYVVRGGPQJGSAVNMTGSHGRQW 143
Qy	1402	VDFVHAYKTLRNSKPNMVAPEQYRFCCYDVALEYLES	1438	CC	Qy 150 LRAELAVSTWPNEQVIFERAEVSGGRSGYTAIDQVLSYPCDSPHFLRLGDEVVNAG 209
Db	1396	VDFVFFAAKLTNRKVNVTMDQYHFCYDVALEYEA	1432	CC	Db 144 HOAELAVSTWPNEQVFLKFLAELISPDHKGTGDDLILFSPYCAKAPHFSRNLGDEVVNAG 203
RESULT 14					
AAW41361	ID	AAW41361 standard; protein; 1436 AA.		Qy 210 QNATFOCIATGDRDAVHNKLMQRNGEDIPVATQINHFRFAASPRQLQEVTKTDDLYR 269	
XX	AC	AAW41361;		Db 204 QNASFQCMAGRAAEAHFFIQRSQGVLYPAGYRHISHRFLATPLASVGRSEQDLYR 263	
XX	XX			Qy 270 CYTQSERGSGVSNPFAQOLIVREPPRPTAPOLLGVCGPTYLQIQLNANSIIGDGPILIKEV 329	
XX	XX			Db 264 CVSQAPRGAGVSNFNPLAIVKEPVTPAPPQLRAGSPTYLIQLNANTSIGDGPVIRKEI 323	
OS	OS			Qy 330 YRMTESSWTETHAVNAPTYKLWHLDDPTEBIRVILTRPGEGGCTLGPGPPLITRCAEP 389	
FH	Key	Location/qualifiers		Db 324 YRMARGPWAEVHVNLLXTYKLWHLDDPTEVLSVLLTRPGDGCTGRGPPLISRTCAEP 383	
FT	Misc-difference	158		Qy 390 MRTPTKLKIAIBIQARRIAVDMESLGNTIRCHTFNVTICHTYFRG -HNEKSADCLDDMP 447	
FT		/label= "unknown"		Db 384 TRAPKGIAFLQARQLTQMQEPLGINVTRCTAYASLCRYLGSINQIRECYKMER 443	
FT		/note= "encoded by TWT"		Qy 448 KAPQHVVNHLPPYPTVNSLKMILTNPGRKESBTETLQTQDPEVGPVPKSLSQGTSPENKI 507	
FT	Misc-difference	340		Db 444 GASRTIKNLNPLFRNTVRLTNPNSRKEGEVTTQDVEPGGIAAESLTFTPLEDMI 503	
FT		/label= "unknown"		Qy 508 FLNWKEDLPNGITIQTYEISYSSIRSFSDPAVPGAVGPOTVSNLWNNSTHVMHLHPCTTY 567	
FT		/note= "encoded by YGC"		Db 504 FLKWWEEQEPNGLITQYBISYQSISSSDPAVNVPGPRRTISKRLNEYHVSNLHPCTTY 563	
XX	XX			PN WO9744458-A1.	
XX	XX			PD 27-NOV-1997.	
XX	XX			DB 22-MAY-1997; 97WO-US009056.	

Qy	568 QFFIRASTVKGFPATAINTVNISAPTLPPDLYGDASLINEATTITVILRPAOKGAPI	627	KW neuroprotective; antiparkinsonian; protein therapy; EST;
Db	564 LFSVRARTSKPGQALTEITTNISAPSFDYADMPSPLCESENTITVILRPAQRGAPI	622	KW expressed sequence tag.
Qy	628 SAYTVEELPHPRTRKREGAMEBCYCOPPTVYQNAMSGGADPYFAELPPGNLPEPAPFTV	687	XX Homo sapiens.
Db	623 SVIQVVEEEPRDRREPQADQDCSPVLFETALRGVLHYFGAELAASSLLEAMPFTV	682	XX
Qy	688 GDNRITYQGFNNPPLAPRKCGYNIPYQAMSSVKEKETKTCQRIATKAATEBEVIDPPAKQT	747	XX WO20022260-A2.
Db	683 GDNQTYRGPFWNPPLPPLPRKAYLIYFQASHLKGETRLNCIAKACKSKEPLEVSQRS	742	XX PD 21-MAR-2002.
Qy	748 DRVVKTAGISA-GILVFILLLVILVILVRSKLAKRDAKGNTROEMTMVNAMDRSYA	806	XX 10-SEP-2001; 2001WO-US06015.
Db	743 EEMGLLIGCAGGLAVLILGLGAAIVIIRGKPVNMTK-ATVNYRQEKTMMSAVDRSTT	801	XX PR 11-SEP-2000; 2000US-00659671.
Qy	807 DQSTLHAEDPLSITFMDOHNSPRYENHS-ATAEBSRRLDVPRVLCETESTESPYOTQGQLH	864	XX PA (HYSE-) HYSEQ INC.
Db	802 DQSTLQBEDRUGLSMADPAGSPRQDQRSGCVTEASLLGGSPRPGKRGSPHTQGQLH	861	XX XX
Qy	865 PAIRVADLLOHNLMLKTSDSYSGKREKEYESFEGQSASWMDYAKKDNONRAKRYGNLIAVDH	924	XX DR WPI: 2002-292408/33.
Db	862 PAVRVADLLOHNMKTAEGFXKQBEYESFEG---WDAWKKDGLKSGRQEFPVSAYR	917	XX DR N-PSDB; ABN32707.
Qy	925 SRVLIQWPDPSSDXINANYIDGQRPSPHYIATGQPVHETVDFWRMWTQEQSACIVMV	984	XX XX
Db	918 HHVKLHPLMIALPDADYISANYIDGYHRSNHPFIATQGPKEPMIDFWRMWTQEQSACIVI	977	CC The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke CC
Qy	985 TNLYEVGRVRCYKWPDDTEVYGFKVTCVEMPAEYVTRFTLERGSYNEIREVKOPH	1044	CC
Db	978 TKLVEVGRVACSRWPEDSMGMDIKITLKVTKTETAEYVTRFTALERGSYSAHBRVQPH	1037	CC
Qy	1045 FTGNDPDHGVPYHATGSLLSFIRRVLKLSNPNPSAGPIVWCHCSAGAGRTGCYXVIDIMLMARR	1104	CC
Db	1038 FTAWEHGPVPYHATGSLLAFTRRVKASTPDAPIVTHCSAGTGCTGCVYLVDWMLDMAEC	1097	CC
Qy	1105 EGVDIYNCTYKALSRRIANNVOTEHQYIFIHDAEACCGETAIPVCEPKAAVYDFMRI	1164	CC
Db	1098 EGVDIYNCTYKTLCSRVMNIQTEHQYIFIHDAEACCGETTPVNFRATREMIRI	1157	CC
Qy	1165 DSOTNSSLHLKDFBOTTINSYSPRLQAEDCSTAICPRNHDGKRFDMLPPDRCPLPELTING	1224	CC Sequence 1462 AA;
Db	1158 DPQSISSSQREEFPLNSYSPPLDVEECSITALLPRNRDKNRSMVLPPLPFLISSG	1217	PT
Qy	1225 ESSNYINAALMDSYDQPAPIVTOYQPLPTVKDPTWLYDYGCTSIVMNEVDLSQG--	1281	Query Match 59.4%; Score 457.5%; DB 5; Length 1462;
Db	1218 DPNNYINAALTDSTSRTSAAFITVTLHPLQSTTPDFWRVLYDYGCTSIVMNLQNSNSAWP	1277	Best Local Similarity 57.6%; Pred. No. 0; Matches 849; Conservative 236; Mis matches 340; Indels 49; Gaps 9;
Qy	1282 CPQTWPEEGMLRYGPIQVBEMCSNCSDNCDVIRNIFRICNTRPQEGYLMQQFOYLGWASH	1341	QY 1 MDTPAAAALPAFVALLLSPWPWLGSAQGQFSAGGCTPDDGPGAQDYHQDL-YDDEFWTH 59
Db	1278 CLQYWPEPGRQYGLMEVTFVPSGTANEDLVSRRFVQNSRQLQGHLLRHFQFLRWASY	1337	QY 1 MASTLAAL---SILLRIQLQPLPFGARQSAQPGCSFDEHYNSCGYSVALGTINGFTWEQ 56
Qy	1342 REVGSKRSPLKTLILOVEKMQEENKEGEERTITHCLNGGRSGMFCAGIGIVEMVKRNQV	1401	QY 60 VSADQPHYLPPMPEQGSTMIVDSSHDPBKEPKARLQLPMTMKENDTCIDPSYLYSQKGLN 119
Db	1338 RDTPSKRAFLHLIAEVDRWQAE--SGDERTVHCLNGGRSGRTFCACATVLEMIRCHSL	1395	QY 57 INTTEKPMULDQAVPTGSFMMVNNSSGRASQOKAHLLPLTKENDTCIDPHYFSSRDRSS 116
Qy	1402 VDVPHAVKTLRNSKPNMTAPEQYRFYCVALELES 1438		QY 120 PGUNLTVYRNKGFLANP1WNNTGFTGRMLRAELAVSVVTEGWKVAELAISTSPWPHXYQVFEAEVSGGRSGY 179
Db	1396 VDVFFPAAKTLRNYKPNMVTMDQTHFCYDVALEYEA 1432		QY 117 PGALNVVYKVNQGQNPQPNVNSVSVTTGQFVPSVSLJRHGPQY 176
RESULT 15			QY 180 IADDIQVLSYPCDKSPHPLRIGDVEVNAGQATPQCIATGRDHWYKLNQLRNGEDIP 239
ABB97521	1 standard; protein; 1462 AA.		QY 177 IAVDBVRVLAHPCKAPHLRLQVNEVNGQATFQCLAGKWSQHDGLWLQQWNGRDTA 236
XX			QY 240 VAQTKNINHRFAASFRLOBVTKDQDLYRCVQSERGGVSNFQLVREPPPJAQQ 299
AC			QY 237 LMTRVNHRRFSATVSYADTAQRSVSKYRCVRSRDGSSGVSNVYAEVLYKEPTPIAPE 296
XX			QY 300 LLGYPYTLQIQLNANSITGDPJIIKVEYRMTGSSTEHAVNAPTYKLWHDPTDLY 359
XX			QY 297 LLAVGATLWIKPANSITGDPJIIKVEYRMTGSSTEHAVNAPTYKLWHDPTDLY 356
DT	27-JUN-2002 (first entry)		QY 360 BIRVLTTRPGEGETGNGLPGPPLIRTRKCAFPMRTPKTLKIAEQARIADVWEISGYNITR 419
XX			QY 357 EIRVLTTRPGEGETGNGLPGPPLIRTRKCAFPMRTPKTLKIAEQARIADVWEISGYNITR 416
DB	Novel human protein SEQ ID NO: 789.		QY 420 CHPNVTICYHYPRGNESKADLMDPKAPQHVVNHPPTVNSLRMLTNPGRKESE 479
XX	Human; antianaemic; vulnerability; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;		

Result No.	Score	Query Match	Length	DB ID	Description	
1	7692	99.8	1439	2 US-08-449-644-2	Sequence 2, Appli	
2	7692	99.8	1439	2 US-08-087-244A-2	Sequence 2, Appli	
3	7571	98.2	1457	2 US-08-652-971-3	Sequence 3, Appli	
4	7571	98.2	1457	2 US-08-449-644-1	Sequence 1, Appli	
5	7571	98.2	1457	2 US-08-087-244A-1	Sequence 1, Appli	
6	7571	98.2	1457	2 US-08-991-258A-3	Sequence 3, Appli	
7	7571	98.2	1457	2 US-08-769-399-3	Sequence 3, Appli	
8	7571	98.2	1457	3 US-08-991-953A-3	Sequence 3, Appli	
9	4807	62.4	1452	2 US-08-449-644-8	Sequence 8, Appli	
10	4807	62.4	1452	2 US-08-087-244A-8	Sequence 8, Appli	
11	4791	62.1	1452	2 US-08-652-971-4	Sequence 4, Appli	
12	4791	62.1	1452	2 US-08-991-258A-4	Sequence 4, Appli	
13	4791	62.1	1452	2 US-08-769-399-4	Sequence 4, Appli	
14	4791	62.1	1452	3 US-08-991-953A-4	Sequence 4, Appli	
15	4586.5	59.5	1436	2 US-08-652-971-2	Sequence 2, Appli	
16	4586.5	59.5	1436	2 US-08-991-258A-2	Sequence 2, Appli	
17	4586.5	59.5	1436	2 US-08-769-399-2	Sequence 2, Appli	
18	4586.5	59.5	1436	3 US-08-991-953A-2	Sequence 2, Appli	
19	4076.5	52.9	777	4 US-09-949-016-7158	Sequence 7158, Ap	
20	3725.5	48.3	1075	4 US-09-949-116-8108	Sequence 8308, Ap	
21	1529.5	19.8	1501	2 US-08-447-464-3	Sequence 3, Appli	
22	1529.5	19.8	1501	2 US-08-716-679-3	Sequence 3, Appli	
23	1487.5	19.3	1911	1 US-08-348-006B-5	Sequence 5, Appli	
24	1487.5	19.3	1911	2 US-08-800-825A-5	Sequence 5, Appli	
25	1487.5	19.3	1911	5 US-09-158-657-5	Sequence 5, Appli	
26	1487.5	19.3	1911	5 PCT-US94-10166-5	Sequence 5, Appli	
27	1187	15.4	793	4 US-09-280-597-3	Sequence 3, Appli	
	29	1172.5	15.2	802	1 US-08-015-985-1	Sequence 1, Appli
	30	1172.5	15.2	802	4 US-09-280-597-1	Sequence 1, Appli
	31	1172.5	15.2	807	4 US-09-949-73-56	Sequence 7356, Ap
	32	1168	15.2	538	4 US-09-743-492A-9	Sequence 9, Appli
	33	1143	14.8	699	1 US-08-348-006B-7	Sequence 7, Appli
	34	1143	14.8	699	2 US-08-800-825A-7	Sequence 7, Appli
	35	1143	14.8	699	3 US-09-158-657-7	Sequence 7, Appli
	36	1108	14.4	249	2 US-08-685-92-8	Sequence 8, Appli
	37	1108	14.4	249	2 US-09-144-925-8	Sequence 8, Appli
	38	1085.5	14.1	560	4 US-09-949-016-70786	Sequence 10786, A
	39	1023.5	13.3	2314	4 US-09-816-703A-2	Sequence 2, Appli
	40	1022.5	13.3	2308	1 US-08-015-973-1	Sequence 1, Appli
	41	1022.5	13.3	2308	2 US-08-448-164-1	Sequence 1, Appli
	42	1022.5	13.3	2308	3 US-08-081-929-2	Sequence 2, Appli
	43	1022.5	13.3	2308	4 US-10-000-954-2	Sequence 2, Appli
	44	1017.5	13.2	1442	1 US-08-015-986A-3	Sequence 3, Appli
	45	1017.5	13.2	1442	2 US-08-446-363-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-449-644-2
; Sequence 2, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ulrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Puchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSEINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query Match	Length	DB ID	Description
1	7692	99.8	1439	2 US-08-449-644-2	Sequence 2, Appli
2	7692	99.8	1439	2 US-08-087-244A-2	Sequence 2, Appli
3	7571	98.2	1457	2 US-08-652-971-3	Sequence 3, Appli
4	7571	98.2	1457	2 US-08-449-644-1	Sequence 1, Appli
5	7571	98.2	1457	2 US-08-087-244A-1	Sequence 1, Appli
6	7571	98.2	1457	2 US-08-991-258A-3	Sequence 3, Appli
7	7571	98.2	1457	2 US-08-769-399-3	Sequence 3, Appli
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9	4807	62.4	1452	2 US-08-087-244A-8	Sequence 8, Appli
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11	4791	62.1	1452	2 US-08-652-971-4	Sequence 4, Appli
12	4791	62.1	1452	2 US-08-991-258A-4	Sequence 4, Appli
13	4791	62.1	1452	2 US-08-769-399-4	Sequence 4, Appli
14	4791	62.1	1452	3 US-08-991-953A-4	Sequence 4, Appli
15	4586.5	59.5	1436	2 US-08-652-971-2	Sequence 2, Appli
16	4586.5	59.5	1436	2 US-08-991-258A-2	Sequence 2, Appli
17	4586.5	59.5	1436	2 US-08-769-399-2	Sequence 2, Appli
18	4586.5	59.5	1436	3 US-08-991-953A-2	Sequence 2, Appli
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21	1529.5	19.8	1501	2 US-08-447-464-3	Sequence 3, Appli
22	1529.5	19.8	1501	2 US-08-716-679-3	Sequence 3, Appli
23	1487.5	19.3	1911	1 US-08-348-006B-5	Sequence 5, Appli
24	1487.5	19.3	1911	2 US-08-800-825A-5	Sequence 5, Appli
25	1487.5	19.3	1911	5 US-09-158-657-5	Sequence 5, Appli
26	1487.5	19.3	1911	5 PCT-US94-10166-5	Sequence 5, Appli
27	1187	15.4	793	1 US-08-015-985-3	Sequence 3, Appli

Query Match Score 7692;
Best Local Similarity 99.9%;
Pred. No. 1, DB 2; Length 1439;

Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Qy	1 MDTAAALPAVALIISPAVLGSQGQSAGCTEDDGPACDYHDLDDDEWTV 60	Qy	1081 HCSAGAGRGTGCVTYIDIMDMAERGVVDIYCVRSLRSRINMVQTEEOYIFIDDALE 1140
	Db	1 MDTAAALPAVALIISPAVLGSQGQSAGCTEDDGPACDYHDLDDDEWTV 60	Db	1081 HCSAGAGRGTGCVTYIDIMDMAERGVVDIYCVRSLRSRINMVQTEEOYIFIDDALE 1140
	Qy	61 SAQEPHYLPPENPMQSYMIYDSSDHDPGEKARLQLPMTMKENDTHCLDFSTLYSOKGLNP 120	Qy	1141 ALCGCTTAIPVCEFFAYFDMIRIDSQTNSHLDKBFTQTLNSVTPLQAEDCS1ACLPRN 1200
	Db	61 SAQEPHYLPPENPMQSYMIYDSSDHDPGEKARLQLPMTMKENDTHCLDFSTLYSOKGLNP 120	Db	1141 ALCGCTTAIPVCEFFAYFDMIRIDSQTNSHLDKBFTQTLNSVTPLQAEDCS1ACLPRN 1200
	Qy	121 GTLNILRVNKGPLANPIWNTGFTGRDMLRRAELAVSTFWNEQYVIFAEVGSGRSGYI 180	Qy	1201 HDKNFMDMLPPDRCLPFLITDGESSNTNALMDSYROOPAFTYQVPLPNTKDFWR 1260
	Db	121 GTLNILRVNKGPLANPIWNTGFTGRDMLRRAELAVSTFWNEQYVIFAEVGSGRSGYI 180	Db	1201 HDKNFMDMLPPDRCLPFLITDGESSNTNALMDSYROOPAFTYQVPLPNTKDFWR 1260
	Qy	181 ADDIQVLSYPCDKSPHFLRGDVEVNGQATFOCIAFGDAVANKLWLRQRNGEDIYV 240	Qy	1261 LVDYGCSTSIVMLNEVDLSQGCPOTWPEEGMLRYCPIQVBCMSCSMDCDVNR1PRICNL 1320
	Db	181 ADDIQVLSYPCDKSPHFLRGDVEVNGQATFOCIAFGDAVANKLWLRQRNGEDIYV 240	Db	1261 LVDYGCSTSIVMLNEVDLSQGCPOTWPEEGMLRYCPIQVBCMSCSMDCDVNR1PRICNL 1320
	Qy	241 AOTKNIHRFAASFRILQEVTKTDQDLRYCUTQTSERGSVNSPAQIIVREPPRAPPQI 300	Qy	1321 TRPOQGYLMYQQPOYLGASHREPGSKRSFLKL1LQVERKQEWKEGEGRTTIICLNGG 1380
	Db	241 AOTKNIHRFAASFRILQEVTKTDQDLRYCUTQTSERGSVNSPAQIIVREPPRAPPQI 300	Db	1321 TRPOQGYLMYQQPOYLGASHREPGSKRSFLKL1LQVERKQEWKEGEGRTTIICLNGG 1380
	Qy	301 LGVGPYLLIONANSTIGDGPILKEVEYMTSGSWTETHAVNAPTYKLWHLDDPDTYE 360	Qy	1381 GRSGMFCAIGIVVENVKRQNVDVPHAVKTLRNSPKNMVAPEQRFCDYVALELESS 1439
	Db	301 LGVGPYLLIONANSTIGDGPILKEVEYMTSGSWTETHAVNAPTYKLWHLDDPDTYE 360	Db	1381 GRSGMFCAIGIVVENVKRQNVDVPHAVKTLRNSPKNMVAPEQRFCDYVALELESS 1439
	Qy	361 IRLVLTTRGEGTGLPOPPLTRTKCAEPMRPTKTLKIAEQARRIANDWESLGNITRC 420	Qy	RESULT 2
	Db	361 IRLVLTTRGEGTGLPOPPLTRTKCAEPMRPTKTLKIAEQARRIANDWESLGNITRC 420	Db	US-08-087-244A-2
	Qy	421 HTFVNNTIYCHYPRGHNESKADCLMDPRAPOHVNLHPYTNSLKMILNPEGRKSEE 480	Qy	Sequence 2, Application US/08087244A
	Db	421 HTFVNNTIYCHYPRGHNESKADCLMDPRAPOHVNLHPYTNSLKMILNPEGRKSEE 480	Db	Patent No. 5863755
	Qy	481 TLIQTDPEVGPGPVVKSLQGTSFENKLFILVKEPLDQNGITTOYEISYSSIRSFSDFAVPV 540	Qy	GENERAL INFORMATION:
	Db	481 TLIQTDPEVGPGPVVKSLQGTSFENKLFILVKEPLDQNGITTOYEISYSSIRSFSDFAVPV 540	Db	APPLICANT: Schlessinger, Joseph
	Qy	541 AGPPQTYSNLWNSTTHIYFMLHPTGTYQEFFIRASTYKGFPTAINVTNTNISAPLDPYE 600	Qy	APPLICANT: Sap, Jan M.
	Db	541 AGPPQTYSNLWNSTTHIYFMLHPTGTYQEFFIRASTYKGFPTAINVTNTNISAPLDPYE 600	Db	APPLICANT: Ulrich, Axel
	Qy	601 GVDASLINEATTIVLRLPAQAKGAPISAYQVTEELHPRHTKREGAMECYQVPVYQN 660	Qy	APPLICANT: Vogel, Miriam
	Db	601 GVDASLINEATTIVLRLPAQAKGAPISAYQVTEELHPRHTKREGAMECYQVPVYQN 660	Db	APPLICANT: Richs, Miriam
	Qy	661 AMSGGAPYYFAAEELPPNLPEPAPFTYGDNRITYQGFPNNPLAPRKYNTYQAMSSVKE 720	Qy	TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSEINE
	Db	661 AMSGGAPYYFAAEELPPNLPEPAPFTYGDNRITYQGFPNNPLAPRKYNTYQAMSSVKE 720	Db	NUMBER OF SEQUENCES: 11
	Qy	721 TKTQCVRIATKATEEPPVTPDPAKQDTRVKGIAIGSLVFLILVVKSKLA 780	Qy	CORRESPONDENCE ADDRESS:
	Db	721 TKTQCVRIATKATEEPPVTPDPAKQDTRVKGIAIGSLVFLILVVKSKLA 780	Db	ADDRESS: PENNIE & EDMONDS
	Qy	781 KERKDANGNTROEMTHNMNAMRSYAQDSTLHAEDPLSITMDQHNFSPRVBNHSATAES 840	Qy	STREET: 1155 Avenue of the Americas
	Db	781 KERKDANGNTROEMTHNMNAMRSYAQDSTLHAEDPLSITMDQHNFSPRVBNHSATAES 840	Db	CITY: New York
	Qy	901 SRLLDVPRYLCEGTESTPSYQTCGKQHNLMTSDSYGKFKEYESFFRGQSA 900	Db	STATE: New York
	Db	901 SRLLDVPRYLCEGTESTPSYQTCGKQHNLMTSDSYGKFKEYESFFRGQSA 900	Db	COUNTRY: U.S.A.
	Qy	961 PYVETTYDFWRMTWQEQSACIYVNLIVEGRVCKYKWPDTTEVGFKTYTCVEMPLA 1020	Db	ZIP: 10036
	Db	961 PYVETTYDFWRMTWQEQSACIYVNLIVEGRVCKYKWPDTTEVGFKTYTCVEMPLA 1020	Qy	COMPUTER READABLE FORM:
	Qy	1021 EYVVRTFTLERRGYNEIREVKQFHFTGPDPDHEGVYHATGLLSFIRRKLNSNPSAGP1VV 1080	Db	MEDIUM TYPE: Floppy disk
	Db	1021 EYVVRTFTLERRGYNEIREVKQFHFTGPDPDHEGVYHATGLLSFIRRKLNSNPSAGP1VV 1080	Qy	COMPUTER: IBM PC compatible
	Qy	Best Local Similarity 99.8%; Pred. No. 0; Length 1439;	Db	OPERATING SYSTEM: PC-DOS/MS-DOS
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	SOFTWARE: Patent-In Release #1.0, version #1.25
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	CURRENT APPLICATION DATA:
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	APPLICATION NUMBER: US/08/087,244A
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	FILING DATE: 01-JUL-1993
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	CLASSIFICATION: 435
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	ATTORNEY/AGENT INFORMATION:
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	NAME: Cotuzzii, Laura A.
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	REGISTRATION NUMBER: 30,742
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	REFERENCE/DOCKET NUMBER: 7683-042
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	TELECOMMUNICATION INFORMATION:
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	TELEPHONE: 212-750-9090
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	TELEFAX: 212-869-8864/9741
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	INFORMATION FOR SEQ ID NO: 2:
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	SEQUENCE CHARACTERISTICS:
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	LENGTH: 1439 amino acids
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	TYPE: amino acid
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	TOPOLOGY: linear
	Qy	99.9%; Pred. No. 0; Length 1439;	Db	MOLECULAR TYPE: Protein
	Db	Query Match Score 7692; DB 2; Pred. No. 0;	Qy	US-08-087-244A-2

Matches	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;	
Qy	1	MDTTAAALPAFVALLLSPWPLGSAQQGFSAGCCTFDGGACGCDYHDLDDFEWTVY	60						Qy 1081 HCSAGAGRTGCYIVIDIMLDMAERGVVDIYCNYKALRSRRINMVQTEQYIFIHDAILE 1140
Db	1	MDTTAAALPAFVALLLSPWPLGSAQQGFSAGCCTFDGGACGCDYHDLDDFEWTVY	60						Db 1081 HCSAGAGRTGCYIVIDIMLDMAERGVVDIYCNYKALRSRRINMVQTEQYIFIHDAILE 1140
Qy	61	SAQEPHYLPPEMPOSYMTDSSDHDPGEKARLOLQPTMKENDTHCIDFYLLYSQGKINP	120						Qy 1141 ACGCETALPVCEPKAYFDMIRISQTNSSHLKEDEFQTLNSTPRLQAEDCSIACLPRN 1200
Db	61	SAQEPHYLPPEMPOSYMTDSSDHDPGEKARLOLQPTMKENDTHCIDFYLLYSQGKINP	120						Db 1141 ACGCETALPVCEPKAYFDMIRISQTNSSHLKEDEFQTLNSTPRLQAEDCSIACLPRN 1200
Qy	121	GTNLILVRVNGKPLANPIWNTGFTGRDWLRAELAVSTWPNEYQVTPAEVGSGRSGYI	180						Qy 1201 HDKNRFMDMLPPDCCLPFLITIDEDESSNTYNAIMDSYRQPAAFVTQPLPNTVKDFWR 1260
Db	121	GTNLILVRVNGKPLANPIWNTGFTGRDWLRAELAVSTWPNEYQVTPAEVGSGRSGYI	180						Db 1201 HDKNRFMDMLPPDCCLPFLITIDEDESSNTYNAIMDSYRQPAAFVTQPLPNTVKDFWR 1260
Qy	181	AIDDIQVISYPCDKSPHEFLRGLDVEVNAGSONATFOCIATGRDAVNKLWLQRNGEDI	240						Qy 1261 LYDYGCTSIWMLNEVDLSQGCPQWPEFGMLRYGPIQECMSCSMDCCDVINRIFRICNL 1320
Db	181	AIDDIQVISYPCDKSPHEFLRGLDVEVNAGSONATFOCIATGRDAVNKLWLQRNGEDI	240						Db 1261 LYDYGCTSIWMLNEVDLSQGCPQWPEFGMLRYGPIQECMSCSMDCCDVINRIFRICNL 1320
Qy	241	AQTNNINHERRFAASRFLQEVTKDQLYCVTQSERSGSVSNFAQLIVEBPPRDIAPPOL	300						Qy 1321 TRPOEGYLMLVQOPOYLGMASHREVPGSRSFLKLLOVEKQEWKQEWKQEWKQEWBCEEGEGRTIHCLNGG 1380
Db	241	AQTNNINHERRFAASRFLQEVTKDQLYCVTQSERSGSVSNFAQLIVEBPPRDIAPPOL	300						Db 1321 TRPQEGLMLVQOFYLGASHREVPGSRSFLKLLOVEKQEWKQEWBCEEGEGRTIHCLNGG 1380
Qy	301	LGVGPYTLILQLNANSITGNGPITLKEVBYRMTSGSWTHTHVNAPTYKLWHLDPDTYE	360						Qy 1381 GRSGMFCAGIVVEMKRQNVVDFHAVTLRLNSKPNNVVAPEOYRFCYDVALEYLESS 1439
Db	301	LGVGPYTLILQLNANSITGNGPITLKEVBYRMTSGSWTHTHVNAPTYKLWHLDPDTYE	360						Db 1381 GRSGMFCAGIVVEMKRQNVVDFHAVTLRLNSKPNNVVAPEOYRFCYDVALEYLESS 1439
Qy	361	IRVLILTRPSEGCTGLPGPLPLITRKCAEMRTPKTLKAEIQARIATWESGYNITRC	420						RBSLT 3 US-08-652-971-3
Db	361	IRVLILTRPSEGCTGLPGPLPLITRKCAEMRTPKTLKAEIQARIATWESGYNITRC	420						; Sequence 3; Application US/08652971
Qy	421	HTEFNVTICHYFRGNESKADCLMDPKAQHVNNHLPHPTVNSLKMILTNPEGRKESSE	480						; Patent No. 5814507
Db	421	HTEFNVTICHYFRGNESKADCLMDPKAQHVNNHLPHPTVNSLKMILTNPEGRKESSE	480						; GENERAL INFORMATION:
Qy	481	TIIQIDEDVPGPVPKSLQGSTSFENKIFLNKEPLDNGLITOTYEISYSIRSFDPAVY	540						; APPLICANT: Cheng, Jill
Db	481	TIIQIDEDVPGPVPKSLQGSTSFENKIFLNKEPLDNGLITOTYEISYSIRSFDPAVY	540						; APPLICANT: Lasky, Laurence A.
Qy	541	AGPPOTVSILWNSTPHVEMWHLHPSTYQFFIRASTVKGFPATAINTTNISAPTLPLYE	600						; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
Db	541	AGPPOTVSILWNSTPHVEMWHLHPSTYQFFIRASTVKGFPATAINTTNISAPTLPLYE	600						; NUMBER OF SEQUENCES: 10
Qy	601	GVDSLNETATTITVLLRAQAKAPISAYQIVVEELHPRTRKEAGAMECYQVPVYQN	660						; CORRESPONDENCE ADDRESS:
Db	601	GVDSLNETATTITVLLRAQAKAPISAYQIVVEELHPRTRKEAGAMECYQVPVYQN	660						; ADDRESSEE: Genentech, Inc.
Qy	661	AMSGCAPPYFAAELPGNLPPEPAFTVGDNRTYQGFNNPLAPRKGNVYFOAMSSVERE	720						; STREET: 460 Point San Bruno Blvd.
Db	661	AMSGCAPPYFAAELPGNLPPEPAFTVGDNRTYQGFNNPLAPRKGNVYFOAMSSVERE	720						; CITY: South San Francisco
Qy	721	TKTCVCRITAATEEPFVLPDPKOTDRVVKLAGISAGILVFLLLVILVKKSLA	780						; STATE: California
Db	721	TKTCVCRITAATEEPFVLPDPKOTDRVVKLAGISAGILVFLLLVILVKKSLA	780						; COUNTRY: United States
Qy	781	KRKDAMGNTROEMTHVNAMDREYADQSTLHAEDPLSTFMDQHNSPRYENHSATES	840						; ZIP: 94040
Db	781	KRKDAMGNTROEMTHVNAMDREYADQSTLHAEDPLSTFMDQHNSPRYENHSATES	840						; COMPUTER READABLE FORM:
Qy	841	SRLLDVPRLCEGTESPYTGOLHPAIRADLQHINLMTSDSYGFKEYESFFEGOSA	900						; COMPUTER: IBM PC compatible
Db	841	SRLLDVPRLCEGTESPYTGOLHPAIRADLQHINLMTSDSYGFKEYESFFEGOSA	900						; OPERATING SYSTEM: PC-DOS/MS-DOS
Qy	901	SWDVAKKCOONRAKRYGNITAYDHSRVVILQPVEDDPSSYINANYGYQRPHYIATQG	960						; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
Db	901	SWDVAKKCOONRAKRYGNITAYDHSRVVILQPVEDDPSSYINANYGYQRPHYIATQG	960						; CURRENT APPLICATION DATA:
Qy	961	PVHBTVDWRMIWQEASCIVMTNLVEGRVYKCYKWPDDTEVYGDJKVTCVEMELA	1020						; APPLICATION NUMBER: US/08/652, 971
Db	961	PVHBTVDWRMIWQEASCIVMTNLVEGRVYKCYKWPDDTEVYGDJKVTCVEMELA	1020						; FILING DATE:
Qy	1021	EYVVRTFTLERRGYNIEIREVKQPHFTGWFHDGYHYATCQLLSPTRVYKSNPPSAGITVY	1080						; CLASSIFICATION: 435
Db	1021	EYVVRTFTLERRGYNIEIREVKQPHFTGWFHDGYHYATCQLLSPTRVYKSNPPSAGITVY	1080						; ATTORNEY/AGENT INFORMATION:
Qy	1021	EYVVRTFTLERRGYNIEIREVKQPHFTGWFHDGYHYATCQLLSPTRVYKSNPPSAGITVY	1080						; NAME: Dreger, Ginger R.
Db	1021	EYVVRTFTLERRGYNIEIREVKQPHFTGWFHDGYHYATCQLLSPTRVYKSNPPSAGITVY	1080						; REGISTRATION NUMBER: 33, 055

Qy 1 MDTTAAALPAFVALLSPWLLGSAQGOFSGGCTFDGPGACDHYDDDFEWHV 60
 Db 1 MD-VAAAALPAFVALMLYPLLSALGEOFAGGTIDGPGACDHYDDDFEWHV 59
 Qy 61 SAQEPHYLPPMPOGSYMIYDSSDHDPGEKARLQLQPTMKENDTHCIDEFSYLISOKGLNP 120
 Db 60 SAQEPHYLPPMPOGSYMMVDSNNHDPGEKARLQLQPTMKENDTHCIDEFSYLISOKGLNP 119
 Qy 121 GTLNILVRVNGP LANPIWNTGFGDRDWRAELAUSTTFNNEQVIFRLEVSQRSGYI 180
 Db 120 GTLNILVRVNGP LANPIWNTGFGDRDWRAELAUSTTFNNEQVIFRLEVSQRSGYI 179
 Qy 121 ADDIQVLSYPCDKSPPHFLRLGDEVNAQONATFOCIATGRDAVNKLWLRNQREDDIPV 240
 Db 120 ADDIQVLSYPCDKSPPHFLRLGDEVNAQONATFOCIATGRDAVNKLWLRNQREDDIPV 239
 Qy 241 AQTKNINHRRFAASFLQEVTKTDDOLYRCYTOSERGSVSNFAQLIVREPRTAPPOL 300
 Db 240 AQTKNINHRRFAASFLQEVTKTDDOLYRCYTOSERGSVSNFAQLIVREPRTAPPOL 299
 Qy 301 LGVGPYTLQIQNANSTIGDPIILKEVEAMTSGWTETHAVNAPTYKLWHDDETEV 360
 Db 300 LGVGPYTLQIQNANSTIGDPIILKEVEAMTSGWTETHAVNAPTYKLWHDDETEV 359
 Qy 361 IRLVLTTRPGEGETGLPSPPLTRTKCAEPMTPTKTLKIAETQARRIADWESLGYNITRC 420
 Db 360 IRLVLTTRPGEGETGLPSPPLTRTKCAEPMTPTKTLKIAETQARRIADWESLGYNITRC 419
 Qy 421 HTFVNITICHHYFRGHNESKAQCLDMDPKAPOHVNHLPPTNVSLKMILTNPEGRKESSE 480
 Db 420 HTFVNITICHHYFRGHNESKAQCLDMDPKAPOHVNHLPPTNVSLKMILTNPEGRKESSE 479
 Qy 481 TIIQTDDEVPGVPVIGLQGTSFENKFLINKEPLDNGITQKETISSKTSRSFDPAVP 540
 Db 480 TIIQTDDEVPGVPVIGLQGTSFENKFLINKEPLDNGITQKETISSKTSRSFDPAVP 539
 Qy 541 AGPPQTVSNLNWNSTHFMHHRPGITYQFFIRASTYKGFPTAINTVNTISAPTLPDYE 600
 Db 540 APPQTQTVSNLNWNSTHFMHHRPGITYQFFIRASTYKGFPTAINTVNTISAPTLPDYE 599
 Qy 601 GVDASLINEATTITVILRPAQKGAPTAQYQIVVEELHHPHRTKREAGAMECYQVPVTYQN 660
 Db 600 GVDASLINEATTITVILRPAQKGAPTAQYQIVVEELHHPHRTKREAGAMECYQVPVTYQN 659
 Qy 661 ANGGAGAYFAAELPPGNLPERAPFTGDNNTYQGFPNPLAPRKYNIYQAMSSVEKE 720
 Db 660 ALGGGAPYFAAELPPGNLPEPAPFTGDNRTYKGFNPNNPLAPRKYNIYQAMSSVEKE 719
 Qy 721 TKHQCVRLATK-AATEBEVIDDPAKQDIDRVVKLAGISAGLVLVLLVKKSKL 779
 Db 720 TKHQCVRLATK-AATEBEVIDDPAKQDIDRVVKLAGISAGLVLVLLVKKSKL 779
 Qy 780 AKKRKDAMNTROEMTMVNANDSYAQSPLHAEDPSITMDOHNSPRY----- 831
 Db 780 AKKRKDAMNTROEMTMVNANDSYAQSPLHAEDPSITMDQINPSPRLNDPLVPT 839
 Qy 832 ---ENISATAEESRLLDPVRLCEGESPYQTGQLHPAIRVADLQHINLMKTSDSYGF 887
 Db 840 AVLDENHATAEESRLLDPVRLCEGESPYQTGQLHPAIRVADLQHINLMKTSDSYGF 899
 Qy 888 KEEYESFPEQGQASWYAKDNRAKRYGNLTAYDHSRVLQVEDPSSDYINANYI- 946
 Db 900 KEEYESFPEQGQASWYAKDNRAKRYGNLTAYDHSRVLQVEDPSSDYINANYI- 946
 Qy 947 ----DGYQRPSPHYIATGSPVHETVYDWRMIWOEQSACIVMVNLIVEGRVTKCYKWPD 1001
 Db 960 IWLWYRDGQRPSPHYIATGSPVHETVYDWRMWMQEACIVMVNLIVEGRVTKCYKWPD 1019
 Qy 1002 DTEVYGDPRKVTCHEMPLAEVTRTFLERRGYNETIPEVKQFHFTGMPDHGPYHATGLL 1061
 Db 1020 DTEVYGDPRKVTCHEMPLAEVTRTFLERRGYNETIPEVKQFHFTGMPDHGPYHATGLL 1079
 Qy 1062 SFIRRVKLSNPPSAGGIVHCSAGAGRIGTCYIVIDIMDMAERGVVDTIYNCVKALRR 1121

Db 1080 SFIRRVKLSNPPSAGGIVHCSAGAGRIGTCYIVIDIMDMAERGVVDTIYNCVKALRR 1139
 Qy 1122 INMYQTEBQWIFIHDALEACLGCTAIPCEFKAYFDMIRISQTSNSSLKDFQTLN 1181
 Db 1140 INMYQTEBQWIFIHDALEACLGCTAIPCEFKAYFDMIRISQTSNSSLKDFQTLN 1199
 Qy 1182 SVTPRLOAECSCIACLPRNHDKNRKFDMLLPDRCFLPLITIDGESNYINAALMSYROP 1241
 Db 1200 SVTPRLOAECSCIACLPRNHDKNRKFDMLLPDRCFLPLITIDGESNYINAALMSYROP 1259
 Qy 1242 AAFTVTOQPLPNTYKDFWRLVYDYGCTSIWMLNEVDLSOGCPQWPEEGMRLYGPQVEC 1301
 Db 1260 AAFTVTOQPLPNTYKDFWRLVYDYGCTSIWMLNEVDLSOGCPQWPEEGMRLYGPQVEC 1319
 Qy 1302 MSCSDCDVNRIFPICNLTRPQEYLMYQFOQVIGWASHREVPSKRSPLKLTLQVEKW 1361
 Db 1320 MSCSDCDVNRIFPICNLTRPQEYLMYQFOQVIGWASHREVPSKRSPLKLTLQVEKW 1379
 Qy 1362 QEENKEGEGRITIHLCLNGGGRSGMFCAGIGVVMKRONVYDVFHAKTLRNSKENMVEA 1421
 Db 1380 QEECBEGEGTIHLCLNGGGRSGMFCAGIGVVMKRONVYDVFHAKTLRNSKENMVEA 1439
 Qy 1422 PEQYRFCDYVALEYLESS 1439
 Db 1440 PEQYRFCDYVALEYLESS 1457

RESULT 4
 ; Sequence 1, Application US/08449644-1
 ; Patent No. 585612
 / GENERAL INFORMATION:
 / APPLICANT: Schlessinger, Joseph
 / APPLICANT: Sap, Jan M.
 / APPLICANT: Ulrich, Axel
 / APPLICANT: Vogel, Wolfgang
 / APPLICANT: Fuchs, Miriam
 / TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSEINE
 / TITLE OF INVENTION: PHOSPHATE-KAPPA
 / NUMBER OF SEQUENCES: 11
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: PENNIE & EDMONDS
 / STREET: 1155 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: U.S.A.
 / ZIP: 10036
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/449,644
 / FILING DATE: 24-MAY-1995
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/087,244
 / FILING DATE: 01-JUL-1993
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Coruzzi, Laura A.
 / REGISTRATION NUMBER: 7683-042
 / REFERENCE/DOCKET NUMBER: 30,742
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 212-659-9090
 / TELEFAX: 212-659-8864/9741
 / TELEX: 66141 PENNIE
 / INVENION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1457 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-449-644-1

Query Match 98.2%; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDITAAAALPAFAVALLISWPWPLIGSAQQGCTPFDGGACDHYDDPEWYV 60
Db 1 MD-VAAAALPAFAVALLISWPWPLIGSAQQGCTPFDGGACDHYDDPEWYV 59

Qy 61 SAQPHYLPEMPQSYYMIVDSSEDPGKARLQOPTMKENDTHCIDFSYLLYSQKGILNP 120
Db 60 SAQPHYLPEMPQSYYMIVDSSNHDPGKARLQOPTMKENDTHCIDFSYLLYSQKGILNP 119

Qy 121 GTLNILVRLVRNKGPLANPINVNTGFGDRDLRABLAIVSTWPNEQVIFAEVGGRSGV 180
Db 120 GTLNILVRLVRNKGPLANPINVNTGFGDRDLRABLAIVSTWPNEQVIFAEVGGRSGV 179

Qy 181 ADDIQVSYPCDKSPHFLRGLDGVBNAGQNAQATFOCIATGRDAVNKLWLQRNGEDIPV 240
Db 180 ADDIQVLSYPCDKSPHFLRGLDGVBNAGQNAQATFOCIATGRDAVNKLWLQRNGEDIPV 239

Qy 241 AQTENINHRRFAASFRLOQVTKTQDQLFCVTCVQSERGSVSNSAQLIVTEPPRPIAPPQI 300
Db 240 AQTENINHRRFAASFRLOQVTKTQDQLFCVTCVQSERGSVSNSAQLIVTEPPRPIAPPQI 299

Qy 301 LGVQPTYLILQLNANSIIGDGPILKEVYRMTGSWTHAANAPTYKLWHLDPTYE 360
Db 300 LGVQPTYLILQLNANSIIGDGPILKEVYRMTGSWTHAANAPTYKLWHLDPTYE 359

Qy 361 ITRVLTRPGEGGTSUPLGPPLITRTKCAEPMRTPTKTLKAEIQCARRIAVWESLGYNITRC 420
Db 360 ITRVLTRPGEGGTSUPLGPPLITRTKCAEPMRTPTKTLKAEIQCARRIAVWESLGYNITRC 419

Qy 421 HTENVNTICHTYFRGNESKADCLMDPKAPQHVNHLPPYTNSLKMINTNPGRKESSE 480
Db 420 HTENVNTICHTYFRGNESRADCLMDPKAPQHVNHLPPYTNSLKMINTNPGRKESSE 479

Qy 481 TIIQDDEDPGPVVKSLQGTSFENKIFNWKPELDPNQIITOEVISYSSRSDPAVYV 540
Db 480 TIIQDDEDPGPVVKSLQGTSFENKIFNWKPELDPNQIITOEVISYSSRSDPAVYV 539

Qy 541 AGPPQTWSNLWNSTHVNHLHPGTTYQFIRASTVKGCPATAINTTNISAPTLPDYE 600
Db 540 AGPPQTWSNLWNSTHVNHLHPGTTYQFIRASTVKGCPATAINTTNISAPSLPDYE 599

Qy 601 GVDASLNETATTITVLLRAQKAQCAPISYQIVVEELHPRTRREAGAMECYQVPVTYQN 660
Db 600 GVDASLNETATTITVLLRAQKAQCAPISYQIVVEQLHPRTRREAGAMECYQVPVTYQN 659

Qy 661 AMSSGAPYFAELPGNIDPEPAFTVGNRITYGFWNPLAPRKGTNYFQAMSSVKE 720
Db 660 ALSSGAPYFAELPGNIDPEPAFTVGNRITYGFWNPLAPRKGTNYFQAMSSVKE 719

Qy 721 TKTQCVRIATK-AATEEPVIPDPAKOTDRVKTAGISAGILVILLVVVJLKKSKL 779
Db 720 TKTQCVRIATKAAATEEPVIPDPAKOTDRVKTAGISAGILVILLVVVJLKKSKL 779

Qy 780 AKERKDAMGNTROQEMTHNAMESYADSTLHADPSITMDQHNSPRY----- 831
Db 780 AKERKDAMGNTROQEMTHNAMESYADSTLHADPSITMDQHNSPRLNDPLVPT 839

Qy 832 ---ENHSATAESSLRLDPYRLCEGTEPYQTCQLHPIRVLADLQNLMTKSDSTGF 887
Db 840 AVLDENHATAESSLRLDPYRLCEGTEPYQTCQLHPIRVLADLQNLMTKSDSTGF 899

Qy 888 KEEYESFFRGQSASWDACKDNRAKNRGNILAYDHSAVLQVEDDPSSDYINANYI- 946
Db 900 KEEYESFFRGQSASWDACKDNRAKNRGNILAYDHSRVLQVEDDPSSDYINANYI- 959

Qy 947 ----DGKORPSHVIATQOPVHETVYDFWRMIVQEQAQJMVNTNLVEGRVKCYKWPD 1001

Db 960 IWLYRDGYORPSHVIATQOPVHETVYDFWRMIVQEQAQJMVNTNLVEGRVKCYKWPD 1019

Qy 1002 DTEVYGDPEKVTVCYMEPLABEVYVRTFTLERRGYNIREVKOFHTGWDHGVPYHATGIL 1061
Db 1020 DTEVYGDPEKVTVCYMEPLABEVYVRTFTLERRGYNIREVKOFHTGWDHGVPYHATGIL 1079

Qy 1062 SFIRRVLISNPPSAGPITVHCSAGAGRGCYTYVIDIMLDMAEREGVYDLYNCYKALRSR 1121
Db 1080 SFIRRVLISNPPSAGPITVHCSAGAGRGCYIVIDIMLDMAEREGVYDLYNCYKALRSR 1139

Qy 1122 INMVOTEBOXYIIFHDIALEACLGCTAIPVCEPKAYFDMIRIDSQTNSHLYKDFOTLN 1181
Db 1140 INMVOTEQYIIFHDIALEACLGCTAIPVCEPKAYFDMIRIDSQTNSHLYKDFOTLN 1199

Qy 1182 SVTPRLOQEDCSACALPANHDKORPMDMLPPDDECLPFLITIDGESNSVINAALMSYROP 1241
Db 1200 SVTPRLOQEDCSACALPANHDKORPMDMLPPDRCLPFLITIDGESNSVINAALMSYROP 1259

Qy 1242 AAFTVTOXPLNTVYDFWRLVYDGCITSIVMNEVDLSOGCPOYWEPEGMRLRYGPJOVBC 1301
Db 1260 AAFTVTOXPLNTVYDFWRLVYDGCITSIVMNEVDLSOGCPOYWEPEGMRLRYGPJOVBC 1319

Qy 1302 MSCSMDCDVINRIFRICNLTRPQEGLMYQQOQYLGASHREVPGSKRSFLKLILQVEKW 1361
Db 1320 MSCSMDCDVINRIFRICNLTRPQEGLMYQQOQYLGASHREVPGSKRSFLKLILQVEKW 1379

Qy 1362 QEWKKEGERTIHLNLNGGRSGMFCAIGIVENVKRONVVDVFHAVKTLRNSKPNMVEA 1421
Db 1380 QEWKKEGERTIHLNLNGGRSGMFCAIGIVENVKRONVVDVFHAVKTLRNSKPNMVEA 1439

RESULT 5
US-08-087-244A-1
; Sequence 1, Application US/08087244A
; Patent No. 5863755
; General Information:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ulrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROLINE
; NUMBER OF SEQUENCES: 11
; TITLE OF INVENTION: PHOSPHATASE KAPPA
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087-244A
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30-742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 6614 PENNIE
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-087-24A-1

Query Match 98.2%; Score 7571; DB 2; Length 1457;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Db 900 KEEYESFFEGQSASWDVAKKDQNRAKNRYGNTIAYDHSRVTLQPVEDDPSSDYINANYID 959
 Qy 947 - - - DGYQPSKXIAATOGPHETTYDFKTMWQOSACIYMTNLVEGRVKCYKWPD 1001
 Db 960 IWLYRDGYQPSHYATOGPHETTYDFKTMWQOSACIYMTNLVEGRVKCYKWPD 1019
 Us-08-087-24A-1

Db 1002 DTEVYGFKVTCVENEPLAEYVVRFTLERGYNTRREVQHFPTGPWPDIGVPTAGTLL 1061
 Db 1020 DTEVYGDFTKTCVENEPLAEYVVRFTLERGYNTRREVQHFPTGPWPDIGVPTAGTLL 1079

Qy 1062 SFIRVKLSNPPSAGPIVHCSAGAGRGTGCVIVIDIMLDNAERGVYDLYNCVKALRSRR 1121
 Db 1080 SFIRVKLSNPPSAGPIVHCSAGAGRGTGCVIVIDIMLDNAERGVYDLYNCVKALRSRR 1139
 Qy 1122 INMVQTEEQYIFIAHLEACLGSTAIPCEPKAYFDMIRIDSOINSHLKDFOQTIN 1181
 Db 1140 INMVQTEEQYIFIAHLEACLGSTAIPCEPKAYFDMIRIDSOINSHLKDFOQTIN 1199
 Qy 1182 SVTPRLQAEDCSIACLPRHFDKRNMDLPDRDCFLTLIDGESEYYINAALMSYRQP 1241
 Db 1200 SVTPRLQAEDCSIACLPRHFDKRNMDLPDRDCFLTLIDGESEYYINAALMSYRQP 1259
 Db 1242 AAFTVTOYPLPNITYDFWRLVYDGCSTYMLNEVDLSOCCPQYVPEEGMLRYGPQVEC 1301
 Qy 1260 AAFTVTOYPLPNITYDFWRLVYDGCSTYMLNEVDLSOCCPQYVPEEGMLRYGPQVEC 1319
 Db 1302 MSCSDCDVNRIFICNUTRPQEGGLYLMVQFOQIGWASHREPGSKPSFLKLILQVEKW 1361
 Qy 1320 MSCSDCDVNRIFICNUTRPQEGGLYLMVQFOQIGWASHREPGSKPSFLKLILQVEKW 1379
 Db 1362 QBEWKGEGRTIHCUNGGRSGMCAIGIVEMVYKRQNTVDFHAVKTLRNSKPNVEA 1421
 Qy 1380 QEECPEGTTIHCUNGGRSGMCAIGIVEMVYKRQNTVDFHAVKTLRNSKPNVEA 1439
 Db 1440 PEQRFCDYVALEYLESS 1457

RESULT 6
 US-08-991-258A-3
 ; Sequence 3, Application US/08991258A
 ; Patent No. 592887
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Jill
 ; ADDRESS: Flehr, Houbach, Test, Albritton & Herbert, LLP
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/991258A
 ; FILING DATE: 17-DEC-1997
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/652,971
 ; FILING DATE: 24-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; RENEWAL/DOCKET NUMBER: A-63478-3/WHD/MTK
 ; TELECOMMUNICATION INFORMATION:

Qy 780 AKKRKDAMGNTQEMTMVNMADRSYADQSTHAEDPLSITMDQINSPRY----- 831
 Db 780 AKKRKDAMGNTQEMTMVNMADRSYADQSTHAEDPLSITMDQINSPPLNDPLVPT 839
 Qy 832 - - - ENHSAEAESSRLIUDPRYLCGETSPYOTGOLHPAIRADLQHINLMKTSDSYGF 887
 Db 840 AVLDENISATASSRLIUDPRYLCGETSPYOTGOLHPAIRADLQHINUMKTSDSYGF 899
 Qy 888 KEEYESFFEGQSASWDVAKKDQNRAKNRYGNTIAYDHSRVTLQPVEDDPSSDYINANYI- 946

TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 98.2%; Score 7571; DB 2; Length 1457;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDTPAAALPAVALLLSPWPLIGSAQGFSAGGCTFDGGACDYHDLDDDFEWYHV 60
 Db 1 MD-VAAALLPAVALLLSPWPLIGSAQGFSAGGCTFDGGACDYHDLDDDFEWYHV 59

Qy 61 SAQEPHYLLPEMPQCSTMIVDSSHDPGKARLQLOPTMENDTCIDFSELLYSOKGLNP 120
 Db 60 SAQEPHYLLPEMPQCSTMVDSNHDPGKARLQLOPTMENDTCIDFSELLYSOKGLNP 119

Qy 121 GTLNILVRLVNGKPLANPINVNTGFTGRDVLRAELAVSTWPNEYQVIFPAEVSGCRSGT 180
 Db 120 GTLNILVRLVNGKPLANPINVNTGFTGRDVLRAELAVSTWPNEYQVIFPAEVSGCRSGT 179

Qy 181 ADDIQVLSYPCDKSPDHPLRQLGDEVNAQONATFOCIATGRDAVNKLWLQRNGEDIPV 240
 Db 180 ADDIQVLSYPCDKSPDHPLRQLGDEVNAQONATFOCIATGRDAVNKLWLQRNGEDIPV 239

Qy 241 AQTQINHRRFAAFLRQLQTYTKTQDLYFCVTQBERGSVSNSNFAQLIVREPPPIAPPOL 300
 Db 240 AQTQINHRRFAAFLRQLQTYTKTQDLYFCVTQBERGSVSNSNFAQLIVREPPPIAPPOL 299

Qy 301 LGVGPYLLIQLNANSIIGDGPILLKEVYRMTSGSWTHAYNAAPTYKLWHLDPDTYE 360
 Db 300 LGVGPYLLIQLNANSIIGDGPILLKEVYRMTSGSWTHAYNAAPTYKLWHLDPDTYE 359

Qy 361 IRLVLTTRPSEGTTGSPGPILLTRTKCAEBMRPTPKTLKTAEIQARIARRAIDWESLGYNITRC 420
 Db 360 IRLVLTTRPSEGTTGSPGPILLTRTKCAEBMRPTPKTLKTAEIQARIARRAIDWESLGYNITRC 419

Qy 421 HTENVTICHYFRGNHNESKADCLMDPKAPOHVNLPHPTNVLKMLTPSGRKSEE 480
 Db 420 HTENVTICHYFRGNHNESKADCLMDPKAPOHVNLPHPTNVLKMLTPSGRKSEE 479

Qy 481 TIIQTDDEDYGPVPEVKSLQSTSFEKINFKINWKPELPNGNITOTOYESISIRSFDPAVY 540
 Db 480 TIIQTDDEDYGPVPEVKSLQSTSFEKINFKINWKPELPNGNITOTOYESISIRSFDPAVY 539

Qy 541 AGPPOTVSNLWNSTHVNMLHPSTTYQPFIRASTVKGFPATAINTVNNISAPTLPDYE 600
 Db 540 AGPPOTVSNLWNSTHVNMLHPSTTYQPFIRASTVKGFPATAINTVNNISAPSPLPDYE 599

Qy 601 GVDASLNETATTITVLLRAQAKGAPISQYIVVEHLHRTREAGAMECYQVPTVQN 660
 Db 600 GVDASLNETATTITVLLRAQAKGAPISQYIVVEHLHRTREAGAMECYQVPTVQN 659

Qy 661 AMSGGAPYYFAELPPGNIPLPEAPTFGNRITYQGFNNPLPAPKGNTNYFQAMSSVKE 720
 Db 660 ALSGGAPYYFAELPPGNIPLPEAPTFGNRITYQGFNNPLPAPKGNTNYFQAMSSVKE 719

Db 721 TKTQCVRIATK-AATEPEVPIIDPAKOTDRVKLAGISAGILYPLLLVILVKKSKL 779
 Db 720 TKTQCVRIATKAATEEPEVPIIDPAKOTDRVKLAGISAGILVILLVILVKKSKL 779

Qy 780 AKERKDAMGNTQEMTHNMAMDSEYADSTLHAEDPLITMDQHNSPRY----- 831
 Db 780 AKERKDAMGNTQEMTHNMAMDSEYADSTLHAEDPLSLTMQHNSPRLNDPLVPT 839

Qy 832 --- ENHSATAESSRLLDVPRLCGTESPYQTGQLHPAIRVADLQHNLMTSDSYGF 887

Db 840 AVLDENHSAETESSRLLDVPRLCGTESPYQTGQLHPAIRVADLQHNLMTSDSYGF 899
 Qy 888 KEYESFFGQSASWDVACKDQNRKRYGNTIAYDHRSVYLOPVEDPSSDYZINANYI- 946
 Db 900 KEYESFFGQSASWDVACKDQNRKRYGNTIAYDHRSVYLOPVEDPSSDYZINANYID 959
 Qy 947 --- DGYORPSHYIATQGPVHETVYDFTWVQACIYMTNLVEGRVCKCYKYWD 1001
 Db 960 IWLYRDGYQRPSHYIATQGPVHETVYDFTWVQACIYMTNLVEGRVCKCYKYWD 1019
 Qy 1002 DTEVYGDPRVTCYEMPLAEVVTFTLERRGNEIREVKQFHFTGPDPHGVPYHTGJL 1061
 Db 1020 DTEVYGDPRVTCYEMPLAEVVTFTLERRGNEIREVKQFHFTGPDPHGVPYHTGJL 1079

Qy 1062 SFIRRVLKSNPSSAGPIVHCSAGAGRGCYIIVIDIMDMAEREGVVDLYNCYKALRSRR 1121
 Db 1080 SFIRRVLKSNPSSAGPIVHCSAGAGRGCYIIVIDIMDMAEREGVVDLYNCYKALRSRR 1129
 Qy 1122 INMYQTEEQYIIFTHDAILEACLGCTEAIPUCEPKAYFDMIRIDSQTNSHLLKDFOTLN 1181
 Db 1140 INMYQTEEQYIIFTHDAILEACLGCTEAIPUCEPKAYFDMIRIDSQTNSHLLKDFOTLN 1199
 Qy 1182 SVTPRLOAQEDCSTAICLPRNHDKORFMDMLPDPCFLPLITDGESSNVINAALMSYROP 1241
 Db 1200 SVTPRLOAQEDCSTAICLPRNHDQRMFMPLPDRCLPLPLITDGESSNVINAALMSYROP 1259
 Qy 1242 AAFTVTOQPLPNYTKDFYLTVYDGTCTVMLNEVDLUSGCPOTWPEECMLRYGPQYEC 1301
 Db 1260 AAFTVTOQPLPNYTKDFYLTVYDGTCTVMLNEVDLUSGCPOTWPEECMLRYGPQYEC 1319
 Qy 1302 MSCSMDCD0V1NRIFRICN1LTRPQEGLMVQQFQYLGASHREVPGSKRSFLKLILQVERK 1361
 Db 1320 MSCSMDCD0V1NRIFRICN1LTRPQEGLMVQQFQYLGASHREVGSKRSFLKLILQVERK 1379
 Qy 1362 QEWKGEQRSTIHCNNGGRSGMFCAIGIVVENVKRONVVDVFHAVTKLNRSKPNMVEA 1421
 Db 1380 QEWKGEQRSTIHCNNGGRSGMFCAIGIVVENVKRONVVDVFHAVTKLNRSKPNMVEA 1439
 RESULT 7 US-08-769-3
 Sequence 3, Application US/08769399
 ; Patent No. 5976852
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheng, Jill
 ; APPLICANT: Lasky, Laurence A.
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd.
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/769,399
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055

Page 8

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; REFERENCE/DOCKET NUMBER: P1033
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-1168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-769-399-3

Query Match 98.2%; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDTPAAALPAFVALLLSWPLGSAQGFSAGCTFDGPGACDHYDLYDDFEWTHY 60
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  1 MD-YAAALPAFVALLLYPWPLGSAQGFSAGCTFDGPGACDHYDLYDDFEWTHY 59

Qy 61 SAQEBHYPPEMPQSYMIVDSSDHDPEGEARLQLPTMKENDTTCIDFESYLQSGKLNP 120
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  60 SAQEPHYPPEMPQSYMVDSSNEDPGEARLQLPTMKENDTTCIDFESYLQSGKLNP 119

Qy 121 GTLNLYRVNKPLANPIWNTGFTGRDLWRLAELAVSTWPNEYQVIFAEVSGGRSGYI 180
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  120 GTLNLYRVNKPLANPIWNTGFTGRDLWRLAELAVSTWPNEYQVIFAEVSGGRSGYI 179

Qy 181 ADDIQQLVSPCDKSPHFLRGDVENAGNATOCIATGRDAVNKLWQRNGEDDIPV 240
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  180 ADDIQQLVSPCDKSPHFLRGDVENAGNATOCIATGRDAVNKLWQRNGEDDIPV 239

Qy 241 AQTKINNIRRAFAASFRQLQEVTKTDOLYRCVTSQERSGSVSNFAOLIVREPPIAPPQL 300
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  240 AQTKINNIRRAFAASFRQLQEVTKTDOLYRCVTSQERSGSVSNFAOLIVREPPIAPPQL 299

Qy 301 LGVGPFTLLIQLNANSIIGDPGPIILKEVEYRMTSGSWTETHAVNAPTYKWLHLDDETEY 360
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  300 LGVGPFTLLIQLNANSIIGDPGPIILKEVEYRMTSGSWTETHAVNAPTYKWLHLDDETEY 359

Qy 361 IRLVLRPCEGGTTGLGPPLITRTRCAEPKRTPKTLKIAEQARRIADWESLGYNITRC 420
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  360 IRLVLRPCEGGTTGLGPPLITRTRCAEPKRTPKTLKIAEQARRIADWESLGYNITRC 419

Qy 421 HTFNYTICHTYFRGNINESKADCLNDPKAQHVNHLPPPTNVSLKMLTNPEGRKESEE 480
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  420 HTFNYTICHTYFRGNINESKADCLNDPKAQHVNHLPPPTNVSLKMLTNPEGRKESEE 479

Qy 481 TI IQTQDVEDYGPGPVYKPSLQSTSFKENKIFLWKPELDPNGLITOYEISYSSSIRSDFDAPVY 540
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  480 TI IQTQDVEDYGPGPVYKPSLQSTSFKENKIFLWKPELDPNGLITOYEISYSSSIRSDFDAPVY 539

Qy 541 AGPPQTWSNLNSTHVFMELHPGTYQFFTRASTVKGFGPATAINTVNINASPLPDYE 600
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  540 AGPPQTWSNLNSTHVFMELHPGTYQFFTRASTVKGFGPATAINTVNINASPLPDYE 599

Qy 601 GVDASINETATTITVLRLPAQKGAISAYQIVWELPHPRTKREGAMECYQVPTVYQN 660
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  600 GVDASINETATTITVLRLPAQKGAISAYQIVWELPHPRTKREGAMECYQVPTVYQN 659

Qy 661 AMSGGAPYYFAAEELPFGNLDEPAPFTVGDNRTYQGFWNPLAPRKCYNNYFQAMSSVEKE 720
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  660 ALSGCAGAPYYFAAEELPFGNLDEPAPFTVGDNRTYKGFWNPLAPRKCYNNYFQAMSSVEKE 719

Qy 721 TKTQCVRIAKT-AAEEPEVITPDPAKQTDVVKIAGISAGLVFILLVVLIVKSKL 779
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  720 TKTQCVRIAKTAAEEPEVITPDPAKQTDVVKIAGISAGLVFILLVVLIVKSKL 779

Qy 780 AKKRKDAMGNTQEMTHMNAMDSTSADQSTLHAEDPLSITFMDDONFSPRY----- 831
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  780 AKKRKAAGMNTQEMTHMNAMDSTSADQSTLHAEDPLSITFMDDONFSPRLNDLVTPT 833

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APPLICATION NUMBER: US 08/652,971
 FILING DATE: 24 MAY 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3449
 TELEX:
 QUERY FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-991-953A-3

Query Match 98.2%; Score 7571; DB 3; Length 1457;
 Best Local Similarity 97.3%; Pred. No. 0; Mismatches 6; Indels 20; Gaps 4;
 Matches 1419; Conservative 13; Nucleotides 61

Qy	1 MDTRAAALPAFAVALLLSPWPLIGSAQGFSAGCTFDGPGACDYHDLYDDPEWTV 60	Db	1 MD-VAAAALPAFAVALLLSPWPLIGSAQGFSAGCTFDGPGACDYHDLYDDPEWTV 59
Qy	61 SAQEPHYPPEMPQSYYMIDSSDGPKEARLQOPTMENDTHCIDFYLQLSOKGUNP 120	Db	60 SAQEPHYPPEMPQSYYMWDSSNNDGPKEARLQOPTMENDTHCIDFYLQLSOKGUNP 119
Qy	121 GTLNLYRVRNKGPLANPTWNTGTGRDNIRAEAVSTFWPNEQQVIFRAEVSGGRSGYI 180	Db	120 GTLNLYRVRNKGPLANPTWNTGTGRDNIRAEAVSTFWPNEQQVIFRAEVSGGRSGYI 179
Qy	181 ADDIQVLSSYPCDKSPHPFLRGDVENVAGONATFCIATGRDAVNLKMLQRNGEDIPV 240	Db	180 ADDIQVLSSYPCDKSPHPFLRGDVENVAGONATFCIATGRDAVNLKMLQRNGEDIPV 239
Qy	241 AOTKININHERRFAASFRQLQVTTKTDLYCUTQBERGSVSNFQLTREPPPIAPPOL 300	Db	240 AOTKININHERRFAASFRQLQVTTKTDLYCUTQBERGSVSNFQLTREPPPIAPPOL 299
Qy	301 LGVGPYTLJLQLNANSIIQDGPIIKEYFYRMISGSWTETHAYNAPTYKLWHLDDPTEYX 360	Db	300 LGVGPYTLJLQLNANSIIQDGPIIKEYFYRMISGSWTETHAYNAPTYKLWHLDDPTEYX 359
Qy	361 IRLVLLTRPREGGTGLPGLPPLITRYKCAEMPRTPKTLKABIOQARRIAVWESLGYNITRC 420	Db	360 IRLVLLTRPREGGTGLPGLPPLITRYKCAEMPRTPKTLKABIOQARRIAVWESLGYNITRC 419
Qy	421 HTFNVNTICHYFRGENESTRADCLMDPKPQHVNHNLPPTYNSLKMILTNPERKSEEE 480	Db	420 HTFNVNTICHYFRGENESTRADCLMDPKPQHVNHNLPPTYNSLKMILTNPERKSEEE 479
Qy	481 TIIQDDEYDGPVPVYKSLQCTSEFNKILNKEPPLDPNGITQYEISYSIRSFPDPAVY 540	Db	480 TIIQDDEYDGPVPVYKSLQCTSEFNKILNKEPPLDPNGITQYEISYSIRSFPDPAVY 539
Qy	541 AGPPTVSNLWNSTHVFMLHPGTTYQFFIRASTVGGPATAINVTNISAPTLPDYE 600	Db	540 AGPPTVSNLWNSTHVFMLHPGTTYQFFIRASTVGGPATAINVTNISAPTLPDYE 599
Qy	601 GVDSLNEATTITVLLRPAQKAPISAYQIVYEBLHPRTKREAGAMECYOPVYTN 660	Db	600 GVDSLNEATTITVLLRPAQKAPISAYQIVYEBLHPRTKREAGAMECYOPVYTN 659
Qy	661 AMSGGAPYVFAAEELPPGNLPEPAPTFVGNRTYQGFNNPLAPRKGYNMFQAMSSVKE 720	Db	660 ALSGGAPYVFAAEELPPGNLPEPAPTFVGNRTYQGFNNPLAPRKGYNMFQAMSSVKE 719
Qy	721 TKTQCVRIATK-AATEEPEVTPDPAKQTDRVKTAGISGILVPLLVLVIVKSKL 779	Db	

RESULT 9
 US-08-449-644-B
 Sequence 8, Application US/08449644
 Patent No. 5856162
 GENERAL INFORMATION:
 APPLICANT: Schlesinger, Joseph
 ADDRESS: San Jose, CA
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449, 644
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/087, 244
 FILING DATE: 01-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Couzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET INFORMATION:
 TELEPHONE: 212-750-9090
 TELEFAX: 212-869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-449-644-8

Query Match 62.4%; Score 4807; DB 2; Length 1452;
 Best Local Similarity 60.8%; Pred. No. 0;
 Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;

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Qy 4 TAAAALPAVALLILSEPLIGSAQGCTFDGGPGACDHYDDDFEWVHVSAAQ 63
Db 3 TGTCLATLAGLL-----TAAGTFTSGCGLDFPSTCGSSSEGDDFWQVNTL 54
Qy 64 EPHYLPPMPQSYYMIVDSSDHDPGEKARLQLPTMKENDTHCIDSYLLYSQKGLNPCTL 123
Db 55 TKPTSDWMPSSMLVNASGRPEQGRHLJLPOLCKNDTHCIDFPYFVSSKSNSPPGLL 114
Qy 124 NLLVRVNGKPLANPIVNTGFGRDWRAELAVSTWPNEVQVIFAEVSGRSGYIAID 183
Db 115 NYVKVYNGNGLPNINNSGDPTRTNRAELAISTWPNFQVIFEV-TISGHQGYLAID 173
Qy 184 DIOVLSPYCPDKSPLSPHFLRLGDYEVNAGONATFOCIATGRDAYHNLWLQRNGEDIPVAQT 243
Db 174 EYVKLGHCPTRPHFLRQNVEVAGAFATCSCAAGRIVGDRNLQIDVRDPLKEI 233
Qy 244 KNINHRRFAASRFLQEVTKTDOLYRCVTOSERGSVSNFAQLIVREPPIAPPOLLGV 303
Db 234 KVTSRRFAIASPNVNTKRDAGKVRMIRTEGGVGISNYAELVKEPVPIAPPOLASV 293
Qy 304 GPTYLILQNLANSIIGDOPPLIKEVYRMTSSWTHEVAPTYKLWILDPTDEYIRV 363
Db 294 GATYLWLNQNLANSINGGPPIVAREVECTASWWNDRQPVDSITSYKIGHLDPTDEYEISV 353
Qy 364 LITRPGEGTGLGPPLTRTCAEPMRTPKTLKIAE1QARRIAVDMESLGYNITRCHTF 423
Db 354 LITRPGEGTGSGPALTRTCADPGRGPRLLEVEKVSQITIWPFGVNVTRCHSY 413
Qy 424 NYTICHYHFRGHNESKAD-CLDMDPKAPQHVNHNLPPTYNVSLKMLTNPGRKESSET 481
Db 414 NLTVHYCIVQVGGQEVRVEWSWDTEHSHPQHTNLSPTYNVSKLILMNPGRKESQEL 473
Qy 482 IOTDVEDPGPVPKVSLQGTSSENPKFLNWRPLDNGITYOYESYSISISFDPAVVA 541
Db 474 IVQTDDEPQGAVTESLGQSTFEKIFQWRPETOYTIVETYKAVSSFDPEDLS 533
Qy 542 GPPQTWSNLNSTHVPMNHLHGTTYOFIRASTVKGPAINTVNISAPTLPDYEG 601
Db 534 NOSGRVSKLGNETHFLFFGLYGGTTSFIRASTAKFGPPATQFTKISAPSMPAYE- 592
Qy 602 VDASLNETATTIVYLREPAQAKGAPSAYQTYVEELHPRHTKREAGAMECYQVPTYQNA 661

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593 LETPINQDTNTVTWILKAHSRGAVSVTIVVEBPRPRRTKKTTBILKCYPVPPHFQNA 652
 662 MSGGADPYFAEALPPGNI DEPAPFTGDNITYQGQWNPLAPRKCGNNTYQFAMSSVKEF 721
 653 SLLNQQYFAEFPDSDLQAQPFITGDNKNTYNGTWNTPLPKSYRIVFQAAASRANGET 712
 722 KTQCVRIATAATEPEVLPDPAOTCDRVVKGASAGILVFLILLVLLVLIVKSSKLAK 781
 713 KIDCQVANVKA-TPKPPEPEKTDYKTAGIAGLFLVFLVYVMKVKLAK 771
 782 KRKDANGNTROEMTMVNANDRSYADQSTLHAEDLSITMDOINSPRY----- 831
 772 KRKEITMSSTRQEMTMVNANDSKSYAEGQGNCDE--AFSMNDTHLNGRSVSSPSFTMK 828
 832 -----ENHSAITAESSBRILLDPRY-LCEGTESPYQGCOLHPAIRVDLHQH 875
 829 TNTLSTSVPNSYYPBETHMASDTSLVQGHTYKREPADVYQGCOLHPAIRVDLHQH 888
 876 INLMKTSDSYGPKEYESPEQGQASWDAKKODNRAKRGYNTIAYDHSRVLQPVEDD 935
 889 ITQMCACFGFKEYESPEQGSPWDSAKKDENMRKRGYNTIAYDHSRVLQVTEGD 948
 936 PSSDVANTIDYQDPRSHYIATQPVHETVYDFWRFMIIQEQSACIVMTNLVEGRVKC 995
 949 TNSDTINGNVTGHRPNNIATQPMQETIYDFFRMWHENTASIMVNLVGRVKC 1008
 996 KYWPPDDTEYGFVKTVCMEPLAEYVVTFTLERRGYNENEYKQFHETGWPDHGVY 1055
 1009 CKYWDDETEYKDKIVTLLTLLABYVTKFAVFRKGVBHEIREQRFHETGWPDHGVY 1068
 1056 HATGLLSFIRRKVUSNPSPSAPIVHCSAGAGRTCTYIVDIDLMAERGVVDYNCVK 1115
 1069 HATGLGFYFQVKSSSPSGPLVTHCSAGAQTGCFIVDIDLMAERGVVDYNCVK 1123
 1116 ALRSRPNMYYQTEEOYTFIHDIALEFACLGCTTAIVCPEKAYFMIRIDSQTSNSSLHKD 1175
 1129 ELRSRPNMYYQTEQVFIHDIALEFACLGDTSVASQVRSLYHMNKLQDQTNSQIKE 1188
 1176 BFOQINSUTPLQADCSIAICLPRHDKORFMDMLPPDRCLPFLITIDGESSSNYINAALM 1235
 1189 EFRTLNMTPLRVEPCSIALPRHEKNCRMDIIPDRCLPFLITIDGESSSNYINAALM 1248
 1236 DSYRQPAAFIVTQYPLPNTYDFWFLVYDYGCTSVMLNEDLSQCCPQYNEPEGMRLYG 1295
 1249 DSYKQPSAFIVTQHLPNTYDFWFLVYDYGCTSVMLNEDLSQCCPQYNEPEGMRLYG 1308
 1296 PIQVBCMSNDCDVTRIPICNLTROQEGLYMQQFOTLGWSHREVPESKRSPFLKI 1355
 1309 PIQVFVPSADLEDLISRIFYIYNARPQDGYRMQQFQFLGWPMYRTDPVSKRSPFLKI 1368
 1356 LQVEKNOEWKEGECPITIHCNGGSRSGMFCAJGIVVEMVKRONTYDVFAVKTLRNSK 1415
 1369 RQDVQKQEYNGGBGETVHLLNGGSRSGTCAISIVCEMLRHQRTVDVFAVKTLRNSK 1428
 1416 PMVVAPEQYRFRCYDVALEYLES 1438
 1429 PMVVDLQDKFCYEVALEINS 1451

RESULT 10
 US-08-087-244A-8
 ; Sequence 8, Application US/08087244A
 ; Patent No. 5863755
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlessinger, Joseph
 ; APPLICANT: Sap, Jan M.
 ; APPLICANT: Ulrich, Axel
 ; APPLICANT: Vogel, Wolfgang
 ; APPLICANT: Fuchs, Miriam
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROLINE
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:

ADDRESSSE: PENNIS & EDMONDS
STREET: 1115 Avenue of the Americas
CITY: New York

COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,244A
FILING DATE: 01-JUL-1993

CLASSIFICATION: 435

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8

SEQUENCE CHARACTERISTICS:

LENGTH: 1452 amino acids

TYPE: amino acid

STRANDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US -08-087-244A-8

Query Match Score 4807; DB 2; Length 1452;
Best Local Similarity 60.8%; Pred. No. 0;
Matches 889; Conservative 326; Indels 42; Gaps 8;

Qy 4 TAAALPAVALLLSPWPLLGSAQFSAAGCTFDGPGACDTHQDLYDDFEWVHVSQ 63

Db 3 TLGICLATLAGLL -----TAGETSGGCLDEPYSTCGYSQSBDDFNWEQVNLL 54

Qy 64 EPHYLPPENPQGSYMIVDSSSDHDPEKEKALQLOPTMKENDOTHCDFSYLISOKGLNPCTI 123

Db 55 TKPTSDPWNPSGSMLVNNSGRPEQCRAHILLPQLKENTHCIDHYFSSKSNSPPGIL 114

Qy 124 NLLRVNKCGPLANPWNVTGFTGRDWLRKLAESTWPNPEYQVTFEAETGGSGSYIAID 183

Db 115 NVYKVNNNGPLGNPNTWNISCDPTTWNRAELAISTWPNFYQVTFEV-TSGHOGYLAID 173

Qy 184 DQVLSYPCDPSKPHFLRLGDVEVNAQONATEFOCIATGRDAHVNLWLQRNRNGDIPVACT 243

Db 174 EVKLQGHPCTRTPHLRQNVEVNAQFQCSAIGRTVAGDRWLWQGDVRDAPLK 233

Qy 244 KTNINHRFAASFRLOEVTKNDQDLYRCVTOSERGSGSNFAOLIVREPRPRIAPPQLGV 303

Db 234 KVTSRRRFASENVNTTRGRDAGYRCRMRTGEVGISNYAELVKEPPVIAAPPQQLASV 293

Qy 304 GPTLILQNANSLIGDPILKILEVEYRMTSGSWTETHAVNAPYKWLWLDPEYEYR 363

Db 294 GATYWIQNANSINGDPIVAREVEYCTASGSNDQPVDSTSYKIGHLDPEYEYSV 353

Qy 364 LLTREGEGETGTLGPBPPLTRTKCAEPMRPTKTLKAEIQAARRTAVDWEGLYNITRCHTF 423

Db 354 LLTREGEGETGSGPGLRTRKCAADPMRGRKLCLEVEVGSRQTIRWEFGYNTRCHSY 413

Qy 424 NVTICHYFHGNESKAD - CLDMDPKAPOHVVNHLPPYTINUSKMLTNPGRKESKEET 481

Db 414 NLTHYHCYQVGGQEYREVSMDTENSHPQHTNLSPTNVSYKLILNPGRKESQUEL 473

Qy 482 LIQDEDVCPVPSLQGTSSENKIFLWKKEPDENGNTQYISYSIRSFSDFDAVVA 541

Db 474 IVQTDDELLPFCAVPTEISQSTSFEKIFLQWRREPQTGYTILBITYKAVSSFPDEIDIS 533

Qy 542 GPPOTVSNLNWNSTHVFMLHPGTYQFFIRASTVKGFSPATAINVNTNISAPTLPDYEG 601

Db	534 NQSGRVSKLGNETHFLPFGGLYPGTTYSFTIRASTVKGFSPATNQFTKISAPSMPAYE- 592
Qy	602 VDASINNETATTITVLRLRPOAKGAPISAQOIVVBLHPRTKREGAMCYQVPTVYQNA 661
Db	593 LETPANQTONTVMLKPASHRGAVPSVQIVVBEERPRTKKTBEILICVLPVPHFQNA 652
Qy	662 MSGGAPYYFAAEIPLPGNLPDEPAPVYQGDNRTYQGFWNPNPLAPRKGNYNTFQAMSVEKET 721
Qy	653 SLLNSQQYPAEFPADSLQQAOPPTIDGNKNTYQNTWNTPLPKYSRITYFQAASRANGET 712
Db	722 KTQCUTRIAKAATEEPEVLPDPAKOTDRVVKIAGTAGLIVFILLVVLIVKSKLAK 781
Qy	713 KIDCVQVATKGA-TPKPVPEPEQCDHTVKIGVAGLIVFLGVUVMKCKLAK 771
Qy	782 KRKDAMGNTQEMTMNAMDRSADOSTLHAEDPLSITFMDQINFSPEY----- 831
Db	772 KRKETMSSTRQEMTMVMSMDSKSYAEGTNCDE --AFSEMDTNTLNRSVSSPSFTMK 828
Qy	832 -----ENHSATAESESRRLDVPRY-LCEGTESPYOTGOLHPAIRVADLHQ 875
Db	829 TNTLSTSVPNSYYDEDTMAMDSITSLVQSHTYKREPADVPTQGOLHPAIRVADLHQ 888
Qy	876 INLMKTSDBYGFKEYESPFEGQASWDVAKDODRAKRNKGNTIAYDSRSRVLQPVEDD 935
Db	889 ITQMKCAEGYGFKEEYESPFEGQASPWMSAKDDEMRMKNYGNIAYDHSSRVLQTIEDG 948
Qy	936 PSSDIXTINAXYIDGQRPXHIAOTCPVHETYDWRMWTQEQSACIVMNTNLVEGRVRC 995
Db	949 TNSDDINGNYIDGHRPNHIAOTGPIMQETYDWRMWMHNTAS:IMVNTNLVEGRVRC 1008
Qy	996 KYKWPDDTEVYGFPKVTCVEMPLAEYVFTPLERGYNENEIREVKQFHTGWPBDHGVPY 1055
Db	1009 CKYWPDDTEVYKD1KVT1BTETLAEVYVFTAYVFTAYVFTAYVFTAYVFTAYVFTAYVFT 1068
Qy	1056 HATGLSFIRRVLUSNPPAGP1VWHCSAGAGRTGTYV1VIDIMUDMAEREGVVDLNYCVK 1115
Db	1069 HATGLGFVTRQVSKSPSSAGPLVTHCSAGAGRTGCFIVIDIMUDMAEREGVVDIYNCVY 1128
Qy	1116 ALRERRINNVQTEQQYFPHDATEACUCGETAIPVCBETKAAYDMDISOTNSHLD 1175
Db	1129 BLRSRVRNNVQTEQQVFLQHDALEACLGQTSPTASQVRSLYDMMKLDQTMNSQIK 1188
Qy	1176 BPFQTSNISUTPRLQADEDCSTAICLPBNHDKRNFMMLPPDRCLPLFTIDGESSNNIAALM 1235
Db	1189 EFRTLNMTPTRVEDCSTALLPRHEKNCRMDILPPDRCLPLFTIDGESSNNIAALM 1248
Qy	1236 DSYRQPAAPITVQPLNTVKDFWRLVYDGC7SIUMLINEVDLSQGCPQYWPEBGMRLYK 1245
Db	1249 DSYKQPSAIVTQHPLPNTVKDFWRLVYDHC7SVMLNDVDPAQLCPQYWPEBGMRLYK 1308
Qy	1296 PIQYBMCMSMDCDYINRFRICNTLTPQEGYLMVQQFOLGLWASHREVPGSKRSFLKLJ 1335
Db	1309 PIQYBFSADLBEPISIRFRTYNAARPDGYRNQVQQFLGNYMIRDTPVSKSFFLKLJ 1348
Qy	1356 LOVEKQEWKEGRGRTI1HCLNGGRSGMFCAGTIVEMVRQMVVDYFHAVKTLRNSK 1415
Db	1369 RQVQWQZQYNGGEGPTVHCLNGGRSGRTFCASITVCEMLRHQRTVDYFHAVKTLRNSK 1428
Qy	1416 PNMYEAPBOYRCYDVALEYLES 1438
Db	1429 PNMYDLDQYFCYDVALEYLNS 1451

RESULT 11
US-08-652-971-4
Sequence 4, Application US/08652971
; Patent No. 5811507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA

NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech Inc.
 STREET: 460 Point San Bruno Blvd.
 CITY: South San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94180

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,971
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Drexler, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1033

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 225-3216
 TELEFAX: (415) 952-9881
 TELEX: 910 371-7188

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid

STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-652-971-4

442 -CLMDMPAPOYVNLHPPYTVNLLPNTPECRKESSETIQTDEDPGPYEVKSICG 500
 433 VSMDTDSHPQHTITNLSPYTNVSKLILMNPCKRKESEBLTQTDIPGAVTESIG 492
 501 TSFENPKIPLNWKEPLDPMNGSITQVEBISYSIRSFDPDAVEVAGPQTQVSLLNS 550
 493 SAEEKPKIPLWREPTQTYVITTEYITKAVSSDPEILSNOSGRVQLGNETHFLFG 552
 US-08-991258A-4 ; Sequence 4, Application US/08991258A
 US-08-991258A-4 ; Sequence 4, Application US/08991258A
 442 -CLMDMPAPOYVNLHPPYTVNLLPNTPECRKESSETIQTDEDPGPYEVKSICG 500
 433 VSMDTDSHPQHTITNLSPYTNVSKLILMNPCKRKESEBLTQTDIPGAVTESIG 492
 501 TSFENPKIPLNWKEPLDPMNGSITQVEBISYSIRSFDPDAVEVAGPQTQVSLLNS 550
 493 SAEEKPKIPLWREPTQTYVITTEYITKAVSSDPEILSNOSGRVQLGNETHFLFG 552

TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE PHOSPHATASE, PTP LAMBDA

NUMBER OF SEQUENCES: 10

ADDRESS/ENCE ADDRESS:

STREET: FLEHR, HOMBACH, TEST, ALBRITTON & HERBERT, LLP
4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0., Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,258A

FILING DATE: 17-DEC-1997

CLASSIFICATION:

435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/652,971

FILING DATE: 24-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Dreser, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK

TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 781-1997

TELEFAX: (415) 398-3249

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US - 08-991,258A.4

Query Match Score: 62.1%; Score: 4791; DB: 2; Length: 1452;

Best Local Similarity: 61.3%; Pred. No: 0;

Matches: 885; Conservative: 205; Mismatches: 320; Indels: 34; Gaps: 7;

Qy 23 LIGSAQGFSAGGGCTFDGGPGACDTHQDLYDDFEWVHVAQAEPHYLPPBMPQGSYIVDS 82

Db 14 LLTDTAGETSSGGCLFDEPYSTCGYSQAEDDFNWEQVNTLTKPTSDPMPGSFMLVNT 73

Qy 83 SDHDGEKAHLQLQPMKENDTHC1DFSYL1YQSQKLNPGLN1LYRVNKGPLANPIWNT 142

Db 74 SGKPGEGQRASHLPLQIKENDTHC1DFYFVSSKSNAAPGLN1YVKNONGPLGPWNTS 133

Qy 143 GFTGRDWLRAELAVSTFWPEYQTFEAWSGGREGYIAADDIOVLSYCDKSPHFLRG 202

Db 134 GDPTRTHWRAELA1STFWPNFQVIFEV-VTSRSHGGLADEVKVLGHCTRTHFLR1Q 192

Qy 203 DVEYNAGQWATFOCIATGRDAVHNKLWLQRNGDEDIPVQTKNINHRRPAAFRQLQETK 262

Db 193 NVEVNAQOFATFOCSAIGRTVAGDRILWQDVRDAPLKEIKVTSRRTASFNVNNTK 252

Qy 263 TDQDLYRCVTOSERSSGVNSFAQLTVREPRPIAPPQLLGVPYLLIQLQANANS1IGDP 322

Db 253 RDAGKYRCM1CTEGGVISNYAELVVKPEPVIAQQLAVGATLWLQNLANSINGDGP 312

Qy 323 TILKEVEYRATSGS1ETHAWNAPTYKWHLDPTDEYEYRVLUTRPGBCGTGLGPPIIT 382

Db 313 IVAREVEYCTASGS1NDRQPUUDTSYKIGHLDPTDEYEYSLTRPGBCGTGSGPALRJ 372

Qy 383 RTKCAEPMRTPKTLKIAEQARRIATWDWESLGYN1NTRCHTENVTCYHFRGNHESKD- 441

Db 373 RTKCAEPMRSPRKLESVVERSRQQTIRWEPFGYNVTRCHSYNLTHYGQVGGEQYRVE 432

Qy 442 -CLMDPDKAOPHVNWHLPPTVNSLKM1TNPGRKESBET1QDDEPVGPyVVKSLG 500

Db 1435 YLES 1438

Db 1448 YLN 1451

RESULT 13

US - 08-763-399-4

433 VSWDDTNSSHQHTITNLSPYTNVSYKL1MNPEGKESQELTVQTDDEDLPGAVPTESIQG 492	Db
501 TSFENRIFLNKWEPEIDPQNGLITQYRISYSSIRSFPDVAVGPPOTVSNIWNSTHVFYH 560	Qy
493 SAFEKFIFLOWREPPQTYGVTILBTITYKAVSSFFPEIDLSNQSSRVSUGNETHFLFFG 552	Db
561 LHPGTTQYOFFTRASTVKGFQPAT1INVNTNISAPLTDYGVDA8SLNETATTIVLRLPA 620	Qy
553 LYPGTTYSPTRASTAKGRSPATNQFTKISAPMPATE-FETLNUQDNTVTVNLKPA 611	Db
621 QAKGAPIASQYQIVYELPHPTKREAGAMECYQFVTYQAMSGGAPYPPAAELPGNLP 680	Qy
612 QSRGPVSYQIVWEEPERPTKCTEILKCPVBFHFQNQASILNSQYFFAAEPADSLQ 671	Db
681 BPAPTTVGDNRTYQOFWNPLAPRKSYNNYQANSVSEKEETKTOCVRIATKAATBPEVI 740	Qy
672 AAQPTTIGDNKTYKNGYWWNTPLPHKSYRYYQASRANGESETKIDCVRATKGAV-TPKPV 730	Db
741 PDPAKQTDYRUVKIAQISAGILVFLILLVILYKXSKLAKKRKDA1GNTQREMTHMVNA 800	Qy
731 PEPEQTDHVTKIAQIVAGILFVFLGVLVNRKRLAKKRKETMSSRQENTVMVNS 790	Db
801 MDRSYADQSTLHAEDPLSTIPMDQHNFSPRY-----ENHS 835	Qy
791 MDKSYAEOGTCNCDE--AFSMGTM1NLRGSVSSPSSFTMKNTNLSTSVPNSYYPPDETIT 847	Db
836 ATAESSRLLDVPRY-LCEGTESPYQTQGQHPAIRVADLQLQHNTQMKCAEGYFKEYYESF 894	Qy
848 MASDTSISLAQPHTYKREAAADVPTQGTQLHPAIRVADLQLQHNTQMKCAEGYFKEYYESF 907	Db
895 FEGQESASWYDACKDNRAKNGYNTIADYHDSRVLQVDEDPSSDPIYANYIDGYQRPSPH 954	Qy
908 FEGQQAPWDASKBNRMKRNQGNTIAVDSRVQLMLEGDNNSDINGYIDGTHRPNH 967	Db
955 YIATGQPHVETVYDFWRM1WQEQSACIVMVNTNLYEVGVRKCYKWPDDTEVYGDFTKVTCV 1014	Qy
968 YIATGQPMQETIYDFWRMWHNTAS1MVNTNLYEVGVRKCCYKWPDDTEIYKOKIKVTLI 1027	Db
1015 EMEPLABYVRFITLERRGYNEIRVKQPHFTGPFDPHGVPYHAATGFLLSFIRRKLNSNPPS 1074	Qy
1028 DTELLIAEYYVTFVAKRGIHEIREIRQHFTGFTGPDHGPYHATGFLLGFPQVSKSPPN 1087	Db
1135 HDATLAEACGETA1PVCFKA1YPMIDQTSQNNSSH1KDEPOTLNSTYPRLOADEDCSI 1134	Qy
1148 HDATLAEACLGDT1SPASQVRSLYYDMNKLDPQNTNSQ1KEEFTLNMVPTLRLVEDCSI 1207	Db
1195 ACLPRNHDKNRFMMLPPDRCLPLP1TIDGESSNTYINAALMDSYRQPAAFIVTOYPLPNT 1254	Qy
1208 ALLRNHEKNCMDLPPDRCLPLTIDGESSNTYINAALMDSYRQPAAFIVTOYPLPNT 1267	Db
1268 VQDFWRLYDYGCTSIVMLNEVDSLQGCPQWPEGMRLRYGP1OYECMSMDCDVINR1 1314	Qy
1315 FRICNLTRQEGYLMLQQFQYLGMASHRREVPGSKRSFPLKILQVKEWKEGEGR1II 1374	Db
1328 FRLYNASRQDGHRMVOQFQFLGPMPYRTDPVSKRSLKLIROQDVKWQBEYNGCEGPFTV 1387	Qy
1375 HCUNGGRGGMFCAGIVVBMVRQNQVYDVFHVAKTLLNSKPNVNEAPEQYRFCDYVALE 1434	Db
1388 HCUNGGRGSSGTFCAISIVCEMLRQHRTDVHAKTLLNSKPNVMDLQYKFCYEVALE 1447	Qy

Sequence 4, Application US/08769399
 Patent No. 5976852
 GENERAL INFORMATION:
 APPLICANT: Cheng, Jill
 APPLICANT: Lasky, Laurence A.
 TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd.
 CITY: South San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/769, 399
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REFERENCE DOCKET NUMBER: P1033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 952-3216
 TELEFAX: (415) 952-9881
 TELPFX: 910 371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1452 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-769-399-4

Query Match 62.1%; Score 4791; DB 2; Length 1452;
 Best Local Similarity 61.3%; Pred. No. 0;
 Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;

Qy 23 LIGSAQGFSAGGCTEDDGPGACDYHDLYDDPEWVHSQAOPHYDPEMMQGSTMIVDS 82
 Db 14 LLITTAAGETFGSGCLPDEPYSTCGYSQADDEDENWEQNTLTKPTSDPMPGSPFLMLNT 73

Qy 83 SDHPGEKARLOLPTMKENDTHCIDSFLYLSYQSKGLNPGTINILVRVNKGPLANPIWNT 142
 Db 74 SGKPGEGORHLLPQLKENDTHCIDSFLYFVSSKNSNAAPGLINVVVKNGPQGNP IWNIS 133

Qy 143 GFPGRDWIRAEALAVSTWPNEQYQIFERAEVSGGRSGCYAIDDIOLVSYCPDKSPHEFLRG 202
 Db 134 GDPTRTWRRAELAISTWPNFQYQIFEV-VTSGHQGYLAIDEVKVLGHPCRTPHPFLRIQ 192

Qy 203 DVEVNAGGNAATQCIATGTDAYHKLWLRQRNGEDIVAQTKNIHRRPASFRLOEVTK 262
 Db 193 NYEVNAGFAFQCSAIGRTVAGDRLWQGDYVRDAKETKVTSRRIFLASNVNTTK 252

Qy 263 TDODLYRCVTOBERSGSGVSNFAOLIIVREPPIAPPOLLGPGPTYLJQLNANSIIGDGP 322
 Db 253 RDAGKRYCMICBGGVGNSYNAELVVRPPVAPPQASVATYWIQLANSINGDGP 312

Qy 323 ILKEYEVYRMITSGSWTEHVNAPTYKWHLDPPDTYEIRVLTRPGBGTGLPGPLIT 382
 Db 313 IVAREVEYCTASGSWNDRQPVDSYKIGHLDPPDTYEIVSLTRPSEGTCSPGPALRT 372

Qy 363 RTKCAEPRTPTKIAIQARRIAVDWESLGYNITCHTENTICHYFRCHNESKAD- 441
 Db 373 RTKCADPDRGPRCLEVVEYKSVRQITRMEPFGVNTRCHSNTLVHGVQGGQEYREE 432

Qy 442 -CLDDMDPKAPQHVVVJHLPPYTIVNSLURMILTNPEGGRESEPTIIQDDEDVPGPVPVKSLOG 500
 Db 433 VSWDDDNSHQHTTINLSPVSKILIMPEGRKESQDLTVQDFAVPTEPIQ 492

Qy 501 TSFENKIFLWKPEPLDPNGTITOXBISYSSIRSFDPAVPGPPQTVSNLWNSTHVFHM 560
 Db 493 SAFERKIFLOWREPPQTYLITVLYKAVSSRPSVSKGNETFLFFG 552

Qy 561 LHPGTYQFSTRASTKGFADPATINTNMISAPLPDYGVDASLINEATTITLIRPA 620

Db 553 LYPTTYSFTSTRASTAKGFCEPATNQFTKISAPPMPAYE-FETPLNQNTNTVWLKPA 611

Qy 621 QAKGAPIASAYQIVVWBBLHPTRKAGAMECYQVPTVYONAMSGGAPYYPAEELPGNLP 680

Db 612 QSRGPVSVQIVVDBBERPRTKTEILCKYPVHQNQASLINSQYPAEEPADSLQ 671

Qy 681 EPAPFTVGDNRTYQGEWNPLPAPRKGNTYQFAMSSVSEKEKTKTOCVRIATAATEPEPEV 740

Db 672 AAQPPTIGDQTKNTYQGNTWNTLPHHSYRITYQAARANGETKIDCRVATKGAV-TPKPV 730

Qy 741 PDPAKOTDRYUKINGIASAGLIVFLILLVVVLLIVKSKLAKKRDAMGNTQEMTHMNA 800

Db 731 PEPEKOTDHTKIASTVAGTILFLGTVLVMKCRKKTMSSTRQEMTMVNS 790

Qy 801 MDRSYADQSTLHAEDPLSITEMDQINFSPY-----ENHS 835

Db 791 MDKSAEQGTCNDE--AFPMGTRNLNGS 847

Qy 836 ATAESSRLLDQPYR-LCEGTESPYTGQHPAIRVADLQHINLNMTKTSDSYGFKEYESF 894

Db 848 MASDTSLSLAQPHTYKKREADVPGQGLPAIRADLQHITONTKCAEGYGFKEYESF 907

Qy 895 FEGQASWDYAKKQDNPKAQKBYGNLIAJBDHSRSLVIAQVEDPSSSYDINANYDQRPSPH 954

Db 908 FEGQASPDASKDDETRMKNRYGNLIAJDHSRVLQMLQEDBNNSYDINGYIDGTHRNPH 967

Qy 955 YIATQPVHETVYDFWRMTMQEQSACIWMVNLVBNGRVYCKYKWPDDTEVYGVDFKVTVC 1014

Db 968 YIATQCPMQTIDYDTRMWHENNTASIMMTNLVBYGRVCKCYKWPDDTEYKDKVTLI 1027

Qy 1015 EMEPAEYVYRTFLERRGNEIREVKOFHFTGWDHGVPYHATGGLSFIRVKLNSNPPS 1074

Db 1028 DTELLEYATRFAEKRGTHEIRQFHTGWPBHGVPHTAGLGFVRQVKSKSPPN 1087

Qy 1075 AGPVVYHCSAGAGRTGCYIVIDIMDMAEREGVYDLYNCYKALRSRINMYQTEOYIFI 1134

Db 1088 AGPVVYHCSAGAGRTGCYIVIDIMDMAEREGVYDLYNCYRELRSRVMVYQTEOYIFI 1147

Qy 1135 HDAILBACLCBETAIVCEFKAYEDFMIRIDSQTSNSSLXDEFQTLNSTPRLQADCSI 1194

Db 1148 HDAILBACLCBETAIVCEFKAYEDFMIRIDSQTSNSSLXDEFQTLNSTPRLQADCSI 1207

Qy 1195 ACPLRHHDKMRFMDMLPPDRCLPFLITIDGESNTINAALMDSYROPAAFIVTQYPLPNT 1254

Db 1208 ALLPRHHEKRCMIDIPPDRLCLPFLITIDGESNTINAALMDSYKOPSAFIVTQYPLPNT 1267

Qy 1255 VKDFEWPLVYDYGCTSIVMLNEVDI-SQGCPQYWPEEGMLRYQPIOYECMSMCMDCYINRI 1314

Db 1268 VRDFWFLVLDYHTCSVMLNDVDPAOICPQTWENGVHRHPIQYERSABLEEDBSRI 1327

Qy 1315 FRICNLTRPQEGCLMYQFOYLGWASHREVPGSKRSPLKLILQVEEKEGEGRITII 1374

Db 1328 FRIVNARSRPQGHRYQFQFLGMYRDTDVSKRFKLJRVQDKWQEVGGEGPRTV 1387

Qy 1375 HCLNGGRSGMFCAGIUVENVKRQNVDFHAVTILRNSKPNMVAPEQRFCDYALE 1434

Db 1388 HCLNGGRSGTFCASIVTCMELRHQRTLVRNNKPNMVDLQDQYKPCYEVALE 1447

Qy 1435 YLES 1438

Db 1448 YLNS 1451

RESULT 14
US-08-991-953A-4
Sequence 4, Application US/0891953A
Patent No. 6083748
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE PHOSPHATASE, PTP LAMBDA
TITLE OF INVENTION: NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-953A-4

Query Match Score 4791; DB 3; Length 1452;
Best Local Similarity 61.3%; Pred. No. 0;
Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;

Qy 23 LGSAQGQTSAGGCTPDDPGACDYHQDLYDDPFMWVHSQAQEPHYLPPMPQSYYMIVDS 82
Db 14 LLTAAGETTSGGCUCDFEYSTCGYSQAEDDEWQVNTLTKEITSDEPMPSGSFMLVNT 73
Qy 83 SDHDEGEKARQLQPLTMKDNDTHCIDFSYLLQKGLNPGLTILVRYNKGPLANPINNT 142
Db 74 SGKPEGQRHLLPOLKENDTHCIDFHYYFVSSKSNAAQPLGLNVTKVNGPLGPINNS 133
Qy 143 GFTGRDWLRAELAVSTFWPNPEYQVIFEAESVGGRSGYIAIDDIQVSLCDKSPEHFLRG 202
Db 134 GDPTRTWHAEELAISTFWPNFYQVIFEV-VTSGHCGYLADDEVKLGHCTRPHFR1Q 192
Qy 203 DVEINAGQNTFOCJATGRDAHNLWLQRNGDI PVQTKTNINHRRFAASPLQEVTK 262
Db 193 NVEYNAGQFTFOCSAIGRTVAGDLWLQIDVRDAPLMKEIKYTSSRRIASENVNTK 252
Qy 263 TDQDLYRCQTOSERSGSVNNAQOLVREPRPRPIAPPOLLGVPGLYTLIQLNANSIIGDGP 322
Db 253 RDAKGYRCMICTEGGVGINSYAEVLVKEPVLAQPLQASGATLWVQLNANSINGDP 312
Qy 323 ILKEVEYRMSTSGSWTETHAWNAPTYKLMWHLDPDTYEYTRVLLTRPGECCGTGLPGPPLT 382
Db 313 IVAEVEYCTASGSWNDRQFDSTSYSKICHLDPDTEYEYTSVLLTRPGECCGTGSPGPALRT 372

Qy 383 RTKCBEPMRTPKTLKIAEQARRIAVDWESLGYNTTRCHTENVTCYHFRGHNESKAD- 441
Db 373 RTKCBDPMRGPKRLEVETKSROLTIRWEPFGYNWTRCHSYNLTWTHYGVQVGGQQVRE 432
Qy 442 -CLDMDPKAQPHVNHLPPTVNSLKMILTNPBEGRKESEETIIOQDEDVPGPVPWKSLOG 500
Db 433 VSWDIDNSHQBHTITNLSPYNTSVKLILMNPEGRKESQELTVQDLEDLGAVPTESIQ 492
501 TSFENKIFUNWKWEPKDPNGTITQETISYTSIRSPDAVPGPCTVSUWNSTHVFHM 560
Qy 493 SAFEKFIFLOWREPTQVGTILVETYKAVSSPPEIDLSNQGRVSXUGNETHFLFFG 552
561 LHPSTTYQFIRASTVKGFGPATAINVNTNISAPTLPDYGVDASLINEPATTTILRPA 620
Db 553 LYPTGTYSFIRASTAKGFGPPATNQFTKISAPSMPAYE-FETPLNQTDNTVTWMLKPA 611
Qy 621 QAKGPAPISAYQIVVVELPHPTKREAGAMECYQVPTVONAMSGGAPYPPAEELEPGNLP 680
Db 612 QSRGPBVPSVYQIVVEERPRTKTTEILKCYPVPHQNASILNSQYFAAEFPADSLQ 671
681 EPAPPTVGDGNRTYQFNNPLAPKQGNYFOAMS SVECEKETKOCVRLATKAATEPEV7 740
Db 672 AAQPPTIGDNKTINGWNTPLPKSYRIVYQAASRANGEBTKIDCVRVATKGAV-TPKPV 730
741 PDPAKOTDRVKLAGISAGILVFLILLVVLIVKSKLAKRKDKAMGNTROEMTHMVA 800
Db 731 PEPEKQTDTVKTAGVIAGILLFVTLIFGVLYMKRKLAKRKDKTMSTROENTVMVNS 790
Qy 801 MDRSYADQSTLHAEDPLSTEMDORHFSPRY-----ENHS 835
Db 791 MDKSYAEQGTCNCDE--AFSPMGTHNLNGRSVSSPSSFTMKTNTLSTSVPNSYYPDEHT 847
836 ATAHSRLUDPVRLQCHPTYKCREADDPVQTCGQHHPA-RAVDLQHITOMKCARGYGFREYESF 894
Db 848 MASDSSLAQCHPTYKCREADDPVQTCGQHHPA-RAVDLQHITOMKCARGYGFREYESF 907
895 REGQASMDVAKDQDNRAKQNRGYNIIAYDHRSVULQPVDDPSSDYINANAYDGXRQPSH 954
Db 908 FEGQASAPDASKCDEBNRMKNRGYNIIAYDHRSVRLQMLLEGDNNSDYINGNYIDGXRPNH 967
Qy 955 YIATQGPHEBTVDWFWMITWQEQSACIVMVNTLVGRVYKCYKWPDDTBVYGDFFKVTCV 1014
Db 968 YIATQGPHEOETIVDWRWMTWHENTASIMVNTLVGRVYKCCYKWPDDTBVYDVKDVKVTLI 1027
Qy 1015 EMEPAIBYVTRTFLTERCNEREVKOFHTGMPDHGPYHATGILLGPFVQKRSPPN 1074
Db 1028 DTELLAEVTRTFAVKEKGTHEIREKROPHFTGMPDHGPYHATGILLGPFVQKRSPPN 1087
Qy 1075 AGPIVVHCSAGA9RTGCTYVIDIMLDMAEREQYDUDYNCVYKALRSRRINMVOTEEQYIFI 1134
Db 1088 AGPIVVHCSAGA9RTGCTYVIDIMLDMAEREQYDUDYNCVYRERSRRINMVOTEEQYIFI 1147
Qy 1135 HDATLEACLGCGTETAPIVCEFKAAVFDMRIDSQNTISHLKDEPOTLNSVTPRLOADECSI 1194
Db 1148 HDATLEACLGCGTISIPASQVRSLYDDANKLDPQTNSQIKEEFPNLNMYTPLVEDCSI 1207
Qy 1195 ACUPRHNDENRFMDLPPCRCLPLITDGESSNYINALMDSYRQPAFIVTOYPLPT 1254
Db 1208 ALLPRNHEKNRMDLIPPRCLPLITDGESSNYINALMDSTKQPSAFIVTOYPLPT 1267
Qy 1255 VDOPWRVLYYDYGCTISIVMLNEVDLSQGCBQWPEGMURYGPQVECMSCSMDCDVINRI 1314
Db 1268 VDOPWRVLYDYGCTISIVMLNEVDLSQGCBQWPEGMURYGPQVECMSCSMDCDVINRI 1327
Qy 1315 FRICNLTRPQEGLYLMVOFOYLGWSHREPGSKRSFLKLILQYBKWOPBWKGEGRITI 1374
Db 1328 FRYNAASRFQDGHRMVOQFQLGWPMYRDTPVSKSFLKLIRQDVNQEEYNGGEQPTVV 1387
Qy 1375 HCINGGSGSGMFCAIGIVYEMVRQNVYDFVHAKTURANSKPNVVAEPOYRFCDYALE 1434
Db 1388 HCINGGSGTFCASIVCEMLRHQRTVDFHAKTLENNKPNVDDLQDQKFCXEVALE 1447

Qy 1435 YLES 1438
Db 1448 YLNS 1451

RESULT 15
US -08-652-971-2
; Sequence 2, Application US/08652971
; Parent No. 5514507

GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreyer, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-7168

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1436
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US -08-652-971-2

Query Match
Best Local Similarity 60.3%; Pred. No. 0;
Matches 854; Conservative 213; Mismatches 331; Indels 19; Gaps 9;

Qy 3 AGCTTGTGGP --ACDYPDLYDDDFEWVHVAQEPHEYLPPMPQQSYIDSSPDHPGE 89
Db 24 AAAGCTTEEAASDPVPVCEFSQAQYDDFQMEQVRIPHGTRTPDLPHGAYLMNAQSHTPGQ 83

Qy 90 KARLQLPMTKENDTHCIDSFLSYLSSOKGLNPSTNLTVLRVKGPLANPWNVTGFTGRDW 149
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Qy 150 LRAELAVSTFWPNPEYQVLFEEAVSGGRSGYIAIDDQVLSPYCDKSPHFLRGDYEVNAG 209
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Qy 330 YRMTSGSSTETHANAPTYKLWHDLDPTDEYEIRVLTTRGEGGTGLPGPPLITRTKCAEP 389
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324 YRMARGPWAEVHVNLTXYKLWHDLDPTDEYEISVULTRPDGGTRGPPLISRTKCAEP 383
390 MRTDKTILKIAEONIARIAIDWESLQYNNFRCHTNVNTCYHYFG -HNESKAQDLDMP 447
384 TRAPGLAFAEIQARQLTQWEPLGYNTRCTHYAVS1CYRTGSHNQTIRECVKMER 443
448 KAPQIVVNH1PPPTVNVSLKMLNTNEGRGESÉETIQTDEDVPGGVPUKSLOGSFENKI 507
444 GASRTKINLPPNTHYRPLLTNEGRRECKEYTFQDVSQJAAESELTIEPLEMI 503
508 FLNWXPBDPENGITQYSESSYRSFDPAVPVACPPOTVSNLWNTTHYFMHLHPGTTY 567
504 FLKWBEPQBNGLTQYSESYOSISSSDPAINVPEPRITSKLNBTIHVSNLHPGTTY 563
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564 LFSVRAARTSNGFGQQLTEITNISAPSF -DYADMPSPGESENITVLLRPACQRGAPI 622
628 SAYQIVVBEIHPHPTKREAGAMECYQVPTYQNAMSGGAPYYFABLPPGNLPEAAPTV 687
623 SVYQIVVEERPRKRREPQDCSVBLTPETAARGLYFGELAASSLLEMFPFY 682
688 GDNRITYQGFNNPPLAPRKGYNTYFOAMSSVEKETTCQYRIATAEPEVIPPDKQT 747
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748 DRUVKINGISA -GIVLVEFLILVLLVLLVLLVLLVLLVLLVLLVLLVLLVLLV
743 EEMGJLJGICAGGLAVLILGAIIVIIRGKPYNTMK -ATVNYRQEKTIMSAVDRSFT 801
807 DQSTRAEDPLSITMDQHNSPBYENHS - ATASSRSLLDVPRVLCGETESPYOTGQHL 864
802 DQSTTQEDERLGLSTMADPQSPDQRSGCYTESSLLGGSPRPCCGKGSPTVGQLH 861
865 PAIRYADLQHONLNUKTSDSYGFKEYESPFEGOSASWYDIAH 924
862 PAVRADLQHONQTKAEGYFKBQYESFPEG --WDATKKKDLKGGRQEPSSAYDR 917
925 SRVILQPVEDPSSDYYINANYIDGQRPShYIATQGPVHETTYDFWRMTMQEQSACIYM 984
918 HHVKLKHPMIADPDAIYISANYIDGTHRSNHFIAQSPKPEMIDYDWRMVWQEQCSAVMI 977
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Qy 865 PAIRYADLQHONLNUKTSDSYGFKEYESPFEGOSASWYDIAH 924
Qy 925 SRVILQPVEDPSSDYYINANYIDGQRPShYIATQGPVHETTYDFWRMTMQEQSACIYM 984
Qy 995 TNLVBENGRVYCYKWPDDTEVYDPKVTCYEMEPAAVYVFTPLERGYNENEIRYKQFH 1044
Qy 978 TKLVIVGTRVYCSRYPPEDSMYGDKITVLYKTTETAEVYVFTFERRGYSARHFRQFH 1037
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Qy 1402 VDVFHVKTURNSKPNVNEAEOYRECVDALLEYLS 1438
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Job time : 39.7887 secs

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OM protein - protein search, using sw model.

Run on: June 1, 2005, 13:44:18 ; Search time 131.676 Seconds
(without alignments)

3777.694 Million cell updates/sec

Title: US-09-887-669-2

Perfect score: 7709

Sequence: 1 MDITAAAALPAFVALLLSP.....EAPEDYRFCYDVALEYLESS 1439

Scoring table: BLOSUM2

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Published Applications AA.*
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Sequence 52, App1
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Sequence 64, App1
Sequence 55, App1
Sequence 45, App1
Sequence 12, App1
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Sequence 15, 1534.5 19.9 1502 10 US-09-887-669-2
Sequence 17, 1509 19.6 1897 17 US-10-482-029-52
Sequence 18, 1505.5 19.5 1907 15 US-10-291-265-250
Sequence 19, 1505.5 19.5 1912 17 US-10-772-636-64
Sequence 20, 1505 19.5 1948 9 US-09-808-602-55
Sequence 21, 1505 19.5 1948 10 US-09-800-198-45
Sequence 22, 1491 19.3 1495 15 US-10-258-666-12
Sequence 23, 1460.5 18.9 2037 15 US-10-087-684-39
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Sequence 25, 1457.5 18.9 2029 15 US-10-087-684-38
Sequence 26, 1457.5 18.9 2029 15 US-10-218-779-38
Sequence 27, 1349.5 17.5 1585 15 US-10-367-493-5569
Sequence 28, 1349.5 17.5 1585 15 US-10-369-493-5570
Sequence 29, 1284.5 16.7 802 17 US-10-777-186-1
Sequence 30, 1187 15.4 793 17 US-10-777-144-3
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Sequence 35, 1172.5 15.2 802 17 US-10-777-186-1
Sequence 36, 1170.5 15.2 807 15 US-10-264-049-3138
Sequence 37, 1118 14.8 699 15 US-10-366-547-65
Sequence 38, 1138 14.8 774 13 US-10-192-1017
Sequence 39, 1132 14.7 700 15 US-10-366-547-63
Sequence 40, 1132 14.7 700 15 US-10-444-795B-793
Sequence 41, 1132 14.7 700 17 US-10-753-267-100
Sequence 42, 1115.5 14.5 642 15 US-10-444-795B-795
Sequence 43, 1109 14.4 305 9 US-09-788-626-9
Sequence 44, 1107.5 14.4 659 15 US-10-366-547-67
Sequence 45, 1085.5 14.1 560 13 US-10-087-192-1020

ALIGNMENTS

RESULT 1
US-09-887-669-2
; Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIORITY APPLICATION NUMBER: 09/234,983
; PRIORITY FILING DATE: 1999-01-21
; PRIORITY APPLICATION NUMBER: 08/087,244
; PRIORITY FILING DATE: 1993-07-01
; PRIORITY APPLICATION NUMBER: 08/049,384
; PRIORITY FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7709	100.0	1439	9	Sequence 2, App1
2	7688	99.7	1439	16	Sequence 284, App
3	7571	98.2	1457	9	Sequence 1, App1
4	4838	62.8	1452	16	Sequence 83, App1
5	4784	62.1	1452	16	Sequence 15, App1
6	4602.5	59.7	1436	14	Sequence 98, App1
7	4564.5	59.2	1444	14	Sequence 22, App1
8	4564	59.2	1463	14	Sequence 22, App1
9	4564	59.2	1463	14	Sequence 343, App
10	4555	59.1	1499	15	Sequence 1283, App
11	4374.5	56.7	1442	16	Sequence 805, App
12	4338	56.3	1430	13	Sequence 34, App
13	2493.5	32.3	623	15	Sequence 1190, App

Qy	61	SAQEPHYLPPMPOGSYMTVDSSDHDPGEKARLOLPTMKENDTHC1DFSYLLSOKGLNP	120		Db	1141	ACLGCTAIPVCEPFKAAYFDMIRIDSQTNSHLDQFQTLNSVTPLQAEDCSIACLPRN	1200
Db	61	SAQEPHYLPPMPOGSYMTVDSSDHDPGEKARLOLPTMKENDTHC1DFSYLLSOKGLNP	120		Qy	1201	HDKNEFMDMLPPDRCLPFLITIDGESSNTINAALDSYROPAAFVTOQPLPNTVTDFWR	1260
Qy	121	GTLNLILVRVNGKPLANPIMWNTGFTGRDMLRAELAVSTWFNEYQVIFAEVGSGRSGYI	180		Db	1201	HDKNEFMDMLPPDRCLPFLITIDGESSNTINAALDSYROPAAFVTOQPLPNTVTDFWR	1260
Db	121	GTLNLILVRVNGKPLANPIMWNTGFTGRDMLRAELAVSTWFNEYQVIFAEVGSGRSGYI	180		Qy	1261	LVDYDGCTSIVMLNEVDLSOGCPOTWPEEGMLRYGPIOBECMSSCMDCDVYNRIFRICNL	1320
Qy	181	AIDDQVLSPCDKSPHFLRQDVETNAQONATFOCIATGRDAVINKLWLQRNEDIDPV	240		Db	1261	LVDYDGCTSIVMLNEVDLSOGCPOTWPEEGMLRYGPIOBECMSSCMDCDVYNRIFRICNL	1320
Db	181	AIDDQVLSPCDKSPHFLRQDVETNAQONATFOCIATGRDAVINKLWLQRNEDIDPV	240		Qy	1321	TRPQQGLMYQOFQLIGWASHREVGSKRSFLKLJLOVERQEWKEGEGRTIIFCLNGG	1380
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Qy							; Publication No. US20000101074A1	
Qy							; GENERAL INFORMATION:	
Db							; APPLICANT: Ghoosh, Soumitra S.	
Db							; APPLICANT: Fahy, Boin D.	
Db							; APPLICANT: Zhang, Bang	
Qy							; APPLICANT: Gibson, Bradford W.	
Db							; APPLICANT: Taylor, Steven W.	
Db							; APPLICANT: Glenn, Gary M.	
Qy							; APPLICANT: Warnock, Dale E.	
Db							; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION	
Qy							; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME	
Db							; FILE REFERENCE: 660088-465	
Qy							; CURRENT APPLICATION NUMBER: US/10/408,765A	
Db							; CURRENT FILING DATE: 2003-04-04	
Db							; NUMBER OF SEQ ID NOS: 3077	
Qy							; SOFTWARE: FastSEQ for Windows Version 4.0	
Db							; SEQ ID NO 284	
Qy							; LENGTH: 1439	
Db							; TYPE: PRT	
Qy							; ORGANISM: Homo sapiens	
Db							US-10-408-765A-284	
Qy							Query Match 99 % ; Score 7688 ; DB 16 ; Length 1439 ;	
Db							Best Local Similarity 99 % ; Pred. No. 0 ;	
Qy							Matches 1436 ; Conservative 2 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;	
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Db	301	LGVGPTYLILQNLANSIIGDGPILIKEKEYRMITSSTHAVAFTYKWLWHLDPTDEYE	360		Db	301	LGVGPTYLILQNLANSIIGDGPILIKEKEYRMITSSTHAVAFTYKWLWHLDPTDEYE	360
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Qy	361	IRVLITRPGEGGTGLFPPLIITRTCAEPMRTPKTLKIAEIQARRIAVDMESLGYNITRC	420		RESULT 3
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Db	421	HTFNVTICHYFRGNESKADCLMDPKAPOHQVNHLPPYTNSLKMILTNPEGRKESSE	480		; Publication No. US20020082397A1
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Db	481	TIIQDDEDPCPVYPSKSLQSTSFKENKIFLWKEPDNGKITOBISSKSISSRSPAPV	540		; APPLICANT: SCHLESSINGER, JOSEPH
Qy	541	AGPPQTIVSNLWNSTHVFMLHPLPHTYQFFTRASTVKGFGPATAINVNISAPTLPDYE	600		; APPLICANT: SAP JAN M.
Db	541	AGPPQTIVSNLWNSTHVFMLHPLPHTYQFFTRASTVKGFGPATAINVNISAPTLPDYE	600		; APPLICANT: UELICH, AXEL
Qy	541	GVDASLINEATTITYVLLRPAOKAPISAQIIVVEBLHPHTRKREAGAMEBCYQVPVTQN	660		; APPLICANT: VOGEL, WOLFGANG
Db	601	GVDASLINEATTITYVLLRPAOKAPISAQIIVVEBLHPHTRKREAGAMEBCYQVPVTQN	660		; APPLICANT: FUCHS, MIRIAM
Qy	601	GVDASLINEATTITYVLLRPAOKAPISAQIIVVEBLHPHTRKREAGAMEBCYQVPVTQN	660		; TITLE OF INVENTION: NODAL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
Db	661	AMSGGAPYKFAELPPGPNLLEPAPPTVGDNRTYQCFWNPLAPRKGYNYFQANSSEVEE	720		; FILE REFERENCE: 038602/1246
Db	661	AMSGGAPYKFAELPPGPNLLEPAPPTVGDNRTYQCFWNPLAPRKGYNYFQANSSEVEE	720		; CURRENT APPLICATION NUMBER: US/09-887-669
Qy	721	TKTQCVRIATAKAATEBEPEVTPDPAKOTDRVVKLACISAGILVFLILLVILTVKSKLA	780		; CURRENT FILING DATE: 2001-10-10
Db	721	TKTQCVRIATAKAATEBEPEVTPDPAKOTDRVVKLACISAGILVFLILLVILTVKSKLA	780		; PRIORITY DATE: 1999-01-21
Qy	781	KKRKDAMGNTROEMTHMVNAMDRSYADQSTLHAEDPLSITMDOHNESPRYENHSATARS	840		; PRIORITY NUMBER: 08-087-244
Db	781	KKRKDAMGNTROEMTHMVNAMDRSYADQSTLHAEDPLSITMDOHNESPRYENHSATARS	840		; PRIORITY NUMBER: 08-049, 3844
Qy	841	SRLLDVPRVLCGETESPYTGQLPAIRADLQHINLAKTSDSYGPKREYESFEGQQA	900		; PRIORITY NUMBER: 08-049, 3844
Db	841	SRLLDVPRVLCGETESPYTGQLPAIRADLQHINLAKTSDSYGPKREYESFEGQQA	900		; PRIORITY NUMBER: 08-049, 3844
Qy	901	SWDVAKKDNQRKARYGNLTAYDHSRVILQVOPVEDDPSSTYDINANITYDGYQRPSHYIATCG	960		; PRIORITY NUMBER: 08-049, 3844
Db	901	SWDVAKKDNQRKARYGNLTAYDHSRVILQVOPVEDDPSSTYDINANITYDGYQRPSHYIATCG	960		; PRIORITY NUMBER: 08-049, 3844
Qy	961	PVHETVYDFWRMIOEQSACIYMTNLVEYGRVCKCYKWPDDTEVYDGPKVTCVEMEPIA	1020		; Query Match: 98.2%
Db	961	PVHETVYDFWRMIOEQSACIYMTNLVEYGRVCKCYKWPDDTEVYDGPKVTCVEMEPIA	1020		; Best Local Similarity: 97.3%; Pred. No.: 0;
Qy	1021	EYVVRTFTLERRGNEIRETKQFHFTGWPDHGVYTAGTGLSFIRRVKSNPPAGTV	1080		; Matches: 1419; Conservative: 13; Mis matches: 6; Indels: 20; Gaps: 4;
Db	1021	EYVVRTFTLERRGNEIRETKQFHFTGWPDHGVYTAGTGLSFIRRVKSNPPAGTV	1080		
Qy	1081	HCSAGAGRCCYIDIMDMAEREGVVDIYNCYKALRSRRINNVQTEEQYIFHDIALE	1140		
Db	1081	HCSAGAGRCCYIDIMDMAEREGVVDIYNCYKALRSRRINNVQTEEQYIFHDIALE	1140		
Qy	1141	ACLCGETAIPVCEPKAAFYDFMDIRIDSQTSNSSLHDEFQTLNSVTPRLOEDCSTAICLPRN	1200		
Db	1141	ACLCGETAIPVCEPKAAFYDFMDIRIDSQTSNSSLHDEFQTLNSVTPRLOEDCSTAICLPRN	1200		
Qy	1201	HDKRFMDMLPPDRCLPFLITIDGESSIONTINAALMDSYQPAAFITVQQLPLNTVKDFVR	1260		
Db	1201	HDKRFMDMLPPDRCLPFLITIDGESSIONTINAALMDSYQPAAFITVQQLPLNTVKDFVR	1260		
Qy	1261	LVDYDGCTSIVMLNEVDLSQCGPOTWPEGMRLYGPQVCEMSCSMDCIVINRIFRICNL	1320		
Db	1261	LVDYDGCTSIVMLNEVDLSQCGPOTWPEGMRLYGPQVCEMSCSMDCIVINRIFRICNL	1320		
Qy	1321	TRPQEGYLMMQFOYLGWASHREVGSKRSPLKLIQKWEEMKEGRITIHCLNG	1380		
Db	1321	TRPQEGYLMMQFOYLGWASHREVGSKRSPLKLIQKWEEMKEGRITIHCLNG	1380		
Qy	1381	GRSGMFCAIGIVVEMVKRQNVDDVHAVTTLRNSKPNMVAPEQYRFYCVDALEYLESS	1439		
Db	1381	GRSGMFCAIGIVVEMVKRQNVDDVHAVTTLRNSKPNMVAPEQYRFYCVDALEYLESS	1439		
Qy	601	GVDAISLNNETATTIVLRLPAAQKAPISAYQIVVYELBPHRTKREAGAMECYQVPTVQ	660		

		CURRENT FILING DATE: 2001-10-10
		PRIOR APPLICATION NUMBER: 09/234, 8833
		PRIOR FILING DATE: 1999-01-21
		PRIOR APPLICATION NUMBER: 08/087, 2444
		PRIOR FILING DATE: 1993-07-01
		PRIOR APPLICATION NUMBER: 08/049, 3844
		NUMBER OF SEQ ID NOS: 13
		SOFTWARE: PatentIn Ver. 2.1
		SEQ ID NO: 8
		LENGTH: 1452
		TYPE: PRT
		ORGANISM: Homo sapiens
		US-09-887-669-8
		Query Match 62.8%; Score 4838; DB 9; Length 1452;
		Best Local Similarity 61.2%; Pred. No. 0;
		Matches 896; Conservative 203; Mismatches 322; Indels 42; Gaps 8
		4 TAAAALPAFAVALLLSPWPLLGSAQGQSAGCTFDGPGACDHYHDLYDDFEWVHVSQA 63
		3 TLGTGATIATLAGLL-----TARGETFSGGCLDEPEYSTCGYSSSEGGDFENWEQVNTL 54
		4 EPHEIDPMPDGSMIVMDSDHDPEKARIQLPINKENDTCIDDSYLLSOKGKNPGLT 123
		55 TKPTSDPWPMSGSLMVLNVAQRPECORAHILPQIKENDTHCIDDHFYFVSSKSNSPGLL 114
		64 NILVRVNKGKPLANPIWNVTGFTGRMLRBLAELAVSTFWPNEXQVIFAEVSGCRGTYAID 183
		947 ----DGYQRESHYIATQGPYHETVTDFTWMWQOQSACIVWMTNLVEGRVKCKWPD 1001
		960 IWLRYDGYQRESHYIATQGPYHETVTDFTWMWQOQSACIVWMTNLVEGRVKCKWPD 1019
		1002 DTEVYGFYKTCVEMEPLAEXVVRTFTLERGYNEIREVQFHFTGWPDHGVPYHATGIL 1061
		1020 DTEVIDDFRTCVEMEPLAETVVRTFTLERGYNEIREVQFHFTGWPDHGVPYHATGIL 1079
		1062 SFIRRVKLNSNPPSAGPIVWHCSAGAGRTGCYIVIDIMLMAEREQSYDITYNCVKALRSR 1121
		1080 SFIRRVKLNSNPPSAGPIVWHCSAGAGRTGCYIVIDIMLMAEREQSYDITYNCVKALRSR 1139
		1122 INMVQTEEQYIPIHDAILEACIGETAIPICEFKAYFDMIRIDSQTNSHLDKEFOTLN 1181
		1140 INMVQTEEQYIPIHDAILEACIGETAIPICEFKAYFDMIRIDSQTNSHLDKEFOTLN 1199
		1182 SVTPRLOAQEDCIACLPRHDKNRFDMLPDRCLPFLITIDGESSNYINRALMDSYROP 1241
		1200 SVTPRLOAQEDCIACLPRHDKNRFDMLPDRCLPFLITIDGESSNYINRALMDSYROP 1259
		1242 AAFIVTOQPLNTVKDFWRVLYDYDGCTISYMLNEVDLSQLCOPQYNPBEGMLRYGPQVEC 1301
		1260 AAFIVTOQPLNTVKDFWRVLYDYDGCTSYMLNEVDLSQLCOPQYNPBEGMLRYGPQVEC 1319
		1302 MSCSMODCDVNRIFCNLIRPQEGMLVQOQYIQLQEVKW 1361
		1320 MSCSMODCDVNRIFCNLIRPQEGMLVQOQYIQLQEVKW 1379
		1362 QEWKEGEGRTHCINGGRSGMFCAIGTIVEMYKRONYDVFHAKTILRNSKPNMVEA 1421
		1380 QECEBEGRTIHINGGRSGMFCAIGTIVEMYKRONYDVFHAKTILRNSKPNMVEA 1439
		1422 PEQYRCYDVALELESS 1439
		1440 PEQYRCYDVALELESS 1457
	RESULT 4	US-09-887-669-8
		Sequence 8, Application US/0987669
		Publication No. US20020082397A1
		GENERAL INFORMATION:
		APPLICANT: SCHLESSINGER, JOSEPH
		APPLICANT: SAP, JAN M.
		APPLICANT: ULLRICH, AXEL
		APPLICANT: VOGEL, WOLFGANG
		APPLICANT: FUCHS, MIRIAM
		TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
		FILE REFERENCE: US6021246
		CURRENT APPLICATION NUMBER: US/09/887-669
		US-09-887-669-8

		Best Local Similarity 60.5% ; Pred. No. 0;	
		Matches 885; Conservative 208; Mismatches 328; Indels 42; Gaps 8;	
Db	772 KRKETMSSTROEMTYVNSMDKSYAEQQGTCNCDB--AFFFMDTHNLRGSVSSPSSFTMK 828	Qy	832 -----ENHSAATAESEPLLDPVRY-LCEGTSRSPYOTGQLPAIRADLQH 875
Qy	829 TNTLSTSVPNSYYDETHTAWSDTSSLVQSHSTYKREPAVVPYQTGQLPAIRADLQH 888	Db	829 TNLKTSDSVKGKEEVESSFFEGOSASWDVAKDQNRAKRYGNITAYDHRSRVLQPVEDD 935
Qy	876 INLMKTSDSVKGKEEVESSFFEGOSASWDVAKDQNRAKRYGNITAYDHRSRVLQPVEDD 948	Db	889 ITOMKCAEGCAGPKKEYESEFFEGOSASWDVAKDQNRAKRYGNITAYDHRSRVLQPVEDD 948
Qy	936 PSSDTYNATYDGYORPSHYIATOGEVHETYDFWRMINOBQSACIVMTNLVEVGRVCC 995	Db	949 TNSDINGNTYDGHPRNHTIATQGMQETIDFWRMVHEINTASIMMTNLVEVGRVCC 1008
Qy	949 TNSDINGNTYDGHPRNHTIATQGMQETIDFWRMVHEINTASIMMTNLVEVGRVCC 1008	Db	996 YKWPDDTEVYGGDFKTVCMPELAEXYVURTFTELERGVNBIREVKQFHGDPHGYV 1055
Db	1009 CKWPDDTEVYGGDFKTVCMPELAEXYVURTFTELERGVNBIREVKQFHGDPHGYV 1055	Db	1009 CKWPDDTEVYGGDFKTVCMPELAEXYVURTFTELERGVNBIREVKQFHGDPHGYV 1058
Qy	1056 HATGLLSFIRVKULSNPPSAGPIVWHCSAAGAGRCCYVUDIMLDMAEREGVVDLYNCVR 1115	Db	1069 HATGLLGFRQVKSKSPSAGPLVTHCSAAGAGRCCPVIDMILDMAEREGVVDLYNCVR 1128
Qy	1116 ALRSRRINNTYDQEYQIIFHDIAECLCGETAP1PCPEPKAYFDMIRLDSQTNTSSHLD 1175	Db	1119 ELRSRRINNTYDQEYQIIFHDIAECLCGETAP1PCPEPKAYFDMIRLDSQTNTSSHLD 1175
Db	1119 ELRSRRINNTYDQEYQIIFHDIAECLCGETAP1PCPEPKAYFDMIRLDSQTNTSSHLD 1175	Qy	1176 EROTINSVTPLQADCSIAC1PLPDRCLPFLITIDGESNSNYINAALM 1235
Db	1189 EFRTLNMVPTPLRVEDCSTAILPRTHEKRCMDL1PPDRCLPFLITIDGESNSNYINAALM 1248	Db	1189 EFRTLNMVPTPLRVEDCSTAILPRTHEKRCMDL1PPDRCLPFLITIDGESNSNYINAALM 1248
Qy	1236 DSYROPAAFIVTQYBPNNTYDFWRLVYDGCSTVMLNEVDLSSGCPQWPBEGMLRKG 1295	Db	1244 9DSYKOPSAFIVTQYBPNNTYDFWRLVYDGCSTVMLNEVDLSSGCPQWPBEGMLRKG 1295
Db	1244 9DSYKOPSAFIVTQYBPNNTYDFWRLVYDGCSTVMLNEVDLSSGCPQWPBEGMLRKG 1295	Qy	1296 P1QYECMSISMDCDVYINR1FRICNLTROPREGYLMYQOFQYLGASHREYPGSKRSFLKL 1355
Qy	1309 P1QYEVSALEED1ISRFRIYNAARPQGSRMVMQFQLGWPMYRDTPVSRSFLKL 1368	Db	1309 P1QYEVSALEED1ISRFRIYNAARPQGSRMVMQFQLGWPMYRDTPVSRSFLKL 1368
Qy	1356 LOVEKWOENKEGEERTHTIHCLNGGRGSMFCAG1IVVEMVKRQNVVDYHAKTKLNISK 1415	Db	1369 RQVDKWQETNGGEGSPTVHCLNGGRSFTFCASIVCMLRQHTVDFHAKTKLNISK 1428
Qy	1416 PNMYEAPEQYRFLQFCYDVALLEYLS 1438	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
Db	RESULT 5	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
Db	US-10-408-765A-83	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	Sequence 83, Application US/10408765A	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	Publication No. US20040101874A1	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	GENERAL INFORMATION:	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Ghosh, Soumitra S.	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Fahy, Eoin D.	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Zhang, Bing	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Gibson, Bradford W.	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Taylor, Steven W.	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Glein, Gary M.	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i APPLICANT: Warnock, Dale E.	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i FILE REFERENCE: 660088-465	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i CURRENT APPLICATION NUMBER: US/10/408,765A	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i CURRENT FILING DATE: 2003-04-04	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i NUMBER OF SEQ ID NOS: 3077	Db	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i SOFTWARE: FastSEQ for Windows Version 4.0	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i LENGTH: 1452	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i TYPE: PRT	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
i	i ORGANISM: Homo sapiens	Qy	1429 PNMYDLIDQYKFCYDVALLEYLS 1451
US-10-408-765A-83	Query Match	62.1%	Score 4784; DB 16; Length 1452;

1.009 CKYWPDDTEIYKDIKVTLIETTELLAEXVIRTPAVEKRGVHEIREIRQFFFTGWPDPDHGVPPY 1068
 Db 1056 HATGLLSPIRVKLSNPPSAGPVINWCSAGAGRTGCYVINDIMLMAEREGVVDLYNCUK 1115
 Qy 1099 HATGLGFVRQVKSKSPSAGPBLVHCSAGAGRITGCFIVIDIMLMAEREGVVDLYNCVR 1128
 Db 1116 ALRSRTRMVQPEEQVIFHDIALEACLGETAIPVCEKAAYEDMIRISQTMNSHLDK 1175
 Qy 1129 EILSRSPVNMVQPEEQVIFHDIALEACLGTSVSPASQVSILYDMNLKPQTNSQIKE 1188
 Db 1126 EFOTLNSVTPLQAEQDCSIACLPRNHDNFMMLPPDRCPLFLITIDGESNSYINAALM 1235
 Qy 1176 EFRFLANVNPPTURVEDSIALPRNHCNRMDIUPDRCPLFLITIDGESNSYINAALM 1248
 Db 1236 DSYRDPAFEVITQYDPLNTVDFEWRLVYDGTCTSIWMLNEUDLSCQQCPYMEETMLRG 1295
 Qy 1249 DSYKQPSAFTVQHPLPNFTWDRLVYDHTCTSVMMLNDVPAOLCPQYWPENSYVHRHG 1308
 Db 1296 PIQEBCMSCSMCDVNRIFRCNLTRPQBGYLMQQFQTYLGWASHREVEPSKRSFLKLJ 1355
 Db 1309 PIQVEPVSADLEEDIISRFYRNARPDQCHRMNQOQFQJGWPMYRDTPYSKRQJALLI 1368
 Qy 1356 LQYEKNOBEWEKEGEGRITIHCLNGGRSGMFCAGIGIVEMYKRONTVDFHAKVTLRNSK 1415
 Db 1369 RQVDKWBEGEYNGEGPTVHCLNGGRSGTFCASISIVCMLRHQRITVDFHAKVTLRNSK 1428
 Qy 1416 PNMVEABQXYRCYDYLELES 1438
 Db 1429 PNMVDLUDQYKFCYEALEYLN 1451

RESULT 6
 US-10-205-219-15
 ; Sequence 15, Application US/10205219
 ; PUBLICATION NO. US20030138803A1
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Lee, Kevin
 ; APPLICANT: Dixon, Alisterair
 ; APPLICANT: Brooksbank, Robert
 ; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
 ; FILE REFERENCE: WI-A-018200
 ; CURRENT FILING DATE: 2002-07-24
 ; PRIOR APPLICATION NUMBER: GB 0118354.0
 ; PRIOR FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 197
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO: 15
 ; LENGTH: 1436
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; FEATURE: Receptor protein tyrosine phosphatase-1 lambda
 ; OTHER INFORMATION: Receptor protein tyrosine phosphatase-1 lambda
 US-10-205-219-15

Query Match 59.7%; Score 4602.5; DB 14; Length 1436;
 Best Local Similarity 60.3%; Pred. No. 0;
 Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;

33 AGCTFDGPG---ACDYHQDLYDDFEMVHVSQAEPHYLPPMPQGSYMIYDSSDHDPG 89
 Db 24 AGCTFEASDPVPPCESQAQDDFQEWQVHIGPGRTRPELPHGAYLMNASQTPGQ 83
 Qy 90 KARLQLPMTKENDTHCIDFSYLLSYOKGNGPSTNLTVYRNKGPLANPNNYGTGFRDW 149
 Db 84 RAHIIFOTLSENTHCQFSYFLYSRDSHSPGTLGIVYRNNGPLGSAVNNMTGSHGRQW 143
 Qy 150 LRALAYSTFWNEYQVTFEEAVSGGRSGSYIAIDIQVLSYPCDKSPHFLLGDVENAG 209
 Db 144 HOAELAVSTFWPNEBFQVLFEEALISPDKHGYIGDILFLFSTPCAKFHSRLGDVENVAG 203

Qy 210 QNATFOCIATGRDAVHNKWLQRRNGEDIPVAGTKNINHRRFANSFRLOQEVTKTDQDLYR 269
 Db 204 QNATFOCMAGRAAEHHPLQRSQGVLYPARGHISHRFLATEPLASVGRSODIYR 263
 Qy 270 CTVQSERGSGVSNPANQOLIVREPPRPIAPPOLLGCVPTYLQIQLANNSIIGDGPILKEVE 329
 Db 264 CVSQAPRAGVSNPNAFELIVEKEPTTAPOLLRACTPYLIQLANNSIIGDGPITRKEIE 323
 Qy 330 YRMISGSWTETHAVNAPTYKLWHIPDDEYEBIRVLUTRPGEGCTUPLITRKCAEP 389
 Db 324 YRMARGPWAHVNLQTYKLWHIPDDEYEBISVULTRPDEGGTRPGRGPPLISRTKCAEP 383
 Qy 390 MRTPTPLKIAEIQARIADWESLQYNIIRCHTFNTLICHYFRG--HNESKADLDMDP 447
 Db 384 TRAPGLAFAETIQARQQUITLOWPEQYVNTCRHCAVSLCYCRYTLEGSHNQTIRECYKMR 443
 Qy 448 KAPOHVNHLPPPTVNSLKMILTMPEGRKESEETLTQTDDEDPGPVPVKSLOGTSFENKI 507
 Db 444 GASRTIKNULPFRIHVRLLTNEBGRKEGVTFQTDDEPVGJIAAESLTFLEDMDI 503
 Qy 508 FLNKKEPLDPLNGITQXEISYSSISBFSDRAPVAGPPTOTVSNTWNSTHVFHMHPGTTY 567
 Db 504 FLKNRREPOEPLGTTQYEISYQSTESSSDPANVPBPRTTSKLRBTYHFSNLHPGTTY 563
 Qy 568 QFFIRASTYKGFPATAINTTNISAPTLDYEGDASLINEATTITVLRAQKGAPI 627
 Db 564 LFSVPAARTSFGFQHALTETTNISAPSP-DYADPSPSIGESENTTIVLRAQKGAPI 622
 Qy 628 SAYQIVVEELHPPHRTKREAGAMECYQVPTVQANMSGAPYFAEABLPPGNLPBPAPFTV 687
 Db 623 SVYQVVEERPRRREPQADCSVPLFETAILRGLVHYFGELAASSLLEAMPFTV 682
 Qy 688 GDNRITYOGEFNPPPLAPRKGYNNYFQAMSSYVEKETKTOCVIATKATEEPEVIPDPAKOT 747
 Db 683 GDNQTYRGFWNPPLPERKATLIVYFAASHKURGETLNCITKARACKESRPLVRSORS 742
 Qy 748 DRUVTAGIASA-GIVYFILLLWVILVKSKLAKRKDAMGNTFQEMTMVNANDRSYA 806
 Db 743 EEMGJLIGCAGGAVALLIGAIIYTRIGKPVMTK-ATVNYQEKTHMSAVDRSET 801
 Qy 807 DOSTLHAEDPLSITPMDOHNSPRYENHS--ATABSSRLDVPRYLCGETESPYQDGQLH 864
 Db 802 DOSTLQDERGLGSMMDAPGSPRDQSRGSGVTEASSLLCGSPRPCCGRGSPHTGQLH 861
 Qy 865 PAIRYADLQHINTMKTSYSGFKEYSEFEGQSASWDYAKDQNRAKRYGNLJAYDH 924
 Db 862 PAVRADLLOHINONKTAEGYGFQKEYYESFEGG--WDTAKKKCDKLKGGRQEPSSAYDR 917
 Qy 925 SRVILQOPVEDPSSSYDINANYIDGKQPSHYIATQGPVHETVYDFWRMINQEOQSACIVMV 984
 Db 918 HHVKLKHPLADPDAYAISANYIDGTHRSNFIQGPKPEMIVDFRMVNOEQCASIUM 977
 Qy 985 TNLVEYGRVYCKYMDPDTTEYQGDFKTCVEMEPLABYVVRTFTLERRGNEIREVKOFH 1044
 Db 978 TKLVBYGRVKCSRYFPESDMYGDKITLVKTETLAEVYVRTFALERGYSARHETRQFH 1037
 Qy 1045 FTGWPDPDHGVPPYHATGCLLSFIRRKVLSNPPSAGPITYVHCSAGAGRGCYIVIDIMDMAER 1104
 Db 1038 FTAWPPHGVPPYHATGLLAFTIRRKAStPDAGPITHCSAGTRGTSYIVIDMLMAEC 1097
 Qy 1105 EGVDVINYCKALRSBRINNQTEOYIFHDIALEACLGCTAIVCEFAAYFDMIRI 1164
 Db 1098 EGVDVINYCKTLCRRVNMQTBEYIFHDIALEACLGCTTVPNEFATYRMIRI 1157
 Qy 1165 DSQTNSSHLKDFOQTLNSVTPRLQEDCSIACLPRNHDKDRFMDMLPPDRCLPFLITIDG 1224
 Db 1158 DPQSNSSQLREFQINTSVTPPLDVECSTALLPRNDRDQRNSMDVLPDRCLPFLISSDG 1217
 Qy 1225 ESSNTNAALMDSYROPAAFIYTQYPLNTYKDFWRLYDYGCTSIVMLNEVDSLQG--- 1281
 :
 Qy 1218 DPNYYNAALTDTSYRSAFIVTLHPLQSTTPDFWLVYDGTCTSMNLNQINQNSAWP 1277
 Db 1282 CPQYWPEGMRLRYGPIQVECMCSMCDVNRIFRICNLTRPQEGLMVQFQYLGWASH 1341

Db	1278	CLQWPSPERQQYGLMEVBFVSGTANEDLVSRRVQNSRSLQEGHLLVRHFQELRWSSY	1337	Qy	1342	REVPSKSPFLKLLOVEKQEWEGEPTIHLNGGGRSGNFCATIVVNVRKRN	1401	Db	1338	RDTPSRKATHLLAEVDKQAE--SGDRTVHCLNGGSRSGTPCACTVLEMIRCHSL	1395
RESULT 7											
US-10-058-270A-98	Sequence 98, Application US/10058270A			Db	1342	REVPSKSPFLKLLOVEKQEWEGEPTIHLNGGGRSGNFCATIVVNVRKRN	1401	Qy	1342	REVPSKSPFLKLLOVEKQEWEGEPTIHLNGGGRSGNFCATIVVNVRKRN	1401
Publication No. US2004029114A1				Db	1338	RDTPSRKATHLLAEVDKQAE--SGDRTVHCLNGGSRSGTPCACTVLEMIRCHSL	1395	Qy	1402	CHTPNTVTCYHYFRGNESKAACLDMDKAPOHVNNHLPYTNYSLRMILTNPGRKSE	479
GENERAL INFORMATION:				Db	1402	CHSTNLTVQYVV--FNQOQEABEVQTSHTYRGLRPMTLRLUJNSPGRMSE	474	Db	1396	VDFHFAVKTLRNSKENMVAPEQYRFCYVALEYLS	1438
APPLICANT: Mack, David H.				Qy	1402	ETIQDDEVPGPVKS1QGTSTENKPLWKEPDNGITOTYEISTSSSIREDFDPAV	539	Qy	1396	VDFPAKTRNRYKPNMFTMDQIFHCYDALEA	1432
APPLICANT: Gish, Kurt C.				Db	1396	ELVQTEEDVPGAVPLS0GGPPEEKYIOWKPNETNGVITYEINKAVGSLDPSAD	534	Db	1396	ELVQTEEDVPGAVPLS0GGPPEEKYIOWKPNETNGVITYEINKAVGSLDPSAD	534
APPLICANT: Afar, Daniel				Qy	1342	VAGPPQTVSNLMNSTHMFMLHPGTTOFFTRASTVKGFPATAINVTTNISAPTLPDY	599	Qy	1342	VAGPPQTVSNLMNSTHMFMLHPGTTOFFTRASTVKGFPATAINVTTNISAPTLPDY	599
APPLICANT: Bos Biotechnology, Inc.				Db	1338	LSSORGKVFKLRNETHLFLPGFLYPTGTTSFIASTAKFGPPVTIAKISAPSMPY	594	Db	1338	LSSORGKVFKLRNETHLFLPGFLYPTGTTSFIASTAKFGPPVTIAKISAPSMPY	594
TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and				Qy	1342	EGYDASLNEBATATTIVLRLPAQAKGAPISAYQYVWEELPHPRTRBAGAMECYQVPTYQ	659	Qy	1342	EGYDASLNEBATATTIVLRLPAQAKGAPISAYQYVWEELPHPRTRBAGAMECYQVPTYQ	659
FILE REFERENCE: 018501-005210JS				Db	1338	NASSLDLSHYFABLKPNLPTQFPTGDNKTYNGYNPNPLSLSKSYIYQALSKANG	653	Db	1338	NASSLDLSHYFABLKPNLPTQFPTGDNKTYNGYNPNPLSLSKSYIYQALSKANG	653
CURRENT APPLICATION NUMBER: US/10/058,270A				Qy	1342	660 NAMGGAPYFAAELPPGLPEPAFPYQDFNRYQGFVNPLAPRKGNIYFOAMQSSVEK	719	Qy	1342	660 NAMGGAPYFAAELPPGLPEPAFPYQDFNRYQGFVNPLAPRKGNIYFOAMQSSVEK	719
PRIOR APPLICATION NUMBER: US 60/263,965				Db	1338	720 ETKHQCVRIATKAATEPEVIPDPDKQTDRVVKIAGISAGILVPLLLVVLLIVKK---	776	Db	1338	720 ETKHQCVRIATKAATEPEVIPDPDKQTDRVVKIAGISAGILVPLLLVVLLIVKK---	776
PRIOR FILING DATE: 2001-01-24				Qy	1342	714 ETKINCVRLATGASTQSNTNTVEPEKQVDNTVMAVGIAGLMFIILIGVMTIKRERN	773	Qy	1342	714 ETKINCVRLATGASTQSNTNTVEPEKQVDNTVMAVGIAGLMFIILIGVMTIKRERN	773
PRIOR APPLICATION NUMBER: US 60/265,928				Db	1338	777 -----SKLAJKRKDAMGNTREQENTHMYNAMDRSYADQSTLHAEDPLSLITFMQDN	826	Db	1338	777 -----SKLAJKRKDAMGNTREQENTHMYNAMDRSYADQSTLHAEDPLSLITFMQDN	826
PRIOR FILING DATE: 2001-02-02				Qy	1342	774 AYSYYSLQRQLAKKQETOSQAQRENGPVASA-DKPTTKLSASRNDEGSSSQDYG	832	Qy	1342	774 AYSYYSLQRQLAKKQETOSQAQRENGPVASA-DKPTTKLSASRNDEGSSSQDYG	832
PRIOR APPLICATION NUMBER: US 09/829,472				Db	1338	827 FSPREYNTISATELSRLJDY---PRYLCEGTTESPYQTGOLHPAIRRADLQLQHTQMKRSQ	883	Db	1338	827 FSPREYNTISATELSRLJDY---PRYLCEGTTESPYQTGOLHPAIRRADLQLQHTQMKRSQ	883
PRIOR FILING DATE: 2001-04-09				Qy	1342	884 SYGFKEEYESFFEQGOSASWDVAKKDQNPRAKNRGNNTIAYDHSRVTLQPVEDDPSSDYINA	943	Qy	1342	884 SYGFKEEYESFFEQGOSASWDVAKKDQNPRAKNRGNNTIAYDHSRVTLQPVEDDPSSDYINA	943
PRIOR APPLICATION NUMBER: US 60/288,590				Db	1338	889 GYGFKEEYEAFLPEPCQTAWSDTADEDENRINKRGNNTISYDHSRVRLVLDGDPHSIDYINA	948	Db	1338	889 GYGFKEEYEAFLPEPCQTAWSDTADEDENRINKRGNNTISYDHSRVRLVLDGDPHSIDYINA	948
PRIOR FILING DATE: 2001-05-04				Qy	1342	944 NYIDGYQRPShYIATQGPVHETYDFWRMIQEOASACTVMNTLVYEVGRVKCYKWPDT	1003	Qy	1342	944 NYIDGYQRPShYIATQGPVHETYDFWRMIQEOASACTVMNTLVYEVGRVKCYKWPDT	1003
PRIOR APPLICATION NUMBER: US 60/294,443				Db	1338	949 NYIDGYHRPRHYIATQGPMQETVDFWRMIQEOASACTVMNTLVYEVGRVKCYKWPDT	1008	Db	1338	949 NYIDGYHRPRHYIATQGPMQETVDFWRMIQEOASACTVMNTLVYEVGRVKCYKWPDT	1008
PRIOR FILING DATE: 2001-05-29				Qy	1342	1004 EYGFDFKTCVENEPLAYVWRFITLGEVNTREVOHFHTFWPDGIVPYHATGLJSF	1063	Qy	1342	1004 EYGFDFKTCVENEPLAYVWRFITLGEVNTREVOHFHTFWPDGIVPYHATGLJSF	1063
NUMBER OF SEQ ID NOS: 141				Db	1338	1009 EYGDIDKYLIEETPLAEVIRIFTVQKGGTHEIRELLFLHTFWPDGIVPYHATGLJSF	1068	Db	1338	1009 EYGDIDKYLIEETPLAEVIRIFTVQKGGTHEIRELLFLHTFWPDGIVPYHATGLJSF	1068
SOFTWARE ID NO: 98				Qy	1342	1064 IRRVKNLSPNSPPSAGPIVWHCSAGAGRGCYIVIDIMDMAEREQYDVIDYNCVKALSRRRIN	1123	Qy	1342	1064 IRRVKNLSPNSPPSAGPIVWHCSAGAGRGCYIVIDIMDMAEREQYDVIDYNCVKALSRRRIN	1123
LENGTH: 1444				Db	1338	1069 VRQYKFLNPPEASPIVWHCSAGAGRGCYIADTM DMAENEGVTDITNCVRELRAQRVN	1128	Db	1338	1069 VRQYKFLNPPEASPIVWHCSAGAGRGCYIADTM DMAENEGVTDITNCVRELRAQRVN	1128
TYPE: PRT				Qy	1342	1124 MVQTBQYQFINDAILEACLGCTAIPCECFKAYFDMRIDSOQTSNSHLKDEFQTLNSV	1183	Qy	1342	1124 MVQTBQYQFINDAILEACLGCTAIPCECFKAYFDMRIDSOQTSNSHLKDEFQTLNSV	1183
ORGANISM: Homo sapiens				Db	1338	1129 IVQTEQYVFWHDAILEACLGCTAIPCEFSLYNNISLDQTSNNSQIDKEFQTLNV	1188	Db	1338	1129 IVQTEQYVFWHDAILEACLGCTAIPCEFSLYNNISLDQTSNNSQIDKEFQTLNV	1188
US-10-058-270A-98				Qy	1342	1184 TPRLQPLNPTVKDFWRLVYDICTCTSIMLNEDVLSQCPQTMPEGMLRGPQIQCMS	1243	Qy	1342	1184 TPRLQPLNPTVKDFWRLVYDICTCTSIMLNEDVLSQCPQTMPEGMLRGPQIQCMS	1243
Query Match 59.2%; Score 4564.5; DB 15; Length 1444;				Db	1338	1189 TPYRPEPDGIGLPRNEDKRNRSMDVLBDRCPLFLPFLSVDGESSNNYNAALMDSHKQPAA	1248	Db	1338	1189 TPYRPEPDGIGLPRNEDKRNRSMDVLBDRCPLFLPFLSVDGESSNNYNAALMDSHKQPAA	1248
Best Local Similarity 58.0%; Pred. No. 0;				Qy	1342	1244 PIYTOQPLNPTVKDFWRLVYDICTCTSIMLNEDVLSQCPQTMPEGMLRGPQIQCMS	1303	Qy	1342	1244 PIYTOQPLNPTVKDFWRLVYDICTCTSIMLNEDVLSQCPQTMPEGMLRGPQIQCMS	1303
Matches 844; Conservative 239; Mismatches 343; Indels 29; Gaps 8;				Db	1338	1249 FVVTQHPLNPTVADFWRFLVFDNCVSMLNENDTAQCMQTPKTSGCYGPQIQCMS	1308	Db	1338	1249 FVVTQHPLNPTVADFWRFLVFDNCVSMLNENDTAQCMQTPKTSGCYGPQIQCMS	1308
1 MDITAAAAPAPVALLLSPWPILLGSAQQFSAGGCTPDGPGACDYHDL-YDDFENWV 59				Qy	1342	1304 CSMDCDVNRIFRICNTRPOEGYLMYQOFQTLGWASHREVPSSKRSFLKLQVKNQ	1363	Qy	1342	1304 CSMDCDVNRIFRICNTRPOEGYLMYQOFQTLGWASHREVPSSKRSFLKLQVKNQ	1363
1 MASLAALU---SLLRLQLPPLPGAROSAPEGCSTPBLHYSNCVSYALGNTGFTMEQ 56				Db	1338	1309 ADIDEDIIFRICNMRPQDSYRIVQHOLQVIGPATRDPSSKRSLLKVRRLERQ	1368	Db	1338	1309 ADIDEDIIFRICNMRPQDSYRIVQHOLQVIGPATRDPSSKRSLLKVRRLERQ	1368
60 VSAOPPHYPPEMFQGSTMIVDSDHDPEGEKARLQPTMKENDTHCIDSYLLYSQCKLN 119				Qy	1342	1364 EWCEGEGTIIHCLNGGSRGMCAJGVVEMYKRQNTYDVFAYKTLRNKSNMVEAPE	1423	Qy	1342	1364 EWCEGEGTIIHCLNGGSRGMCAJGVVEMYKRQNTYDVFAYKTLRNKSNMVEAPE	1423
60 VSAOPPHYPPEMFQGSTMIVDSDHDPEGEKARLQPTMKENDTHCIDSYLLYSQCKLN 119				Db	1338	1369 QYDREGTIVHCLNGGSRGMCAICSVEMIQONLIDVPHIKTLRNKSNMVEAPE	1428	Db	1338	1369 QYDREGTIVHCLNGGSRGMCAICSVEMIQONLIDVPHIKTLRNKSNMVEAPE	1428
57 INTTEKPMQDQAVPTGSFMVNNSGRASQAKHLLPTKENDTHCIDSYLLYSRDES 116				Qy	1342	297 LLGCGPTYLQIOLNANSIIGDGPILKEVYRMTSGSWTETHAVNAPTYKLWHLDPTYE	359	Qy	1342	297 LLGCGPTYLQIOLNANSIIGDGPILKEVYRMTSGSWTETHAVNAPTYKLWHLDPTYE	359
57 INTTEKPMQDQAVPTGSFMVNNSGRASQAKHLLPTKENDTHCIDSYLLYSRDES 116				Db	1338	297 LLGCGPTYLQIOLNANSIIGDGPILKEVYRMTSGSWTETHAVNAPTYKLWHLDPTYE	359	Db	1338	297 LLGCGPTYLQIOLNANSIIGDGPILKEVYRMTSGSWTETHAVNAPTYKLWHLDPTYE	359

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF PROSTATE CANCER
 FILE REFERENCE: MRI-044
 CURRENT APPLICATION NUMBER: US/10/205, 823
 CURRENT FILING DATE: 2005-07-15
 PRIOR APPLICATION NUMBER: 2001-07-25
 PRIOR APPLICATION NUMBER: 60/314, 356
 PRIOR FILING DATE: 2001-08-22
 PRIOR APPLICATION NUMBER: 60/325, 020
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: 60/341, 746
 PRIOR FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: 60/342, 158
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 343
 LENGTH: 1463
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-205-823-343

Query Match 59.2%; Score 4564; DB 14; Length 1463;
 Best Local Similarity 57.5%; Pred. No. 0; Indels 48; Gaps 9;
 Matches 847; Conservative 238; Mismatches 341;

Qy 1 MDITAAAALPAFAVALLPSWPWLGSAACQFSSAGGCTEDFDGPGACDYHDLL-YDDEFWH 59
 Db 1 MASLALARL---SLLRLQLPPLPGARAQSAPGCGCSFDEHSNCGYSVALGTINGFTWE 56

Qy 60 VSAQEPHYLPPEMPOGSMTYVDDSDHDPGKAKARLOLPNPKENDTHCIDSYLLSQKGIL 119
 Db 57 INTTEKEPMKDQAVPTGSMFMVNSSGRASQKAHLPTKENDTHCIDPHYFSSRDRSS 116

Qy 120 PGTMILVYVNGKPLANPIWNVTGTFGRMLRAELAVSTFWPNEXQVIFAEVSGGRSCY 179
 Db 117 PGALNVYVTKYNGPQGNPNVNWVSGVTVBGMVKAELAISTFWPHYQVIFEVSLKGHPG 176

Qy 180 IATDDIOVLSYPCDKSPHFLRGLDVEVNQGQNATFOCIATGRDAVNWKWLQRNGEDIP 239
 Db 177 IAVDEVRVLAHPCKRAPHFLRQNVEVNQGQNATFOCIAGGKWSQHDCLWLQWNGRDTA 236

Qy 240 VAQTKNINRRFAASPRQEVTKDQLRVCYTOSERGGVSNPNAQLYTREPPPPIAPPQ 299
 Db 237 LMTRVUNRRFSATVSVADTAQSVSKRCVIRSDGGSGVSNYAAELIVKEPPPTIAPE 296

Qy 300 LLGGPTVYIQLANSIIGDGPTILKEYTMRGTSWNTETHAVNAPTYKLWHLDPDTET 359
 Db 297 LLVAGATYIWKPNANSIIGDGPTILKEYTMRGTSWNTETHAVNAPTYKLWHLDPDTET 356

Qy 360 EIRVLTRPGEGGTGLPGPLPITRTKCAFPMRTPKTLKAEIQARRIADWESLGYNITR 419
 Db 357 EIRVLTRPGEGGTGPPLTRTCAFPVHGFQNVTEVDIIRARQLTQWEPGYAVTR 416

Qy 420 CHTPNVITYHFRGHNEKACDCLMDPQAPQHVNHLPPTNVSLKMLTNPBGRKSE 479
 Db 417 CHSYNLTVQYOVY--FNGQOYEAEVFIQGSSHTYLRLPPEMTRLRLSNPBRGMSE 474

Qy 480 ETIIQTDPEVPGPVVKSLQGTSPFENKLFPLNKPLDPLNGITTOEYISSSSIRSFSDFDPAV 539

Db 475 ELVVOQEEPDGPAYPLESQQGPPEEKVYIWKWPKNETGVITLYEINKAVESLDPAID 534

Qy 540 VAGPQOTVSNLNMNSTHVFMLHPGTTYOFFIRASTKGFGPATAINVTNISAPTLDY 599
 Db 535 LSSORGKVKLNRNTHLFLVGlyPCTTYSFTIKASTKACFGPPVTRLATKISAPSMPY 594

Qy 600 EGVDASLNSTATITVLLPAQAKGAPISAYQIVVEELPHPRTRKREAGMECYQVPVTYQ 659

Db 595 D-TDTPLNETDTITVMLPAQSGPAPVSYQLVKEERLQKSRRAADIECCSVPSYR 653

Qy 660 NAMSGGAPPYYFAAEIPLPGNLPEPAPFTYQGFVNPLAPRKGYNIYQAMSSSVBK 719

RESULT 10
 US-10-205-823-343
 Sequence 1283, Application US/10296115
 Publication No. US20040053248A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq Inc.
 TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
 FILE REFERENCE: 78-PCT
 CURRENT APPLICATION NUMBER: US/10/296, 115
 CURRENT FILING DATE: 2002-11-18
 PRIOR APPLICATION NUMBER: US03/4488, 725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US09/552, 317
 PRIOR FILING DATE: 2000-04-25
 SEQ ID NO: 1283
 SEQ ID NO: 1478
 LENGTH: 1499

212 ATFOCIATGRDAVNKLWLRNNGEDIPVAOTKINHRPFAASFRLOETVTKTDOFLYRCV 271
 206 ASFQCMAGR AEAFRFLLQRDQSGLAVPAAGVRHISRSPLATPLAAYSRAEQLYRCV 264

272 TOSERGSGS - NFAOLIVRVEPRPTAPPOLLGPGPTYLILQNLNANSIISGDPITLKEYRY 330
 265 SQAPRGTSLSNFABMVKSEPTPAPPQLRAGPTYLILQNLNANSIISGDPITRKEITY 324

331 RMTGSSTWTEHAVNAPTYKLUWHLDPPDTYEKIRVLULTRGGCTGLPGPLITRKYCAEM 390
 325 RMARGPWAETHYAVSLSQTYKLUWHLDPPDTYEKISVLUTRGCGTGLPGPLITRKYCAEM 384

391 RTPKTLKIAIBQARRIAJAVDWSIGNITRCHTNTICHYFRG -HN-----ESKA 441
 385 RAKPLAFAEIQAROLTLQKPEPLGYNVTRCHTYSLCCHYTGLSSHNCQTIPRCEDR 444

442 CLDMDPKAPORVNHLPPTYTNVLMLTNPGEKESETIQTDEDVPGPVPKSLOC 501
 445 CQPLHEEPAL-----SERSRREVLTNPGEKEGKTFQFDDEVSGIAAESLT 497

502 SPENKIFLWKPELDPNGLITOYESYSSTSRSFPAVPGAGPPTQVSNLWNMSITHVFMF 561
 498 PLEMDFLWKPEQEPNGLITOYESYSQTESSDAVNYQA-TSTISKURNETHVFSNL 556

562 HPGTYQFFTRASTYKGFDATAINVTTNISAPTLPDYCGVDASINETATTITVLLPAQ 621
 557 HPGTYLFSUGARIICKFGFQOALTEITIYISAPS -DYADMPSLIGESENNTVLLPAQ 615

622 AKGAPISAYQIVVVEELH -PHRTKREAGAMECYQVPUVTYQANMSGGAPYVFAAEELPPGNL 680
 616 GRGAPISVQVIVBQGSRLRREPGGDCFPBLTFAALARGLVDFGAELAASSP 675

681 EPAPTVGDNRTYQCFMNPIPLAPKGYNLYFOAMSSVEKETKOCVRIKTAATEEPEN 740
 676 EAMPFTVGDNKTYQCFMNPIPLEPKAYLFLQASHLKGETRLNCIRFARKAACKESKR 735

741 PDAKOTDRVVKTAGISA -GILVFILLVILVILVKS-----LAKKRKD 786
 736 LEVQSRSEBMGLLIGCAGLAVLILGAIIVIRKGRDHAYSYYPKPVNMTK---A 791

787 MGNTROEMTMVNAMDTSYADQSTLHAEDPLSLTFRMDQINSPRYENHS--ATAEASSRL 844
 792 TVNTRQEKTTHMMSAIVDRSTTDQSTL---OPPGLSMDTGYSTGEQRGGYTEASSLG 848

845 DVPRYLCEGTESPIOTGOHPAIRDALIQLQHNMKTSYSYGFKEEYESPFEGOSASKW 904
 849 GSPRRPGKGSPYHTVQHAPVADLQHNMKTAEGYGFQEYEEFFEG ---WDA 904

905 AKDDQNRAKNRYGNJIAYDHSRVLQPVDDPSDIYNDGYQRPSHYIATQGPYH 964
 905 TKKDKVURKSROEPMPAYDRVQLHPMGDPNADYINANYIDGYHRSHNFIAQGPKE 964

965 TYDFWERMWIQEOSACIYVNTNLYVEGRYKCYKWPDDTEVYDFKTVTCVEMPLAETYV 1024
 965 MYYDFWRMWQEHCSIVWTKLVEAGCKCSRWPEDDTYGDIKIMVAKTTLAETYV 1024

1025 RTFLERRGYNEIREVKQFHFTGPDPDGHGPYHATGLLSIRRVKLSNPSAGPVVHCSA 1084
 1025 RTFLERRGYNEIREVKQFHFTGPDPDGHGPYHATGLLSIRRVKASTPDAGPVVHCSA 1084

1085 GAGRGCGYVTDIMLDMAREGWYDINYCYKALRSRRRINMVOBEQYIIFTHDALEAC 1144
 1085 GTGRGCGYVLDVWLDMAREGWYDINYCYKTLCSRVMNIQEEQYIIFTHDALEAC 1144

1145 GETAPVCEFKAAYFDMIRIDSQTNNSHILKDEFQTLNSTPLQAEDCSIACLPRNHDN 1204
 1145 GETTIPVSEFKATYKEMIRIDPQNSNSQREEFTLNSTPLDVEEYTSALLPRNRDN 1204

1205 RFMDMLPPBRCLPLITIGESSNTINALMDSYRQPAFIVTQYPLPNNTVDEFWRLYD 1264
 1205 RSMBVLPBPRLPELISTGDSNNYTNALDTSYRASPVTIHLPLQSTTPDEFWRLYD 1264

1265 YGCTSVIWMNEVDLSQG --CPOYWPEEEGMLRYGPIQVCMSCSMDCDVIRFRICNL 1321

Db 1265 YGCTSVIWMNEVDLSQG --CPOYWPEEEGMLRYGPIQVCMSCSMDCDVIRFRICNL 1324

Qy 1322 RPQCLAYMQQFOYIGWASHREVPSCSKREFLKL1QVEKMQEENVEGEGRITINCLNGGG 1381
 Db 1325 RLQBSEHLLVRHFQFRWSAYRDTPDSKAFLHLLAEVDKWAEB-SGDGRTIVHLLNGGG 1382

Qy 1382 RSGMFCAIGIVVENVKRONVYDVFHAKTILRNNSKPNMVEAPEQYRFCDYALEYLES 1438
 Db 1383 RRGTSICALRTVLEMTRCHNLVDVSFAAKTLRNVYKPNMVTMDQTHFCYDVALEYEA 1439

RESULT 12
 US-10-087-993-34
 Sequence 34 , Application US/10087993
 Publication No. US20020169303A1
 GENERAL INFORMATION:
 APPLICANT: Ulrich, Axel
 Aoki, Naohito
 Kim, Yeong Woong
 Wang, Hong Yang
 Chen, Zhengjun
 Naylor, Oliver
 Kharitonov, Alexei Igorevich
 TITLE OF INVENTION: NOVEL PT20, PCP-2, BDPI, CLK,
 AND SIRP POLYPEPTIDES AND RELATED
 PRODUCTS AND METHODS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90011-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSQL for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/087, 993
 FILING DATE: 05-Mar-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/877, 150
 FILING DATE: June 17, 1997
 APPLICATION NUMBER: U.S. 60/019, 629
 FILING DATE: June 17, 1996
 APPLICATION NUMBER: U.S. 60/023, 485
 FILING DATE: August 9, 1996
 APPLICATION NUMBER: U.S. 60/030, 860
 FILING DATE: No. US2002169303A1ember 13, 1996
 APPLICATION NUMBER: U.S. 60/034, 286
 FILING DATE: December 19, 1996
 APPLICATION NUMBER: U.S. 60/030, 664
 FILING DATE: No. US2002169303A1ember 15, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 225/298
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1430 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

Qy 1008 DFKVTCVEMEPLAEYVVRFTFLERRGYNIEREVKOFHFTGMPDHGVPTYHATGLJSFIRY 1067
Db 192 DIKVTLJETTEAIVTIRTAEVKGVHEIREIOPHTFEDHGVPYHATGLJFVRQV 251
Qy 1068 KLSNPDPSAGPVIHVCSAGAERTGCYIVIDIMLDMAEREQGYDVIDNCVKALESRRINMVC 1127
Db 252 KSKSPSAGPVLHVCSAGAERTGCYIVIDIMLDMAEREQGYDVIDNCVRELSRRINMVC 311
Qy 1128 BEQYTFIHDALEACIGEPAIPCEPKAYFDMTRIDSQTSNSSLKUDFQTLSVTPL 1187
Db 3112 EEQYTFIHDALEACTGDSVPSAQSYRSLYDDNKLDPQTNSSIKEFERTLNMVTPL 371
Qy 1188 QADEGSTACIPLPRNHDQNRFNDMLPPDRCLPLITDGESSNYINALMDSYRQPAFTV 1247
Db 3712 RVEDSIALLBRNHEXCRMDILPPDRCLPLITDGESSNYINALMDSYKQPSAFIVT 431
Qy 1248 QYPLPNTVDFWRLYDYGGTSTIVMLNEYDLSOGCPQYWDPEEGMLRYGPIQVECMSCSD 1307
Db 4322 QYPLPNTVDFWRLYDHTCTSVWMLNDVDAOLCPQYWPENGVRHGPQVERVSADLE 491
Qy 1308 CDVNRIFRICNLTPQEGTYLWVQOFGYLWASHREVPGSKRSFLKLLOVEKQBEWKE 1367
Db 4932 EDIISRIFRYNAAPQDGTRMVQOFGYLWASHREVPGSKRSFLKLLOVDKQEOYNG 551
Qy 1368 GEGRTIHCINGGGRSGMCAIGITVEMVRQNYDVFHAKVTLRNNSKPNMVAPEQYRF 1427
Db 552 GEGRTVHCINGGGRSGTCAISIVCMLRHQRTVDFHAKVTLRNNSKPNMVDLLDQYKP 611
Qy 1428 CYDVALEYLES 1438
Db 6112 CYDVALEYLN 622

RESULT 14
US-10-296-115-1390
; Sequence 1330, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO: 1390
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-296-115-1390

Qy 244 KNINERRFAASFRLOEVTKTDQDLVRCVTOSERGGSVSNFAQLIVREPPRPIAPPQLLGV 303
Db 234 KVTSRRFTASFNVNNTTKRDAGYKRCMRTEGGGINSYAEVLYKEPPVPIAPPOLASV 293
Qy 304 GPTYLQINANSTIGDGPIILKEYBYRMTSGSWTETHAYNAPTYKWLHLDPTDBYEIRV 363
Db 294 GATHWQIQLNANSINGDGPIVARETEYCTASGSMDROPVDSSTSCKIGHLDPTDEIEISV 353
Qy 364 LLTRCEGGTGLPGPLITTKCABPMTRKTLKAEIQARRIAWDSEUGYNTIRCHTF 423
Db 354 LLTRCEGGTSPGSPGALTRTKCABPMGERKLEVEVKSRQITRWPQGYNTVRCHSY 533
Qy 424 NVTICHYHRGNESKAD- CLDMDPKAQPHQVYHNLPPTYNLSKMLTNPEGKKESET 481
Db 414 NLTVYCYQVGGQEPYREEVSWDTENSHSPQHTITNLSPTYNLSKMLTNPEGKESQEL 473
Qy 482 LIQTBDBDVPDPVPVSKQLOGTSFENKFIAWKEPPLDNGLITQYETSYSSRSFDAPVVA 541
Db 474 IVQTEBDLPGAVPTISIQGSTFEKIFLQMRPCTQYGVITLYETTYKAVSSFDEIDLS 533
Qy 542 GPPQTVSNLWNSTHVFMLHPGTYQFFTRASTKGFGEATAINVNTNISAPTPDYG 601
Db 534 NQSGRVSKUGNETHLFFGFLPGTYTSFTRASTKGFGPATNOFTKISAPSNPAYE-
Qy 602 VDASINETATTITVLRPAOKGAPIASAOIUVVBLHPRTKREGAMCYQVPTYQNA 661
Db 593 LETPLNQQTDTNTVYMLKAHSRGAFASVSYQIVWEERPRETKKTBTILCYPVPPHFQNA 652
Qy 662 MSGGAPYYFAAEELPGPNLPPAPPTFGDNRITYQGWNPPLA PRKCNITYFQAMSVEKET 721
Db 653 SLLNSQYYFAAEFPADSLQAQPFIDGNKTYNGWNTPLPYKSRYIYQAAASHANGET 712

RESULT 15
US-09-808-602-54
; Sequence 54, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: Macnoughall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15946-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US09/15115A1
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-808-602-54

Query Match Score 2210.5; DB 15; Length 815;
Best Local Similarity 53.2%; Pred. No. 3.2e-154; Mismatches 223; Indels 13; Gaps 5;

Matches 412; Conservative 123; Mismatches 227; Indels 13; Gaps 5;

Qy 4 TAAALPAVALLLSPWPLIGNSAQGQFSAAGGCTPDDGGAQDYHQDLYDDFEWVHVAQ 63
Db 3 TLGTCTLATLAGLLL-----TAAGETSGGCLDFEPYSTCGSQSEDDFNMEQNTL 54

Qy 64 EPHYLPPMFDQGSMIVDSDHDPEKARQLQPLTMKENDPHCIDEFSYLISQKLNPGTL 123
Db 55 TKPTSDPWMSGSEMLVNNSGRPEQRHILLPKQNKENTHICDFHYFSSKNSPPGIL 114

Qy 124 NILYRVNKGPFLANPIIWNVTCFTGMRWLAELAVSTFWPEYQVIFEAFTSGGERGYTAID 183
Db 115 NYVYKVNNQGPFLNPNWNSIDPRTWNAELAISTFWPNFYQVFEV-TTSGHGYLAID 173

Qy 184 DIOVLSYPCDKSPHFLRLDDEVNAGQNTFOCIATGRDAVHNKLWLRQRNGEDIPIACT 243
Db 174 EVKVLGHPCTRPHFLRQINQVNAQGQFTFOCSAIGRTVAGDRILWQGDYDRAPIKEL 233

Db 242 EIMPGGNVUNITCVAVGSPMPYVK-WMQGAEDLTPEDMPVG--RNV-----LEBLTDV 290
 Qy 261 TKTDDQDLKRCUTQSRSQGSVNFQAQLIVREPRPPIAPPOLQVGFTYLLQNLANSIIGD 320
 Db 291 -KDSANYHPCYAMSSLGV-TEAVAQITVKSUPKAAGTPTMVNTATSIITWDSEN--P 345
 Qy 321 GPILEKEVTRMTS--GSWTEATHAVNAPTYKLWHLDDPTEYEIRVILTRPOEGGTGLPGP 378
 Db 346 DFSVSYVIEYSKSSQDPCYQIKEDITTRTISIGGLSPNSEEIHW-SAVNSIGOOPSE 403
 Qy 379 PLITRTKCAEPMRTRPKTIAEIQARRIADWES----LGYNI----- 417
 Db 404 SVVTRGEQAPARPPRNQARMLSLATMIVOWEEPVNGLIRGYVTMEPEHPGNW 463
 Qy 418 -----T 418
 Db 464 QKHNVDDSLLTIVGSLIEDETYTWRVLAFTSVGDGPLSDPIQVKTQOGPGCQPMNLRAEA 523
 Qy 419 RCHTFENVTICYH-----YERGHNESSKADCLMDPDKAOPHVNHHAPPYTNVSLK 466
 Db 524 RSET-SITLSMSPPROSESIXKYLREGVRVORTF--TTSVBDEUKPNTEYAFR 581
 Db 467 MILTNPEG-----RKESBTIIQDDEDVPGPVVKSLQGTSPEENKIFLNWKZPLDPN 518
 Db 582 LAARSPQSLGAFTPQVVRQRTSOSI-----SPKNFKVMTMKTS---VLLSWEFPP-DNY 630
 Qy 519 GLIQYBISYSIIRSSTDPAVYAGPDTQVSILWNSTTHVFMHLHPCTTYQFFI--RASIV 576
 Db 631 NSPTPYKIQYNGL-----TLVDG-----RITTKKLTHLKPHTFYFNFLTNRGSSL 676
 Qy 577 KGF GPA---TAINVTT-NISASPTLPDYEGVDAISLNETATTITVLLRPQAQKGAPISAYQ 631
 Db 677 GLOQQTTTAWTANLINGKPSVAKPDDGF-----IMVLPDGSF-VPVQSF 725
 Qy 632 IYVEELHPR-----TKREAGAMECYO-----VVPVYQNMAGGAPYYFA--AE 673
 Db 726 IVMVPLRKSRSQQFLPLGSPDMDELLIOPDISRLQRSRSLRSRLEVPPYIARFSV 785
 Qy 674 LPPGNLDEPAPSTVQGDNRTYQCFWNPLAAPPKGNNYFQAMSSVKEKTRQCVRATKA 733
 Db 786 LPP-----TYPHPGDQKQYGFDFNRGLREPGRHYVLFVFLAV--LQKSEPT----FAASP 831
 Qy 734 TBEPEVI--PDPAKQTDVVKLAGISAGILVILLIVVI-LIVKSKSLAKRKDAMGNT 790
 Db 832 FSDPFQDNPDPQOPTIVDQEEGIWVQPLAVFICIVIALYKNSKRSKRSEPR 891
 Qy 791 RQEMTHNMVAMDRSYADOSTLHAEDPLSITPNDORNFSPRYENHSATAESSRLLDPRYL 850
 Db 892 KCULLNN-----ADIAFHPKPDPB--MRRNF----- 916
 Qy 851 CEGTESPYQTGOL-HPAIRVADLQHNLMTSDSYGKEEYESFEGQASAWDVAKKDQ 909
 Db 917 ---QTP--GMLSHPPPIADMMAERTLKLDSLKSQYESIDPGQOFTWEHSNLEV 969
 Qy 910 NEAKNRYGNIAIYDHRSVILQPVEDDSSDYNANTIDYQORPSHYTAQGPVHETVYDF 969
 Db 970 NKPKNPZYANVAYDHRSVILQPEGINSDYINANVYDGPQRQNAVIAATQZPLPTEFGDF 1029
 Qy 970 WRMWIQEOEACIYMTVNLAVEGRVKCYXWPD-DTEVYGDPEKTVCEMPLAEXYVRTFT 1028
 Db 1030 WRNWWEQRSATIUMMTRBEKSRIKCDQWPNRGTETYGFQVTLIDTIELATFCVRTFS 1089
 Qy 1029 LERRGYNMIREKQHFHTCPWDHGCVPHATGLSPIRRUKLSNPPSAGPIVHCSAGGR 1088
 Db 1090 LHKNSSSKREVRQFOFTAWPDHGPEXPPTPELAFLRKRKTCNPDPAGPITVHCSAGGR 1149
 Qy 1089 TGCYIVIDIMLDMAEAEVSDIYNCVKALRSRRINWQTEOYIFHDIAEACLGETA 1148
 Db 1150 TGFPIVIAMLERIKPTKTDVYGHFTLMSRQSPNMYQTEOYSFHEALLEAVGCGNT 1209
 Qy 1149 IPVCEFKAYFDMDIRISDQTSNTSHLKDDEFQTLNSVTPLQAOEDCSIALPRLNHDKNRFMD 1208
 Db 1210 VPARSLIYAIQKLAQVEGEHTGMELFEKRL--ANSKAHTSRFISANLPCKKFKRNLVN 1267

Qy 1209 MLPPDRCLPPLITDG-ESSNYINAALMDSYRPAFAFTVTOYPLPNTVKDFWRLVYDYGC 1267
 Db 1268 IMPYSTSTRVCLQPIRGVEGSDYINASFDYQROQAYIATQGPLBETTEFWRMWENNS 1327
 Qy 1268 TSIVMLNEVDL-SQGCPQWPEECMRLRGPIQECMSCSMDCDVNRIFRICNLTRPQE 1325
 Db 1328 TIVVNLTKLREMGREKCHQWPABERSARYQFYVUDPA--EYNMPOYILREFKWTNDAR 1384
 Qy 1326 GY-LMVQQFOYLGWSHREVPGSKRSFLKLUJOVKEWKGRTITHCLNGGRSG 1384
 Db 1385 GQSRTVROFQFTDW PEQGVPKSGGFDFIGQVHKTEOFGQ-DGPISHCAGVGRTG 1442
 Qy 1385 MFCALGIVVEMVKRQNVVDFHAYVTLRNSKPNMVAPEOYRCYDVALEYLES 1438
 Db 1443 VFITLIVLERMRYEGVVDFQTVRMLRTORPAMVQTEDYQFCQAALEYLGS 1496

Search completed: June 1, 2005, 14:02:15
 Job time : 138.676 secs

b	361	IRVLILTRGEGETGLPGPPPLTRTKCAEPWPTPKTLKIAEQARRLAVDNESSLGZNLTRE	420	protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type kappa precursor - mouse
b	421	HTFNTTICHHYFRGHNESKAQCLDMPPDKPAPORTVNLHPPYTNSLKMILNTPEGRKSEB	480	C;Species: Mus musculus (house mouse)
y	421	HSPNTTICHHYFRGHNESKAQCLDMPPDKPAPORTVNLHPPYTNSLKMILNTPEGRKSEB	480	C;Date: 21-Jan-1994 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
b	421	RJiang, Y. P.; Wang, H.; D'Busstachio, P.; Musacchio, J.M.; Schlessinger, J.; Sap, J.	481	A;Title: Cloning and characterization of R-PTP-kappa, a new member of the receptor protein.
y	481	TIIQTDBDVGPVPSLQGTSENKIFLAWKEPLDPNGITQYEISYSIRSFSDFPAVY	540	A;Reference number: A48066; MUID:93233655; PMID:8474452
b	481	TIIQTDBDVGPVPSLQGTSENKIFLAWKEPLDPNGITQYEISYSIRSFSDFPAVY	540	A;Accession: A48066
y	541	AGPQTTSNWNISTHVFMLHPCITYQFRASITYKGFCRATAINTTINSAPTLIDY	600	A;Status: nucleic acid sequence not shown
y	541	AGPQTTSNWNISTHVFMLHPCITYQFRASITYKGFCRATAINTTINSAPTLIDY	600	A;Molecule type: mRNA
b	541	AGPQTTSNWNISTHVFMLHPCITYQFRASITYKGFCRATAINTTINSAPTLIDY	600	A;Residues: 1-1457 <UTA>
b	601	GVDASLINEATTITIVLRLPAAQKAPISAYQTVVEELHPPHTKREAGAMECYQVPVITYQN	660	A;Cross-references: UNIPROT:P35822; GB:L10106; NID:9293771; PID:AAA40021.1; PID:g293772
y	601	GVDASLINEATTITIVLRLPAAQKAPISAYQTVVEELHPPHTKREAGAMECYQVPVITYQN	660	A;Experimental source: brain
b	601	AMSGGAPYYFAELPPGNLPEPAPFTGDNRTYQGFNPPLAPRKGYNNIYFOAMTSVKE	720	C;Complex: after cleavage by a furin-like endopeptidase, the two chains remain associate
y	661	AMSGGAPYYFAELPPGNLPEPAPFTGDNRTYQGFNPPLAPRKGYNNIYFOAMTSVKE	720	C;Supertamily: protease-like endopeptidase, receptor type mu; fibronectin in type III repeat
b	661	AMSGGAPYYFAELPPGNLPEPAPFTGDNRTYQGFNPPLAPRKGYNNIYFOAMTSVKE	720	C;Keywords: glycoprotein phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane; signal sequence #status predicted <SIG>
y	721	TKTQCRBIATK ANTEPEVLPDPAKOTDRVKIAGISAGLIVLILLIIVLIVKSKL	779	F;29-1457 /Product: protein-tyrosine-phosphatase, receptor type kappa, uncleaved #status pre
y	721	TKTQCRBIATK ANTEPEVLPDPAKOTDRVKIAGISAGLIVLILLIIVLIVKSKL	780	F;29-641-641-755 /Domain: extracellular #status predicted <EXT>
b	780	ARKRKDAMGNTQEMTHVMNAMDRSTADQSTHHAEDPLSITMDQINSPRYENHSATB	839	F;293-371 /Domain: immunoglobulin homology <IMM>
b	781	ARKRKDAMGNTQEMTHVMNAMDRSTADQSTHHAEDPLSITMDQINSPRYENHSATB	840	F;293-371 /Domain: fibronectin type III repeat homology <FN3A>
b	781	AKKRKDAMGNTQEMTHVMNAMDRSTADQSTHHAEDPLSITMDQINSPRYENHSATB	840	F;293-371 /Domain: fibronectin type III repeat homology <FN3B>
b	840	SSRLLDQPVRLCEGFTESPYOTCQLHPAIRVADLQLHQLMKTSDSYGFKEEYESFPFGQS	899	F;489-581 /Domain: fibronectin type III repeat homology <FN3C>
b	841	SSRLLDQPVRLCEGFTESPYOTCQLHPAIRVADLQLHQLMKTSDSYGFKEEYESFPFGQS	900	F;593-682 /Domain: fibronectin type III repeat homology <FN3D>
b	900	ASWDVAKKDDQNBPAKQYGNLTAYDHSPVILQPVEDDPSSTYDNYNDGQPSPHYIATQ	959	F;841-1457 /Domain: intracellular #status predicted <INT>
y	900	ASWDVAKKDDQNBPAKQYGNLTAYDHSPVILQPVEDDPSSTYDNYNDGQPSPHYIATQ	959	F;841-1457 /Domain: leukocyte common antigen cytosolic domain homology <LAC>
b	901	ASWDVAKKDDQNBPAKQYGNLTAYDHSPVILQPVEDDPSSTYDNYNDGQPSPHYIATQ	960	F;1218-1442 /Domain: protein-tyrosine-phosphatase homology <PTP2>
b	960	GPVHETVYDFWRMIQWQSACTIVMTNLVEGRVCKCYKWPDTTEVYDFKVTCVMEPL	1019	F;100-139 /Domain: protein-tyrosine-phosphatase homology <PTP2>
y	961	GPVHETVYDFWRMIQWQSACTIVMTNLVEGRVCKCYKWPDTTEVYDFKVTCVMEPL	1020	F;210-415 /Domain: binding site: carbohydride (Asn) (cova)
b	1020	AEVYVPTFTLBERGNEIREVKOFHFTGWDFGVPHATGLISFIRAVKLNSPPSAGPIV	1079	F;210-415 /Domain: binding site: carbohydride (Asn) (cova)
b	1021	AEVYVPTFTLBERGNEIREVKOFHFTGWDFGVPHATGLISFIRAVKLNSPPSAGPIV	1080	F;210-415 /Domain: binding site: carbohydride (Asn) (cova)
y	1080	VHCSAGAGRGTGYVIDIMDMAEREGVYDVTNCVKAIRSRRIINMYTQEYLFHDAIL	1139	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1081	VHCSAGAFRTGCVIDIMDMAEREGVYDVTNCVKAIRSRRIINMYTQEYLFHDAIL	1140	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1140	EACLGCTTAIYPCFCKAYDMRIDQTSNSSLKDFQFQTSVTPQAEQCSIACLPR	1199	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1141	EACLGCTTAIYPCFCKAYDMRIDQTSNSSLKDFQFQTSVTPQAEQCSIACLPR	1200	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1200	NEDKRNFMMLPPDRCLPFLPFLTDGEESNYTNAALMDSYRQPAFIFTQYPLNTVDFW	1259	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1201	NEDKRNFMMLPPDRCLPFLPFLTDGEESNYTNAALMDSYRQPAFIFTQYPLNTVDFW	1260	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
y	1260	PLVYDYGCTSIUMLNEVDSLQSQCPQYVPEGMRLQVCMSCSMDCDYNIRIFCN	1319	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1261	RLVYDYGCTSIUMLNEVDSLQSQCPQYVPEGMRLQVCMSCSMDCDYNIRIFCN	1320	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
y	1320	LTRPQEGYLMMQFOQYLGWASHREVPSSKRSFKLIIQVKEEKGEGFTIHCLNG	1379	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1321	LTRPQEGYLMMQFOQYLGWASHREVPSSKNSFKLIIQVKEEKGEGFTIHCLNG	1380	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
y	1380	GGRSGMFCAGIVVEMYKRQNTYDVFHAKTURNSKPMEVAPEQTRFCYDALEYLES	1439	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1381	GGRSGMFCAGIVVEMYKRQNTYDVFHAKTULRNSKPMEVAPEQTRFCYDALEYLES	1440	F;1106-120 /Domain: binding site: carbohydride (Asn) (cova)
b	1400	Bindsite: substrate phosphate (Arg) #status predicted		Query Match Score: 98.2%; Best Local Similarity: 97.3%; Matches: 1419; Conservatism: 13; No. of Missmatches: 6; Indels: 20; Gaps: 4;
b	1400	Bindsite: substrate phosphate (Arg) #status predicted		Query Match Score: 98.2%; Best Local Similarity: 97.3%; Matches: 1419; Conservatism: 13; No. of Missmatches: 6; Indels: 20; Gaps: 4;
b	1	MDTTAAALPAFYALLLSPWPLIGSAQCSAGCTFDGPGACDYHDLYDDPEWVHV	60	QY 1 MDTTAAALPAFYALLLSPWPLIGSAQCSAGCTFDGPGACDYHDLYDDPEWVHV 60
b	1	MD-VAAAALPAFYALLLSPWPLIGSAQCSAGCTFDGPGACDYHDLYDDPEWVHV	59	Db 1 MD-VAAAALPAFYALLLSPWPLIGSAQCSAGCTFDGPGACDYHDLYDDPEWVHV 59
b	61	SAQRPHYLPPMPGGSYMTVDSSPDHPGEKARLQLOPTMKTNDTHCDFSYLLYSOKGLNP	120	QY 61 SAQRPHYLPPMPGGSYMTVDSSPDHPGEKARLQLOPTMKTNDTHCDFSYLLYSOKGLNP 120
b	60	SAQRPHYLPPMPGGSYMTVDSSPDHPGEKARLQLOPTMKTNDTHCDFSYLLYSOKGLNP	119	Db 60 SAQRPHYLPPMPGGSYMTVDSSPDHPGEKARLQLOPTMKTNDTHCDFSYLLYSOKGLNP 119
b	121	GTINLILVRNKNGKPLANPIKVNVTGFTGRDMLRAELAVSTFWPEYQVIEAVSGGRGSGYI	180	QY 121 GTINLILVRNKNGKPLANPIKVNVTGFTGRDMLRAELAVSTFWPEYQVIEAVSGGRGSGYI 180
b	120	GTINLILVRNKNGKPLANPIKVNVTGFTGRDMLRAELAVSTFWPEYQVIEAVSGGRGSGYI	179	Db 120 GTINLILVRNKNGKPLANPIKVNVTGFTGRDMLRAELAVSTFWPEYQVIEAVSGGRGSGYI 179
b	124	AQTKINHRRFAASFLRQEVTKTDOQLYRCVTOSERGSGVSNAQALIVREPRPAPPOL	300	QY 124 AQTKINHRRFAASFLRQEVTKTDOQLYRCVTOSERGSGVSNAQALIVREPRPAPPOL 300
b	240	AQTKINHRRFAASFLRQEVTKTDOQLYRCVTOSERGSGVSNAQALIVREPRPAPPOL	299	Db 240 AQTKINHRRFAASFLRQEVTKTDOQLYRCVTOSERGSGVSNAQALIVREPRPAPPOL 299
b	301	LGCVGPTTYLIQLNANSIIGDGPIIKEYBYRMITSGSWTETHVNAPTYKLWHLDDPEYE	360	QY 301 LGCVGPTTYLIQLNANSIIGDGPIIKEYBYRMITSGSWTETHVNAPTYKLWHLDDPEYE 360
b	300	LGCVGPTTYLIQLNANSIIGDGPIIKEYBYRMITSGSWTETHVNAPTYKLWHLDDPEYE	359	Db 300 LGCVGPTTYLIQLNANSIIGDGPIIKEYBYRMITSGSWTETHVNAPTYKLWHLDDPEYE 359

481 TIIQTDDEDVPGPVPVKSLQGTSFENKIFLNKEPLDPNGITIOTYBISYSSIRSFDPAVPP 540
 Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 477 VTFQTDDEDVPSGIAAESLTLTIPEDMFLKWEPOEPNLGITQYISQTESSPDANNV 536
 C;Species: Homo sapiens (man).
 C;Accession: S72441.
 R;Crossland, S.; Smith, P.D.; Crompton, M.R.
 Biochem. J. 319, 249-251, 1996
 A;Title: Molecular cloning and characterization of PTP-psi, a novel receptor-like protein
 A;Reference number: S72441; MUID:97024447; PMID:8870675
 A;Accession: S72441.
 A;Status: nucleic acid sequence not shown.
 A;Molecule type: mRNA
 A;Residues: 1-1442 <CRO>
 A;Cross-references: UNIPROT:092735; EMBL:X95712; NID:91666422; PIDN:CAA65016.1; PID:9166
 A;Experimental source: mammary; cell line MCF-7
 C;Genetics:
 A;Gene: fmi
 C;Function:
 C;Superfamily: regulates cellular function by dephosphorylating phosphotyrosine residues
 C;Keywords: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat
 -tyrosine-phosphatase homology
 F:29-188/Domain: MM homology <MAN>
 F:288-336/Domain: fibronectin type III repeat homology <3FR>
 F:910-1130/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match Score 4374.5; DB 2; Length 1442;
 Best Local Similarity 58.5%; Pred. No. 4.7e-289;
 Matches 840; Conservative 202; Mis matches 332; Indels 63; Gaps 18;

Qy 7211 TKTQCYRIATAKATEPEVTPDPAKQTDRVKKIAGISA-GILVFLILLVLLIVKSKL 779
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 7116 TRLNCRIRAKTACKESKRPLEVSQRSEMGUIGICAGGGAVAVLILGAIVIIRKGKP 775
 :|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 780 AKKRKDAMGNTRQEMTHVNAMDRSYAIDOSTLHAEDPLSITFMDOINFSPRYENHS-AT 837
 :|||:|||:|||:|||:|||:|||:|||:
 Db 7776 VNMTK-ATVNTRQEKEHTHMSAVDRSFTDQSTILOEDERLGNISFMDDTHGYSTRGDQESGGVT 834
 :|||:|||:|||:|||:|||:
 Qy 838 AESSRLLDPRVLCGETESPITQGOLHPAIKVADLQLQHINLMKTSDSYGFKEEYESFFEG 897
 :|||:|||:|||:|||:|||:|||:
 Db 835 BASSLGCGSPPRCPGRKGSPYHTQGHPAVRADLQLQHINQMKTAEQYGFQEXYESFFG 894
 :|||:|||:|||:|||:
 Qy 898 QSASWDVAKKODONRAKRNRYGNTIADHSRVLQPVDDPSSDYINANYIGYQRESHYIA 957
 :|||:|||:|||:|||:
 Db 895 ---WDAKKDKVKGKSREQMPAYDRHRVKLHMPMLGPNDAYINANYIGYHRSNHFIA 950
 :|||:|||:|||:
 Qy 958 TOGPVHETVDFWRMIWQEQSACIVMWNLNEVGRYTKCYKWPDDTEVYGBFKUTCVCME 1017
 :|||:|||:|||:
 Db 951 TQGPKEPMVDFWRMWQEHCSIVMWKLVEVGRYKCSRWPEDSDTGYDPIKIMLKVKTE 1010
 :|||:|||:|||:
 Qy 1018 PLAEXYYVTRTFLEERRGNEYIREVKOPHTGMPDFHGVPYHATGLLSPIRTRYKLNSNPPSAGP 1077
 :|||:|||:|||:
 Db 1011 TLAEYYVTRTFALERGGSARIEHVROPHFTAMPEHGVYPYHATGLLAFTRVYKASTPDAGP 1070
 :|||:|||:|||:
 Qy 1078 IVVHCSAGAGRTGCYVTDIMDMAEREGYDVINCYKALRSRRINMVQTEEQYIPIHDA 1137
 :|||:|||:|||:
 Db 1071 IVVHCSAGTAGTCYVTDIMDMAECEGVYDINYCKTLCRSRVMNQIPEEQYIPIHDA 1130
 :|||:|||:|||:
 Qy 1138 ILEACLGCTAIPVCEFKAAVFDMDRIDSOTNISHLDEFOFLNSYSPRQAOEDCSIACL 1197
 :|||:|||:|||:
 Db 1131 ILEACLGCTTIPVSEKATYKEMIRDQPSNNSQUREFOFLNSYSPPLDVECSIALL 1190
 :|||:|||:|||:
 Qy 1198 PRNHDKNRFMDMILPPDRCLPFLITIDGESSNYINAALMDSYROPAFIVTOYPLNTVKD 1257
 :|||:|||:|||:
 Db 1199 PRNRDKNRSMDYLPDRCLPFLISTDGSNNYINAALTDSITRSAFIVLHPLQSTTPD 1250
 :|||:|||:|||:
 Qy 1258 FWRLVDYDGCTSIIVMLNEVDLSQ--CPOWPEEGMLRYGPIQVBCMSCMDCDVIRI 1314
 :|||:|||:|||:
 Db 1251 FWRLVDYDGCTSIIVMLNOLQNSANSANFCLOVWPEPROQYSUMEVEFMSTGADEDLVARY 1310
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 Qy 1315 PRICNLTRPOEGYLMYOFOQYLGWASHREPVPSKRSRSPFLKLQVERWQEEENREGERTII 1374
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 Db 1311 FRVNQISSLQEGHLIVRHQFLURWSAYRTDPDSKKANHLLAEVDKQAE-SGDERTIV 1368
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 Qy 1375 HCINGGSRSGMFCAGIGIVEMYKRONTYDVFHAKTILRNSKPNMVEAPEOYRCYDVALE 1434
 :|||:|||:|||:
 Db 1369 HCINGGSRSGTCACTVLEMIRCHNLVDVFFAAKTLRNYKPNMVTMDQTHFCYDVALE 1428
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 Qy 1435 YLE 1437
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 Db 1429 YLE 1431
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RESULT 6
 S72441
 protein-tyrosine-phosphatase (EC 3.1.3.48) pi - human

N;Alternate names: FMI protein; receptor-like protein tyrosine phosphatase pi
 C;Species: Homo sapiens (man).
 C;Accession: S72441.
 R;Crossland, S.; Smith, P.D.; Crompton, M.R.
 Biochem. J. 319, 249-251, 1996
 A;Title: Molecular cloning and characterization of PTP-psi, a novel receptor-like protein
 A;Reference number: S72441; MUID:97024447; PMID:8870675
 A;Accession: S72441.
 A;Status: nucleic acid sequence not shown.
 A;Molecule type: mRNA
 A;Residues: 1-1442 <CRO>
 A;Cross-references: UNIPROT:092735; EMBL:X95712; NID:91666422; PIDN:CAA65016.1; PID:9166
 A;Experimental source: mammary; cell line MCF-7
 C;Genetics:
 A;Gene: fmi
 C;Function:
 C;Superfamily: regulates cellular function by dephosphorylating phosphotyrosine residues
 C;Keywords: protein-tyrosine-phosphatase homology
 F:29-188/Domain: MM homology <MAN>
 F:288-336/Domain: fibronectin type III repeat homology <3FR>
 F:910-1130/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match Score 4374.5; DB 2; Length 1442;
 Best Local Similarity 58.5%; Pred. No. 4.7e-289;
 Matches 840; Conservative 202; Mis matches 332; Indels 63; Gaps 18;

Qy 35 GCTFDGPG --ACDXHQDLYDDPFPWVAYSQAEPPHYLPPPEMQPGSYMIVDSSDHDPGEKA 91
 :|||:|||:|||:
 Db 33 GCTFPBEGSDPAPVPCYSQAQYDDFWQDPG5-----PAUDPHGSGYLMVNTSOHQPGQRA 85
 :|||:|||:
 Qy 92 RLQLPTMKENDNDTCIDFSYTLQYLSQKGLNPQGTNLTVRNGPLAMPAPIWVNTGFLGTYFGRDWLR 151
 :|||:|||:
 Db 86 HVIFPSLSSENDTHTCQFSYLYSRSQHSPGTLGVYTVRNGPLGAVAVMTGSHGROWTHQ 145
 :|||:|||:
 Qy 152 AELAVSTFWPEYQVIFEAEVSGC3RSGYIAIDDQIQLSYPCDKSKPHFLRGDVEYNAGON 211
 :|||:|||:
 Db 146 AELAVSTFWPEYQVIFEAEVSGC3RSGYIAIDDQIQLSYPCDKSKPHFLRGDVEYNAGON 205
 :|||:|||:
 Qy 212 ATFOCIATGRDVAHNKLWLRNGEDIPVATQKNINMRRAASFLQEQVTKTDQDOLYRCV 271
 :|||:|||:
 Db 206 ASFOQMAAGR-AEAFRFLQORQSGALVPAVGVRHLSRSFLATPLAFAVSRAEQDOLYRCV 264
 :|||:|||:
 Qy 272 TQSERSGSVS-NFAQIIVRERPRPAPPOLIGVGFTYLQIOLANSIIGDQPIILKEVEY 330
 :|||:|||:
 Db 265 SQAPQRGTSLNFAEMVKEPPTPAPPOLLRAFRGTYLQIOLNTSIIIGDQPIVREKEY 324
 :|||:|||:
 Qy 331 RMTSGSSWTETHAVNAAPTYKLWHLDDPTEYEYTRVLLTRPGEETGTLFGPPPLTRTKCAEPM 390
 :|||:|||:
 Db 325 RMARGEWAETHVLSQTYKLWHLDDPTEYEYSLVLTTRPGEETGTLFGPPPLTRTKCAEPM 384
 :|||:|||:
 Qy 391 RTPKTKIAEIQARIAVADWESIGNYNTIRCHTENTVICHYFRG--HN----ESKAD 441
 :|||:|||:
 Db 385 RAPKGCLAFASTQARQQLTONEPLGLNVTRCTYTVSLCYHYLGSNSHNOTIPRCYDRAR 444
 :|||:|||:
 Qy 442 CLDMDFKAPQHVNPLPPQNGLTTQYESYQSSESDPAPVQGPPVPSLOGT 501
 :|||:|||:
 Db 445 CQPLHHEEPAAL---SERSREVLTNPBEGREKGKEYFTQDVEDVPSGIAAESLFTF 497
 :|||:|||:
 Qy 502 SFENK1FLNKWKEPLDNGITTOYEISYSSIRSFDAPVAGPPOTVSNLWNSTHVFMLH 561
 :|||:|||:
 Db 498 PLEDMMFLKWEQBPQNGLTTQYESYQSSESDPAPVQGPPVPSLOGT 621
 :|||:|||:
 Qy 557 HPGT1YLFSLVSGARTGKGFGQQLTETTYIASPL-DYADMPSPLGESENNTVLRPAQ 615
 :|||:|||:
 Qy 622 AKGAPISAYQIVVVELH-PARTKREAGAMECYQVPUTYQNAMSGGAPYYFAELPGCNLP 680
 :|||:|||:
 Db 616 GRGAPISVQVIVETEEQGSRLRREBFGQQDCEPVLFEALLARGLVYDFGRELAAASSLPL 675
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Qy 681 EPAPPTVGDNRRTYQQFWNNPLAPRKGYNTYFOAMSSVEKETKTOCVRATAEPEVYI 740
 Db 676 EAMPPTVGDNKTYGEWNPPIPLEPKAYLTFQAASHLKGTRUNCIRARRAACKESKP 735
 Qy 741 PDPAKOTDRTVYKAGISA-GILVFILLVVILVYKSKK-----LAKKRKA 786
 Db 736 LEVSRSEENGLLIGCAGGIAVLTLLGAIVTIRKGDBHYASYYPPKPVNNTK---A 791
 Qy 787 MGNTQEMTMNAMDYSADQSTLHAEDPLSITFMDQNFSPYENHS-ATPESRSL 844
 Db 792 TVNTRQEKTMMSAVDRSTFDOSTL---QPGPLSFMDTGYSTRGEQGGVTEASSLJG 848
 Qy 845 DVPRVLCEGTBESPYOTGOLEPAIRDLQHINLMRTSDSYGFKEYESEFGEGOSASNDV 904
 Db 849 GSPRPCKGKGSPHTVQHLPAVRDLQHINQMKTAGCYGFKEYEFFEG---WIA 904
 Qy 905 AKKDQNRAKNRGNTIAYDHSRVLTIQPVEDDPSSDYINANVYDGYORPSHYIATQGPVHE 964
 Db 905 TIKKDKDVKGSRQEPMPAYDRHRVLPHPMLGDPNADYINANVYDGYHRSNHFIAUTQGPKE 964
 Qy 965 TUYDFWRM1WQEQSACIVWNTNLVEGRKVCYKTCWPDPDEYVGDPKVTCEMPLAEVYI 1024
 Db 965 MVDYDFWRM1WQEHCSIVM1TKLVEVAGGCKCSRWPEDSDTGYKIMVKTENLAEVYI 1024
 Qy 1025 RTFTLERRGNEYIRETVKQFFPHTGWDHGYPYHATGLLSSTRVQLSNPSAGP1VHCSA 1084
 Db 1025 RTFALELRGGYSARTEVRQFFTAPEHGYPYHTGGLATIRRVAESTPDAGP1VHCSA 1084
 Qy 1085 GAGRTGCGYIVIDIMLDMAREGVYDLYNCYKALSRRIINMVQTEQYIPIHDALEACI 1144
 Db 1085 GTGRTGCGYIVDIMLDMAEGVYDLYNCYKTLCSRCVNMQIOTEQYIPIHDALEACI 1144
 Qy 1145 GETAIPVCPCEKAAYFDMIRDQSNTNSHKEDEFOTLNSTSPRLAEDCSIAC1PRNHDN 1204
 Db 1145 GETTPVSEFKATKEMIDPQNSNSSLQREFQTLSNSTPPLDVEEISALLPRNHDN 1204
 Qy 1205 RFMDVLPPRCLPPLITIGESSNTNALMDSTROPAFIVTOYPLPNTVQDFWRLYD 1264
 Db 1205 RSMDVLPPLRCLPFLISTGDSNTNINALTDSTYTSRAFIVTILPLOQSTTPDFWRLYD 1264
 Qy 1265 YGCTSIVMNEVDSLQS---CPOYWPPEECMILRYGPIOVRCMSCSMDCIVNIRFRICNT 1321
 Db 1265 YGCTSIVMNQLNQDSNSAFCPLQWPEPRQQYGLMEFVMSGTADEDIVARFRVQNTS 1324
 Qy 1322 RPQGTYLMQQFQYLGWASHREVPGSKRASFLKL1LQVKWQEMKEGERGTTIHCINGG 1381
 Db 1326 RLQEGSHLLVTHFOPTRWSAYRTDPESKFLHLAAEVDKWQAE---SGDGTIVHCLNGG 1382
 Qy 1382 RSGMFCATGIVVENVKRONVYDPAVKTLRNKSPEMYBAPEQYRCYDALEYLES 1438
 Db 1383 RRGTSCLARLTLEMIRCNLNDVSPAAKTLRNKYPNMYETMDQHFCYDALEYLEA 1439

RESULT 7
 15148 protein-tirosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
 N;Alternate names: Leukocyte common antigen-related phosphatase
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R;Walton, K.M.; Martelli, K.J.; Kwak, S.P.; Dixon, J. B.; Largent, B. L.
 A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
 A;Accession: 15148; MUID:93357030; PMID:8352346
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Accessories: 1-1501 <WAL>
 A;Cross-references: UNIPROT:Q64605; GB:L19333; PID:9310242; PID:AAA42309.1; PID:9310243
 A;Note: In Genbank entry RATTYRPIOS, release 113.0, the source is designated as Rattus
 R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A;Title: Molecular cloning and expression of a unique receptor-like protein-tirosine-pho

A;Reference number: S46216; MUID:94347119; PMID:8068021
 A;Accession: S46218
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-1501 <ZHA>
 A;Cross-references: EMBL:L12329; PID:9294573; PID:9294574
 C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology
 C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
 F:47-109/Domain: immunoglobulin homology <IMM1>
 F:149-209/Domain: immunoglobulin homology <IMM2>
 F:216-309/Domain: immunoglobulin homology <IMM3>
 F:413-505/Domain: fibronectin type III repeat homology <3FR>
 F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:969-1190/Domain: protein-tirosine-phosphatase homology <PTP1>
 F:1258-1481/Domain: protein-tirosine-Phosphatase homology <PTP2>
 F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted
 F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
 F:1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted
 F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted
 Query Match 19.8%; Score: 1529.5; DB: 2; Length: 1501;
 Best Local Similarity 30.1%; Pred. No. 2.5e-95;
 Matches 419; Conservative 207; Mismatches 470; Indels 296; Gaps 46;
 Qy 205 EVNAGQNATFOCIATGRDAVNKLWLQRNG---EDIPIAQCTKINHRRFAASFRQLQEV 260
 Db 242 EIMPGGNNTITCAVGSPMPYVK-WMQGAEDLTPEDDMEVG--RNV-----LELT 288
 Qy 261 TKTDQDLVRCVTSOBGSESVNPAOLIVREPPIAPPOLLGVGPYPTLLIQLNANSIIIGD 320
 Db 289 DVKDSDANTYTCVAMSSLGV-IEAVAQITVSLPKAPGPVVTENTATSITVTVWDSGN--P 344
 Qy 321 GPITLKEYTRMTS-GSMTEHAVAQNAPTYKLVHLDPTDEYEYRVLTRPGECCGTGLPGP 378
 Db 345 DPVSYVILEYKSKSQDGPKQIKSDITTRYSIGSPNSEYIWV--SAVNSIGQGPSE 402
 Qy 379 PLITRTRKCAEPMTPTKLKIAEIQARRIAVDWES-----LGYNITRCHTNVNTICYH 430
 Db 403 SVVTRTGEQAPASAPRNTQARMLSATMTIVQWEPVEPNGLIRSYRV-----449
 Qy 431 YFRGHNESKADCLMDPQAPHQVNVHLPPYNTVSLKMLTNPGRKESBTIIQT-----485
 Db 450 YY-----TMPEPHPGWQKH-NVD-DSLTTVGSLEDETYTVLAFTS 493
 Qy 486 --DEDVPGEPVPSLQG-----TSFENKFLWKEPLDNGITQYTSYSS-- 530
 Db 494 VGDGPPLSDPQIVKIQGQYGPQMPNLAERAKSETSIGLSNSAPQES--VIKYELLFREGD 551
 Qy 531 -----IRSDFPAYVAGPQPQTVSNLWNNTSTHVPMHLHPCGTYOFFIRASTVKGPGPATAI 585
 Db 552 RGREVGRFDP-----TFAFVYEDLKNTENYAFRLAARSPOQIGAFTAV 595
 Qy 586 -----NVTNINISAPLPL--DYGVDYASLN-BTATTI 613
 Db 596 VCQRTLQASPKNFKVKMIMKTSVLSWEPDNYNSPPT-PYKIQYNGLTDVDRTRKKL 654
 Qy 614 TVLIRP-----AQAKGAPISAYQIVYVTEBLLPHRTKREA-----649
 Db 655 ITHLKRPHTPYNFVLTNRQSSLGLQTV-----TARTAFNMLSGKPSVAPKPDNDGS 707
 Qy 650 ECY--QVPTVYQNAMGGAPYFEEAELP-----PGNLP-----680
 Db 708 VVYLIPDGQSPVTVQN-----YFYIVMPLRKSRRGGQFPILLGSPEDMDLELIODLUSR 759
 Qy 681 -----EPAPFTVCDNRTYQGFNNPLAPRKGNNTYQFQAMS 715
 Db 760 LQRRLRHSROLEVRPYTAARFSILPVAVPNQKQYGGFDNRGLFQHRYVLFVLAV- 818
 Qy 716 SVREKETKQCVRATKATEEEPEV-----PDPAXQDTVYKJAGISAGILYFILUWVLL-L 772
 Db 819 -LQRNEPT-----FAASPSDFPQLDNDPQPTIVDGBEGLIWVGPVLAFFCIVIAI 872

Qy	335 GSWTETHAVNAPTYKLWHDDETEYEIRV-LLTRPGEGGTGLPPPLITTKCAEPMRTP 393	Db	1747 ERSAYQYFVDPKA--EYMPQYILREFKVTDARDGSRTIRRQFDTW-PEGVPKT 1802
Db	777 G-----LTBETTSITVAYTTKGDR--SKPVVTTGAVPGR-- 814	Qy	1348 KRSFKLILQYKEKNGEGRITIHCUNGGSIGMFCAIGITVEMVRQNVDFVFA 1407
Qy	394 KTLKIAEIQARRIAVWDW-----ESLGYNITRCHTFNTVTCHYFRGNESKADCLDM 445	Db	1803 GEGPFDIGQVHKTCBQFGQ-DGPPTVHCSAGVFTGVPITLSIVLTERMRYEGVDMFQT 1861
Db	815 PTMMVSTTAHMTALLQWHPPKELPGFLGRL-----QYRADEARENTIDF 861	Qy	1408 VKTLENSKPNMVEABQYRCYDVALEYLES 1438
Qy	446 DPKAPOHVNLPPPTVNSLXKMLITNPGRKESBTIIQTEDVQGPVP---VKSQGT 501	Db	/ 1862 VKTURTORPAMVQTSDQYOLCYRALEYLG 1892
Db	862 GKDDQHFTVGLHKGATYIIFLAAKQRAGPGEFEKETIPEDASGFQNLRVGLTS 921		
Qy	502 SPENKIFLNKKBPL-DPQNLITOYEISSSSIRSFPDPAVVPAGQPOTVSLWNSTHRYFM 559		RESULT 9
Db	922 TTE---LAMDPPVLAERNGRITNTVYVVDINS-----QHELDQNTGDVHLTL 967	TDHUIK	leukocyte antigen-related protein precursor - human
Qy	560 HLHPGTTYOFFIRASTVKGFGPATAINVTTNISAPTLPDYEGVDASLNSETATTI--TVYL 617	N	Alternate names: leukocyte common antigen homolog
Db	968 GLKPDITYDKVRAHTSKGACP----LSPSIQSRTMP-MEQVPAKNFRVAAAMKTSVIL 1021	C	Species: Homo sapiens (man)
Qy	618 R--PAQAKA-----PISAYQIVV---- 634	C	Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
Db	1022 SWEVPSYSKAVPFPKLYNGSVEVDGHSMRKLIADLOPNTYESEVLMNRGTSAGGLQHL 1081	C	Accession: S03841; JL0051
Qy	635 -----EELLPHRTRKREAGAMECYQPVTYQONAMSGGAPYFAAELPP----GNL--- 679	R	J. Exp. Med. 168, 1523-1530, 1988
Db	1082 VSIRTAPDILPQKPLPASAFLPEDGRFLSLMPQVQDPSLIVSLWYFIVVVP-LDRVGNNLLAPR 1141	A	Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho
Qy	680 ---PE-----PAPETVGDNRTYQGFW 697	A	A; Reference number: JL0051; MUID:8903578; PMID:2972792
Db	1142 WSTPBEELDBLLEATEQQGBEKQRKRRQARLKEYVAAQYDELFBETFLGDKENRYGRY 1201	A	A; Accession: S03841.
Qy	698 NPPLAPRKGYNIYQAMSVKBEKTTQCRIAKTRATESEVPPAKQTDRVVKIAGS 757	A	A; Status: nucleic acid sequence not shown
Db	1202 NRPLSPDLISQCFLVSLKSLKEMPDQK---RYASSPPSDTEIVVQTPAQQOBE-FEMLWYT 1256	A	A; Molecule type: mRNA
Qy	758 AGILVFILLVVVLTIVKSKLAKERKDANGNTQBMETMVNAMDR--SYADQSTLHAE 814	C	Molecule type: mna
Db	1257 GPVLAVILILIVAI---LLFRKR-----RTISPSKSDQEOSTGLKDSLLAHS 1302	C	Residues: 1-1897 <STR>
Qy	815 DPLSTIFMDQHNFSPRYENHSATAESSRLDVPVYLCETGETSPYOTQGQJ-HPAIRADL 872	C	Cross-references: UNIPROT: P10586; EMBL: Y00815; PIDN: CA68754.1; PID: g34267
Db	1303 DPV-----EMRRL-----NYQTGPRDHPPTPITL 1328	C	C; Genetics:
Qy	873 LQHINLMKTSDSYKGKKEYESPFECQSAHSDVAKDQNRAKRNKGNIAYDHSRVILQV 932	F	F; 1-16/Domain: signal sequence #status Predicted <SIG>
Db	1329 ADNTERLKANDGLKLSQEYESIDPQQFTWENSNSEVNPKRNANVIAYDHSRVILJISI 1388	F	F; 17-1897/Domain: leukocyte antigen-related protein #status Predicted <MAT>
Qy	933 EDDPESDYINANYIDGQRFPHYIATQGPVHETTYDFWMRIWOESACTVMTLVEYGR 992	F	F; 18-197/Domain: extracellular #status Predicted <EXI>
Db	1389 DGVPESDYINANYIDGKONAYIATQGPVLPDTEMDFWMRNWEOQIATVMTRLEER 1448	F	F; 19-29/Domain: immunoglobulin homology <IMM2>
Qy	993 VKCYKYWP-DDTEVYGGDFKTYCIVMEPLAEYVVTFTLERRGYNEMIREYKQFHFTGWPDH 1051	F	C; Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
Db	1449 VKCDOWPARGTETYGLIQLVTLDVLLATYTMTRFLALKSGSSSKRELQFQMAWPW 1508	F	C; Keyphrases: phosphotyrosine kinase; protein-tyrosine phosphatase homology <IMM3>
Qy	1052 GYPHATGLLSFIRVKLNSPPSAGPPIVHCSAGGRTGYIVIDIMDMAERGVVDDY 1111	F	F; 20-48/Domain: fibronectin type III repeat homology <IMM4>
Db	1509 GVPEPPTPLAFLRVRVKAICNPLDAGPMVTHCSAGYGRGTFVIDAMLERMKHEKTVDIY 1568	F	F; 44-97, 146-197, 243-289/Disulfide bonds: #status Predicted
Qy	1112 NCVKRALSRISINMYOTEYQYTFIHDAILEACLGCTETAIIVCEFKAYFMDMIRDSQTNS 1171	F	F; 107, 245, 285, 711, 956/Binding site: carbohydrate <FN3D>
Db	1569 GHVTCMRSQARNYMQEIQDQTVFIREALLAEAMCGTHEVILRNLYAHIQLGQVPGESTV 1628	F	F; 1001-1078/Domain: fibronectin type III repeat homology <FN3E>
Qy	1172 HLKDEFOTLNSVTPLQACDSIACLPRNHDKNRFDMLPPDRCLPPLITDG-ESSNYI 1230	F	F; 1251-1274/Domain: transmembrane #status Predicted <IMM>
Db	1629 AMELIEFKLIL-AGSKARASRFISANLPCRFKNLNUINPYELTRVCLQPIRGVEGSDTYI 1686	Qy	F; 1275-1897/Domain: intracellular #status Predicted <INT>
Qy	1231 NAALMDSYRQPAFAFIVTQQLPNTVKDFTRLVLYDGTCTIVMNEVDL--SQGPQYWES 1288	Db	F; 1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
Db	1687 NASFLDGYRQOKAYIATQGQLAESTEDFWRMLWEHNSTIVMLTKLRENGRECKHQYWA 1746	Qy	F; 1365-1586/Domain: protein-tyrosine phosphatase homology <PRP1>
Qy	1289 EGMLRYGPQYECMSICSMDCDVINRIFRCNLTRPQEY-LMVQOFQVLYGWASHREVPGS 1347	Db	F; 1654-1877/Domain: protein-tyrosine phosphatase homology <PRP2>
		Qy	F; 44-97, 146-197, 243-289/Disulfide bonds: #status Predicted
		Db	F; 1538/Active site: Cys (phosphocysteine intermediate) #status Predicted
		Qy	F; 1544/Binding site: substrate phosphate (Arg) #status Predicted
		Db	F; 1829/Active site: Cys (phosphocysteine intermediate) #status Predicted
		Qy	F; 1835/Binding site: substrate phosphate (Arg) #status Predicted
			Query Match 19.6%; Score 1509; DB 1; Length 1897;
			Best Local Similarity 29.1%; Pred. No. 8.9e-94;
			Matches 464; Conservative 223; Mismatches 555; Indels 352; Gaps 59;
		Qy	69 PPENPQG---SYMIVDSSD-----HDPEGEKARIQLOPTMKNDTHCIDFSYLLYSQ 115
		Db	426 PPBENGVLVGRYRYVTPSRRPNAWHKHNTDAGLLTIVGSLPITYSL--RVLAFTA 483
		Qy	116 KGJLNPGTILNLYVRVNGKPLANPIWNTGFTGRDWLRAELAVSTFW--PNE---YQVIF 168
		Db	484 VGDGPSPTIQLVQVPAQP---ADRFQAE---VESDTRIQLSWLPPQERIIMYELVY 537

Db	165	ITWF--KDFLPVDPSTS-----	-NERIKQURSGGQIIESSEETDQGKTECVASNIS	211
Qy	196	--PHEPLIG-DVEVNAGONATEQCIATGRDAVHNKLWLRQRNG	235	
Db	212	AGVRYSSPANLYVVRVRRVARFSTLPSHIMPGENVNTICVAVGSPMVK-WMOGAED	270	
Qy	236	--EDIPVYQTKNNINHRPAASFRQLEQVTKTDDPLYRCVTSQSERGSGVSNFAOLIVRP	291	
Db	271	LTPEDDMVPG -RNV-----LELTIVKDSANYTCUAMSSLGV -IEVAQITVSL	317	
Qy	292	PRPIAPPOJLGVGPFTYLJQLNANSLLIGDPILKLEVEYRMTS --GSNTETHAYNAPTYK	349	
Db	318	PKAPPTPVVETTAATISITIWDSGN--PPVSVTIVYEYRSKSODGPYQIKEDITTRYS	374	
Qy	350	LWHLDPDTETEVIRUVLTLRPEEGGTGLPGPPLITRKCAFPMTPTKTLKAEIQARRIADV	409	
Db	375	IGGLSPNSETBIWW--SAVNSIGQCPSESVTRGEQAFASAARVNOQGRLMSSTMIIQ	432	
Qy	410	WES-----LGNTNTRCHTFNTVTCIHYFRGHINESKAQDCLMDPKAP----OHVYNH	456	
Db	433	WEBPVPNGDIRGIRV-----Y	467	
Qy	457	LPPYTNVSLKMILTNPEGKKESEETIIQT-----DEWDVPGPVPKSIQG-----	500	
Db	468	--DSLLTIVGVSLEDEETYTVRLAFTSVGDGPISDPIQVKTOQGVPGQPQMNFR	518	
Qy	501	--TSEBNKFLPNAKEPLDPGIRIYTOEYISS-----IRSFDPAVPVAGPPTVSNLW	551	
Db	519	AEAKTETSIWLSSPPRQE--IIVKYLEIFKEGDHGREYRNFED-----	561	
Qy	552	NSTHHVFMHLHPGTTYOFFTRASTYKGFGPAT-----AINVTT-----	589	
Db	562	-TTSEPTVEGIKPNTYEYFRLAARSALGLGAAFTPEVRTLQSILPKNPXKVMTKTSTVIL	620	
Qy	590	-----NISAPTLPLP---DVEG - VDASLNBTATIT-----	614	
Db	621	SWEFPNTNSPT -PYKIQNGLNYTDVDRGTTKLUITNLKPTHTPYNFVLMRGNNSMGGIQQ	679	
Qy	615	-----VLLRPAQAKGAPTSAYOIVV-----EELH	638	
Db	680	NVAWTAANMLSREPEVTHPDADEGNVVLVLPDKTSSVQAQAYIVVYBLRSRGQQFTN	739	
Qy	639	PHRTKREAGAMECYQ-----VPVTYQNMMSGGAPPYPAEFLPPGNLPEAPPFTVGDR	691	
Db	740	PLGSPPEEMMLEELQDIARIURRSURHSRQLDFPKP -IYARF--RSLPN -HFVLGDMK	794	
Qy	692	TYQCFWNPPPLAPRKGYNITYQAMSSVEKETKTOCVRIATAKEPEVY----PDPAKOT	747	
Db	795	HYDNFENRALEPGQRYVIFLAVLQ-EPE-----ATFAASPSDPIQLDNPDFPQTLI	845	
Qy	748	DRVVKIAGISAGILVPLLILVY-LIVKSKLAKKRKDGMNTROEMTMVNAMDRTYA	806	
Db	846	DGERGLIWWVGPVLAFFCIVTIAILYKPKDPSKRDSEPRTKCULNN-----A	896	
Qy	807	DQSTLHAEDPLSITMDQHINANTIDGQRPSHIATQGPVHETVYDFTWRMTWBQSCACIVNVT	865	
Db	897	EITPHHPKDPVE--MRRMF-----QTP -- GMWSHP	923	
Qy	866	AIRYADLQHINLMTSDSYGFKEYESEFEQGQSASWMDYKAQKDNQRAKQYGNJIAYDH	925	
Db	924	PIPSELABETEHKANDNIKLKLSQEYESIDPGQOFWTWENSYLNPKRNRYANVIYDHS	983	
Qy	926	RVIQPVDEDDPSDYINANTIDGQRPSHIATQGPVHETVYDFTWRMTWBQSCACIVNVT	985	
Db	984	RVILPIEGVGSYYINANVYDGRKQNDYIACTQPLPTEFGDWTRMWEQRATIVNVT	1043	
Qy	986	NLVVEGRVYKCYKWPD-DTEVYQGDFKVTCEMEPLAEXVTRTFLTERGYNEIREVKOFH	1044	
Db	1044	KLEBSRRIXKCDQWYWPGRGEPYPTPEFLARVYKTCNPDPAGP1VWHCSAGRTGCFLVDA	1104	
Qy	1045	FTGHDGQDGYHATGLLSIRRFLVLSNPPSAGIVWVHCSAGRTGCFLVDA	1104	
Db	1104	FTAWPDHGSPYEPYPTPEFLARVYKTCNPDPAGP1VWHCSAGRTGCFLVDA	1163	

QF	250-304	/Domain: immunoglobulin homology <IMM3>
PF	171-831	/Domain: fibronectin type III repeat domain homology <LAC>
PF	1293-1912	/Domain: leukocyte common antigen cytosolic domain homology
PF	1669-1892	/Domain: protein-tyrosine-phosphatase homology <PTP2>
PF	1553-1849	/Active site: Cys (phosphocysteine intermediate) #status predicted
PF	1559-1844	/Binding site: substrate phosphate (Arg) #status predicted
PF	1844-1850	/Active site: Cys (phosphocysteine intermediate) #status predicted
PF	1850-1855	/Binding site: substrate phosphate (Arg) #status predicted
Query	Match	19.5%; Score 1505.5; DB 2; Length 1912;
Best Local Similarity	29.3%	Pred. No. 1.6e-93;
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Qy	254	SFRLOEVTTKTDODLYRCVTCOSERGSVSNPAOLIVRE--PPRPIAPPOLIGV--GPTYLL 309
Qy	569	SYRQGLKPNLSLYFRLAARSPOQIGAST-AE[SARTMOSKSP]SAPPQDISCTSSPSSTIL 627
Qy	310	IQLNANSIIGDGPILK-EVEYRNTSGSSTETHAY----NAPTYKLWHLDPDTBEYTRV 363
Db	628	:VSWQOPPVKEQNGITTEYTKYTAVDGEKDTPKPHILGIPSDDTKYLLSEOLEKNTBEY--RI 685
Qy	364	LUTRPGBEGGTGLGPPLPLSRTKCAKMPMRPTPKTLKIAEQARRIAYDWE-----L 413
Db	686	TVTAAHTDVGPEESLUSVLJRTNEVDPSPGPRKVYEAVNSTSVDVSRSRSPVPNKQHGQIR 745
Qy	414	GYNITRCHTFENVTICHYFRGHN-----APDQHVYHLPPTYNVNSUKMLTNTNP-----436
Db	746	GYQV-----HYTMENGEKPQGPQMLKDVMLADAQWEEDDTDEHDMLISGLOPE 793
Qy	437	-----ESKAIDLMDMPK-----APDQHVYHLPPTYNVNSUKMLTNTNP-----473
Db	794	TSYSLTVAATTYTKGPGDARSCKPLVSTTGAVPGKRLVTH-----TOMNTALIONHPPVDT 849
Qy	474	-----GRK-----ESEETIIQPD-----486
Db	850	FGPLQGYRLKFGRKDMEPLLTLEFSEKEHFTADHKAGASYYVPRSLARNKVGFEEMVK 909
Qy	487	-----EDVPGSPVPDKPSLOGTSFENKFLWKPEPL--DNGITTYOEISYSSIRSFDPAPV 539
Db	910	EISIEEEVPTGFPQNHLSEGTTSVQLSNQWPPLAERNGNTITKTYLLRDINI--PLIP 967
Qy	540	VAG-----PPQTVSNLNSTHIVMLHPGTYQPFTRASTVKGFGPATAINVTNTNISAPT1 596
Db	968	MEQLLVPADTTMTLG-----LRKDPDTYDVKVRRAHTFSKGPGP-----YSVPVQFRTL 101
Qy	597	PDYEGVDASUNETATIT-VLRL--PAQAKGAP1SAYQI-----VYVELBHPRTKR--644
Db	1015	PVDQVPAKNTHVKAMKTKTSLSWEIPNTNSA--MMPFKLILYDGKMYBEVDGRTATORKL 107
Qy	645	-EAGAMECYQVPVTVQNAMSGGAPYFAAELPPG-----NLPE-- 681
Db	1073	VNLKDEKSYSFVLTNRGNSAGGLQHRTVAKTAPDYLRTKPAFIGTKNL.DGMGTTQLPVEP 113
Qy	682	----- 681
Db	1133	ANENIKGGYLLIIVPLKKSRGKPIKWESPDDEMELDLKEISRKRRLSTRYGREVBLKPV1 119
Qy	682	-----PAPFTGDNRTYQGFMNPPPLAPRKGYNYIQFQAMSSEKEKTKQCVRLATKAAT 734
Db	1193	AAHFDFDVLPTPLTGLDDKHKGFTVYKOLOSQEB-----NLPE-- 681
Qy	735	EEPEVTP--DPKQKTDVVKLAGISAGIL--VFILLVLLVILVKSKE-AKKRDAMGN 789
Db	1247	SDPVYMSMDLQPQPTIDEEGHIIWWGVPLAVVFICIVAILYKRKRAEDESRSKSSSTP13C 130
Qy	790	TROEMTHVNAMDRSYAQSQTSLHADPLSITEMDHOHNFSRPNYHNTATESSRLIDVPRV 849
Db	1307	NKEITSH-----HPTDPVLERLNL----- 132
Qy	850	LCEGTESPYOTGQL--HPAIRVADLJQHINLMKTSDSYGFKEKEYYESFFEGOSASWDVAKK 907
Db	1326	:-----FQPGMASHPP--IPLADHIBRLKANDNLKSQEYESIDPQQFTWEHSNL 137

Qy	908	DQEAKRNRYGNIAVDHSRVILQPVEDPSSDINYANVYDQEQRSPHYIATQGPVHETVY 967
Db	1378	EVNKPKNRVAIYDHSRVILSAEGIPGSDDVNYANVYDGYRKONAYIATQGSLPPEFG 1437
Qy	968	DWEMIWIQEOQSACIVMVNTLVEGRVKCYKWPD-DTEVYGDDEFKVTGEMPLAETYVRT 1026
Db	1438	DWFMIWEOQSACIVMVNTLVEGRVKCYKWPD-QTQWPSROTETGLVQVTLDTBLATYCVR 1497
Qy	1027	FTLERRGNEIREYKQFHFTGPWDHGVPYHATGLISFIRRYKLNSNPDPSAGPIVYHCSAGA 1086
Db	1498	FALYKGNSSEKREVRQFQFTAWPDHGVPERHTPFALFLRRYKTCNPDAQPMVHCSAGV 1557
Qy	1087	GRTGCVYIDIMDMAEREGVYDINCKAALSRRIMVQTEQYIFHDALLEACCGE 1146
Db	1558	GRTGCFVKAAYFDMIRIDSQTNSSHLKDQFDTLNSVTPLQAEDCETACIPLRNHDKNRF 1206
Qy	1147	TAIPCFCEVKAAYFDMIRIDSQTNSSHLKDQFDTLNSVTPLQAEDCETACIPLRNHDKNRF 1206
Db	1618	TEVPARNYLAIQKUTQIEGENVTGMELKEKLAS-SKAHTSRFRFSANLPCKPKFQLR 1675
Qy	1207	MDMLPDPDRCLPFLITIDG-BSSNYINAALMDSYROPAAFVITYOPLPNTVKDFWRLYDY 1265
Db	1676	VNINPYESTRVCLQPIRGVEGSDTYNAASFIDGYROQKAYIATQGPLETTEDFWRMWEH 1735
Qy	1266	GCTSTMVLMNEVLDL-SQGCPQYWPEEGMLYGPQIVCMCSMDCDVINRIRICNUJTRP 1323
Db	1736	NSTIVVMMLTKLREMGREKCHQYPAERSARQYFVDPMA--EVNMPQYILREFKYTDAA 1792
Qy	1324	QEGY-LMVQFOYLGWASHRREVPGSKRSFLKLQILOVKEWQEWKEGGRTI1HCLNGGR 1382
Db	1793	RDGQSRTRVQFQFTDW-PEQGVPKSGEGFIDFIGVQHTKTEOFQGQ-DGPISVHCSAGYGR 1850
Qy	1383	SGMFCAIGIVYEMVYKRONVYDVFHAVKTTLRNSKPNVNEAPEQYRFCTYDALEYLES 1438
Db	1851	TGFVFTLTSVLERMVEYGVWDIFQTVKMLRTQRPMVQTEDYQFSYRAEYLGLS 1906
RESULT 12		
A48758		protein-tirosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor -
C		Keywords: alternative splicing; phosphoprotein; fibronectin type III repeat homology <I>immuno-globulin homology</I>
C		Species: Rattus norvegicus (Norway rat)
C		Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C		Accession: A48758
R		Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.
J		Biol. Chem. 268, 19284-19291, 1993.
A		Title: Cloning and expression of two structurally distinct receptor-linked pro-
A		teins. Reference number: A48758; PMID:83374907; PMID:8396131
A		Status: preliminary
A		Molecule type: mRNA
A		Residues: 1-1496 <PAN>
A		Cross-references: GB:119180
A		Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 28. Phe
C		Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology <I>immuno-globulin homology</I>
C		Keywords: phosphoprotein; phosphoric monoester hydrolase
F	149-209	Domain: immunoglobulin homology <I>imm>
F	216-300	Domain: immunoglobulin homology <I>imm>
F	318-405	Domain: fibronectin type III repeat homology <I>FN3B>
F	411-504	Domain: fibronectin type III repeat homology <I>FN3B>
F	509-599	Domain: fibronectin type III repeat homology <I>FN3C>
F	600-684	Domain: leukocyte common antigen cytosolic domain homology <I>LAC>
F	880-1496	Domain: protein-tirosine-phosphatase homology <I>PTP2>
F	1156-1477	Domain: protein-tirosine-phosphatase intermediate #status predicted
F	1146/Binding site:	substrate phosphate (Arg) #status predicted
F	1129/Active site:	Cys (phosphocysteine intermediate) #status predicted
F	1135/Binding site:	substrate phosphate (Arg) #status predicted
Query Match	19.3%	Score 1490.5; DB 1; Length 1496;
Best Local Similarity	29.4%	Pred. No. 1..1e-92; 1..1

Qy	205	EVNAGONATFQCIATGRDAVHNKLW-LQRNG---EDIPVAQTKNINHRRFAASFRILQEV	260	Qy	1132	IFIHDAILEBACLGCTAIPCEFKAYFDMIRIDSQTNTSSHLCDFDTLNSVTPLQLAQED	1191				
Db	242	EIMPGENVNNTICVA/GSPMPYVK-IMQGADLTPTDDMPVG--RNV-----LELT	288	Db	1190	SFIHADLLAVGCENTTLEKSRVKDQYWPRTGTEYGFICV	1247				
Qy	261	TKTQDLYRCYTOSERGSVSNPAQILIVREPRPPIAPPOLLGVGPFTYLILQLNANSIIGD	320	Qy	1192	CSTACLPRAHDKNRPMMDLPPDRCLPFLITIDG-ESSNYINAALMSYROPAAPTIVTOYP	1250				
Db	289	DVKDSANPYCAYAMSNIGV-IEAVADITVSLKSLPKAPGTVENTATTTVWDAGNPDPV	347	Db	1248	SFTASLPCKNFKNRLVNLNLPYEESRVCLOPIRGVEGSDYNTASFDGYRKQAKATQGP	1307				
Qy	321	GPIIKEKEVTRMTSSWTHAVNAPTYKUWHLDDETEYIRV-ULTRAREGGTGLPGPP	379	Qy	1251	LPNTYKDFWRLVYDUGTSIVMVLNEVDL--SGQGCPQYWPEGMIRYGPLOVCMCSMDC	1308				
Db	348	SYVVLISIIKARM-GRIRSKKTSTTRYSGIGLSNSEEIWIWSAVNSGQA---PSSES	401	Db	1308	LAETTEDENRALWNENSTIVVMLTKLRENGREKCHQYPAERSARYQYFVUDPM--EY	1364				
Qy	380	LITRTPKAEPMRPTKTLKLAETIQARRIAYDVES-----LGVNITRCHTENVTCYH	431	Qy	1309	DVINRIFRICLNFNLTRQEGYLMVQOFQYLGWASHREVPGSKRSPLKLIOVEKWOEWKEG	1368				
Db	402	VVTRIGEQAPASAPRNVOAUNLSATMIVOWEEPVBNGLIRGTRV-----Y	448	Db	1365	NMPETVILREFKVTDARDGSQSTRV-QFTDW-PBQAKPSKGEGFIDFIGVHKTRQFPGQ-	1421				
Qy	432	FRGHNBESKAQCLDMDPKAPOHVNVNHLPPTNVSLKMLTNPGRKESETIITQ-----	485	Qy	1369	EGRTIITHCLNGGGRSGMFCAGIGIVYEMVKRQNIVDVFHAVKTILRNISKPNMVEAPEQYRFC	1428				
Db	449	Y-----TMEPEHHPVGWQKH-NVD-DSSLITVGSLLDETYTVRLAFTSV	492	Db	1422	DGPISHVCSAGVGRGTGVFTLTSIVLTERMYEGVVDIFQTVKVLKLTQRPMQTEDEYQFC	1481				
Qy	486	-DEDVPGPVWRSLOG-----TSPENKFLANWKEPLDNGITIOTYEIYSS---	530	Qy	1429	YDVAE	1434				
Db	493	GDGPLESDP1QVKTQGVPGQPMNLRAEAKSETSGLSWSAPROES--VTKYELLFREGDR	550	Db	1482	FOAALE	1487				
Qy	531	---IRSFDPAVPVAGPPQTVSNLNMSTHVFMLHPGCTYOFFTRASTYKGFGPATA-----	585	RESULT 13							
Db	551	GREVGETFDD-----TTAFVDEDKPNPEYAFRIAARPSPQGLAFTAVV	594	Qy	54489	Protein-Serine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor					
Qy	586	-----NVTINISAPTLP--DYEGVDSLNLSTATITI	614	N;Alternate names: MPTP delta type D precursor							
Db	595	RQRTQAIISPKNFKVTRMIMKTSVSLSWEFFDNTNSP-TPKIQTQNLGLTDVGRTTKKLI	653	N;Contains: protein tyrosine phosphatase, receptor type delta, splice form A							
Qy	615	VLLRP-----AQKQGAPSAYQVIVELPHPRYKREA-----GAWB	650	C;Species: Mus musculus (house mouse)							
Db	654	THLKPTHTFYNFLVTRGSIGGLQTV-----TARTAFNMLSGKPSVYAKPKNDGSIV	706	C;Accession: D54689; As4689							
Qy	651	CY----QVPTTYQONAMSGGAPYFAELP-----PCNLPE-----	681	A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized							
Db	707	VLPDPGQSPVTVQV-----YFTIVMVPLRKSRGQFPILLPSPEMDMLEELIQDLRSLR	758	A;Reference number: A54689; MUID:9336986; PMID:8355697							
Qy	682	-----PAPFTVGDNRTYQCFWNPPLAPRKGNYIQFQAMS	716	A;Status: preliminary							
Db	759	QRRSLRHRSROLEVPRPYIAARFSIILPAPVHPGNQKOYGFNDNRGIEPGRHYVLFVLA-----	816	A;Molecule type: mRNA							
Qy	717	VERETKTOCVRIATAATEPEVIT--PDIAKOTDRVKAGISAGLVILLIUVIT-LI	773	A;Cross-references: UNIPROT:Q64487							
Db	811	LQKNEPT---FAASPFSDPQFDLNPDPQIVDGEEGLIVWIGPVAVFICIVIAL	871	A;Experimental source: brain							
Qy	774	VKSKSLAKRKDKDAGNTQEMTHVNAMDRSYADQSTLHAEDPLSITFMQDHNNFSPRYEN	833	A;Note: sequence inconsistent with nucleotide translation							
Db	872	LYNKRPDSGRKDSEBRTKCILNN-----ADIAHPHPKDPE---MRRINF----	913	A;Sequence extracted from NCBI backbone (NCBIN:136522, NCBIP:136524)							
Qy	834	HSATAESSRLLDVPRYLCGCTESPQYTGQ-L-HPAIRVALLOQHINLMTSDSYGKFKEEB	892	C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology							
Db	914	-----QTP---GMLSHPPPTPITMAHEMERLKLNSLKSQEYE	949	C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoster hydrolysis							
Qy	893	SFFEQQSASVADFVAKRDQNAKRKNRGTNTIYDHSVILQVEDDPSSEPTNANTDGYORP	952	F;114-156/Domain: immunoglobulin homology <IMM3>							
Db	950	SIDPQQFWEHHSLEANRKPKNRYANVIADHSRVLQLEGIMSDTINANTDGYRQ	1009	F;114-156/Domain: fibronectin type III repeat homology <EN3A>							
Qy	953	SHYIATQGPVHETYVDFWMNIWOSACIYWMVNTLNUVEGRVKCYKWPD-DTEVYGFKEV	1011	F;1449-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>							
Db	1010	NAYATQGP1PETQDFWMNVWEOSATVMMTMLEEKSRVKDQYWPRTGTEYGFICV	1069	F;1449-1691/Domain: protein tyrosine phosphatase homology <PTP>							
Qy	1012	TCVEMEPPLABVIRTFLLERRGYNIRETKQFHPTGWPBHGVPYHATGILSFLRVLKLN	1071	F;1339/Active site: Cys (phosphocysteine intermediate) #status predicted							
Db	1070	TLLDTMELATECVRTEFLKINGSSKEKRVTHQFTAWPHGVPEYPTPLAFLRRVKTION	1129	F;1623/Active site: substrate phosphate (Arg) #status predicted							
Qy	1072	PPSAGPIVVHCSAGVGRGTCYIVDILJMAERGVVDDYCNCKALRSRINNVQTECY	1131	F;1629/Binding site: substrate phosphate (Arg) #status predicted							
Db	1130	PPDAGPVVHCSAGVGRGTCFIVDAMLERIRTEKTVDDVGHVTLMRSSRINVMQTEDQY	1189	Query Match Score 19.2%; Best Local Similarity 29.3%; Pred. No. 4.4e-92; Matches 418; Conservative 205; Mismatches 460; Indels 344; Gaps 43;							
Qy	311	QLNANSIIGDGPLILK-EVYRMSTSWSWTHA-----NAPTYKLWHDPLDTEYIRVL	364	Qy	254	SFRQLQBVTKMDQDLYRVCYTSERGSVSNFAOLIVREPPIAPPLQUGV--GPTYLLI	310				
Db	361	SYRLQLKPNSLYFRLSATSPQCLGAST-AEISARTMKQPSAPPQDISCTSPSSTSILV	419	Db	362	PSASGPVYVHCSAGVGRGTCFIVDAMLERIRTEKTVDDVGHVTLMRSSRINVMQTEDQY	364				

297 PVPNKOHGQIRGYQVT-----YYVRLENGBPRGQPIODVMLAEAQWREPEESSD 344
 Qy 453 --VDRHLPPTVNSLKM--_LITINDEGRKESEETIOTEDVFPGPVVKSLQ_GTSFENK 506
 Db 345 YETTISLTLPTTYSITVAAYTTKGDSGARSKPKVUTT----_GAVFAKNFRVAAAMKTS 399
 Qy 507 IFLNKKEPDLDNGIIQYEISYSSRSRSDPAPV--VAGPQQTVSNLWNSTPHVNMLHNG 564
 Db 400 VLLSHWP-----DSYSAVVPKLYNGQSVEVDGHMBKLADLQN 442
 Qy 565 TYQFFI--RASTVKSGPATAINTVNNTNISAPTLPDYEGYDAS--LNEATATT----- 614
 Db 443 TEYSFVLMMRNSSEAGLQLHVSIR----TAPDLLPQKLPASAFLDGRSPLSMPQVDD 497
 Qy 615 -----VLLRPAQAKGAPISA-----YQIVVBEI-----HPBRTKREAGAMEC 651
 Db 498 PSLVRFWFTIVVVPIDRGGENILAPRWTSPTEELDDELLAIEOEGBEKKRRRQAERLK- 556
 Qy 652 YQVPVITYQANMGGAPYFAELPPGNLPEAPFTVGDNRTYQGEWNPPLAPRKGYNIYF 711
 Db 557 -----PVAQV--DELPE--TTFLGDKNYRGEYNRLSPDLSYQCev 596
 Qy 712 QAMSSVEKETKTCQVYRATAKATEPEPVIPDPAKOTDRVYKIAIGTISAGLIVFLILLVYI 771
 Db 597 LASLKEPMDQK---RYASSPYSDETVQVTPAQOCQE-BEMLWVTPYLAVILILIVI 651
 Qy 772 LIVKSKLAKGRKDANGNTROEMTMNANDR--_SYADOSTLHAEDPLSITEMDHNFS 828
 Db 652 AI----LLFCKR-----RTHSPSSKDEQSICGLKDSILAHSSDPMEMRRLN----- 692
 Qy 829 PRYNEHSATAESESSLRLLDVPRLCEGTESPYTOQGLRPARYADLQHNUMLKTSYGFK 888
 Db 693 --YQTPCSASG-----CPNISMPD---_HPPITDLDNIEBLKANDGLKES 736
 Qy 889 BEYESPFEGOSASWDVAKDONRAKRYGNLTAYDHSRVTLIQPVBDPSSDYNANYTDG 948
 Db 737 QYEYESDGGQTWENSNEVYKPNKRNAYTAYDHSRVLRLTSIDGVPGPSDYNANYDG 796
 Qy 949 YQRPHSYIATQGPWHETVYDWFWMQEQSACIVWNTNUVEGRUKCYKWP-DDTEVIG 1007
 Db 797 YRKONAYIATQGPPLPMTGDFWRMWTMREQBKSRTVKCDQWPARTETTG 856
 Qy 1008 DEKVTCVEMPLAETYRTRFLERGYNEREVKOPHTGMWDHGSVPYHATGLLSPIRV 1067
 Db 857 LIQVTLTYBLATYTMRFLHKSSESSEBELRQFOQMAPDHCPEYPTPILAFLRV 916
 Qy 1068 KLSNPPSAGPIVVHCSAGAGTGCYIVIDIMDMAERGVDTYCNCKAALRSRRINMVT 1127
 Db 917 KACNPDLDAVPMVHCSAGVGRIGCFIVIDAMLERMKHETKTDIYGHVTMCRSQRYMVQT 976
 Qy 1128 EEQYIETHDALAEACLGETAIPVCEKAAYFDMIRIDSQTNSSHILKDFOTLNSVTPRL 1187
 Db 977 EDQYVTHEALLEAMCGHTEVLARNLYAHIQKLQGQVPGESVTALELPKLL--ANSKA 1034
 Qy 1188 QAEDCSTAICLPRNHDKNRFDMLPPDRCLPLPLITDG-ESSNYIAALMSYRQPAAFIV 1246
 Db 1035 HTSRFISANLPCNKFKNRDNIMPFLTRVCLQPFRVGESESDYTAASFLCYRQKAYIA 1094
 Qy 1247 TOYPLPNTRVDFWRLVYDYGCTSIVMLNEVDL--SOCGPQYWPPEECMLRYGPIOECMSC 1304
 Db 1095 TGPLAESTEDWWRMLWEHNSLTIWNLTKOREMGREKCHQWPAERSARYQFVVDPMIA- 1153
 Qy 1305 SMDCDVNRIFRICNUTRPOQETI-LMVQOFQYLGASHREYPGSKRSEFLKLIQVKEWQE 1363
 Db 1154 -EYNNEQYIUREFKYTDARDQCSRTRQFOTDW-PEQGVPKTGEGEFDFIGQVHKTKE 1210
 Qy 1364 EWKEGBERTRIHLCLNGGSRSMFCAGIUVENVRKONVUDPHAKTLLRASKPNVTEAPE 1423
 Db 1211 QFGQ-DSPVITYVHCSAGVGRIGCFITISLVEFMRYGVDMQFQTTLTQRPMVQTED 1269
 Qy 1424 QYRFCYTDVALEYLES 1438
 Db 1270 QYQLCYTRAALSYLGS 1284

Scoring table: BIOSUM62									
Gapop 10.0 , Gapext 0.5									
Searched: 1612378 seqs, 512079187 residues									
Total number of hits satisfying chosen parameters:									
1612378									
Minimum DB Seq length: 0									
Maximum DB Seq length: 2000000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database : UniProt 03.1*									
1: uniprot_sprot:*									
2: uniprot_trembl:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.									
Score									
Match									
Length									
DB									
ID									
Description									

1	7638	99.7	1439	1	PTPK_HUMAN	Q15262 homo sapien	Q15262 homo sapien	SEQUENCE FROM N.A.	RP
2	7673.3	99.5	1440	2	086N12	Q8wJ2 homo sapien	Q8wJ2 homo sapien	SEQUENCE FROM N.A.	RP
3	7670.5	99.5	1440	2	Q68DT8	Q6dct8 homo sapien	Q6dct8 homo sapien	SEQUENCE FROM N.A.	RP
4	751	98.2	1457	1	PTPK_MOUSE	P35222 mus musculus	P35222 mus musculus	MEDLINE:97199372; PubMed=8653237; DOI=10.1074/jbc.271.28.16712;	RX
5	4807	62.4	1452	1	PTPM_HUMAN	P28827 homo sapien	P28827 homo sapien	Yang Y., Gil M.C., Choi B.Y., Park S.H., Pyun K.H., Ha H.; "Molecular cloning and chromosomal localization of a human gene homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine phosphatase." Gene 186:77-82 (1997).	RA
6	4791	62.1	1452	1	PTPM_MOUSE	P28828 mus musculus	P28828 mus musculus	Fuchs M., Mueller T., Lerch M., Ulrich A.; "Association of human protein-tyrosine phosphatase kappa with members of the armadillo family"; J. Biol. Chem. 271:16712-16719 (1996).	RA
7	4794	62.1	1486	2	Q68PM4	Q68PM4 mus musculus	Q68PM4 mus musculus	RT	RT
8	4776	61.3	1390	2	Q86V60	Q86V60 homo sapien	Q86V60 homo sapien	"FUNCTION: Regulation of processes involving cell contract and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/plakophilin. Beta-catenin may be a substrate for the catalytic activity of PTP-kappa."	RL
9	4697.5	60.9	1434	2	Q6YI48	Q5yI48 gallus gallus	Q5yI48 gallus gallus	CC	CC
10	4632	60.1	1436	2	Q00197	Q00197 homo sapien	Q00197 homo sapien	"SUBCELLULAR LOCATION: Type I membrane protein; at adherens junctions."	CC
11	4623	60.0	1436	2	Q92850	Q92850 homo sapien	Q92850 homo sapien	"TISSUE SPECIFICITY: High levels in lung, brain and colon; less in liver, pancreas, stomach, kidney, placenta and mammary carcinoma."	CC
12	4608.5	59.8	1436	2	Q35564	Q35564 mus musculus	Q35564 mus musculus	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
13	4602.5	59.7	1436	2	P70125	P70125 mus musculus	P70125 mus musculus	"SIMILARITY: Contains 1 immunoglobulin-like C2-type domain."	CC
14	4588.5	59.5	1454	1	PTPT_MOUSE	Q9pm00 mus musculus	Q9pm00 mus musculus	"SIMILARITY: Contains 1 MAM domain."	CC
15	4581.5	59.4	1439	2	P78379	P78379 homo sapien	P78379 homo sapien	"SIMILARITY: Contains 2 protein-tirosine phosphatase domains."	CC
16	4564	59.2	1463	1	PTPT_HUMAN	Q14522 homo sapien	Q14522 homo sapien	"SIMILARITY: Contains 4 fibronectin type III domains."	CC
17	4550	58.6	1434	2	Q6E5N7	Q6E5N7 brachydanio	Q6E5N7 brachydanio	"SIMILARITY: Contains 1 immunoglobulin-like C2-type domain."	CC
18	4374.5	56.7	1442	2	Q92735	Q92735 homo sapien	Q92735 homo sapien	"SIMILARITY: Contains 1 MAM domain."	CC
19	4352	56.5	1430	1	PTPU_HUMAN	Q92729 homo sapien	Q92729 homo sapien	"SIMILARITY: Belongs to the protein-tyrosine phosphatase family."	CC
20	4343	56.3	844	2	Q8C462	Q8C462 mus musculus	Q8C462 mus musculus	"SIMILARITY: Contains 1 receptor class 2B subfamily."	CC
21	3481	45.2	1195	2	Q9PDR2	Q9PDR2 xenopus laevis	Q9PDR2 xenopus laevis	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
22	2611	34.4	492	2	Q8IV94	Q8IV94 homo sapien	Q8IV94 homo sapien	"SIMILARITY: Contains 1 immunoglobulin-like C2-type domain."	CC
23	2615	33.9	990	2	Q6PDN0	Q5pdn0 mus musculus	Q5pdn0 mus musculus	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
24	2518.5	32.7	502	2	Q9WUJ3	Q9wuj3 rattus norvegicus	Q9wuj3 rattus norvegicus	"SIMILARITY: Contains 1 immunoglobulin-like C2-type domain."	CC
25	2255	29.3	465	2	Q9IB39	Q9ib39 potamotrygon	Q9ib39 potamotrygon	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
26	1913	24.8	617	2	Q66JY9	Q66JY9 mus musculus	Q66JY9 mus musculus	"SIMILARITY: Contains 1 immunoglobulin-like C2-type domain."	CC
27	1706	22.1	542	2	P70643	P70643 rattus norvegicus	P70643 rattus norvegicus	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
28	1539	20.0	1788	2	Q9IAJ0	Q9iaj0 xenopus laevis	Q9iaj0 xenopus laevis	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
29	1534.5	19.9	1502	2	Q9UM81	Q9um81 homo sapien	Q9um81 homo sapien	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
30	1533.5	19.9	1529	2	Q6ZG46	Q6zg46 mus musculus	Q6zg46 mus musculus	"SIMILARITY: Contains 1 fibronectin type III domains."	CC
31	1529.5	19.8	1501	2	Q9QH00	Q9qh00 rattus norvegicus	Q9qh00 rattus norvegicus	"SIMILARITY: Contains 1 fibronectin type III domains."	CC

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Query	Match	Score	DB 1;	Length	1439;
	Best Local Similarity	99.7%			
	Matches	1436;	Conservative	0;	
	2;	Mismatches	1;	Indels	0;
				Gaps	0;
Qy	1	MDTTAAALPAFVALIILSPNPILGSAQGOFSSAGGCTPDDGPACDYHODLYDDFEWVHV	60		
Db	1	MDTTAAALPAFVALIILSPNPILGSAQGOFSSAGGCTPDDGPACDYHODLYDDFEWVHV	60		
Qy	61	SAQEPPHYPPEPMPOGSYMIIVDSSDHDPGEKARLQLQPTMKENDTHC1DFSYLLSQSGKLNP	120		
Db	61	SAQEPPHYPPEPMPOGSYMIIVDSSDHDPGEKARLQLQPTMKENDTHC1DFSYLLSQSGKLNP	120		
Qy	121	GTLNIVLVRNGPPLANPIWNVTGFTGRDWLRALAVSTFWPNYQVIFRAEVSGRSGYI	180		
Db	121	GTLNIVLVRNGPPLANPIWNVTGFTGRDWLRALAVSTFWPNYQVIFRAEVSGRSGYI	180		
Qy	181	AIDDIQVLSPYCDKSPHFLRIGDVEVNAGQNAFCIATGRDAVHNKLWLQRNRGDEDIPV	240		
Db	181	AIDDIQVLSPYCDKSPHFLRIGDVEVNAGQNAFCIATGRDAVHNKLWLQRNRGDEDIPV	240		
Qy	241	AQTQNINHRRAAIFIQLQEVTKTDQDLYRCYTOSERGSVSNPAQLIIREPRPPIAPPOL	300		
Db	241	AQTQNINHRRAAIFIQLQEVTKTDQDLYRCYTOSERGSVSNPAQLIIREPRPPIAPPOL	300		
Qy	301	LGVGPIYTLIQLQANSITGDGPBILKEVEYRMTSGSMWTHAVNAPTYKLWHLDDEYE	360		
Db	301	LGVGPIYTLIQLQANSITGDGPBILKEVEYRMTSGSMWTHAVNAPTYKLWHLDDEYE	360		
Qy	361	IRVLJTRPGEGETGLCPPLITRTKCAEPMRTPKTLKIAEIQARRIAYDVWESLGYNITRC	420		
Db	361	IRVLJTRPGEETGLCPPLITRTKCAEPMRTPKTLKIAEIQARRIAYDVWESLGYNITRC	420		
Qy	421	HTFNVNTICHYFRGHNESKADCLDMPKAPOHQVNHLPYTNSLKMILTNPEGRESEE	480		
Db	421	HTFNVNTICHYFRGHNESKADCLDMPKAPOHQVNHLPYTNSLKMILTNPEGRESEE	480		
Qy	481	TIIQTEDEDPGPGEVPTKSLQGTSFENKFLNWKEPPLDPNGIITOTOEISYSSIRSFPAPVY	540		
Db	481	TIIQTEDEDPGPGEVPTKSLQGTSFENKFLNWKEPPLDPNGIITOTOEISYSSIRSFPAPVY	540		
Qy	541	AGPPOTVSNLNISTHNVPMHLHPGTYOFFIRASTKCFGPATAINVTNTNISAPLDPYE	600		
Db	541	AGPPOTVSNLNISTHNVPMHLHPGTYOFFIRASTKCFGPATAINVTNTNISAPLDPYE	600		
Qy	601	GVDASINBNETATTITVILRPAQKGAPISAYQIVVEELHPHTKREGAMECYQVFTYQN	660		
Db	601	GVDASINBNETATTITVILRPAQKGAPISAYQIVVEELHPHTKREGAMECYQVFTYQN	660		
Qy	661	AMSGGAAFYFAELPGLNLPAPAPFTYQGFNNPLAPAKGTYQVFTYQN	720		
Db	661	AMSGGAAFYFAELPGLNLPAPAPFTYQGFNNPLAPAKGTYQVFTYQN	720		
Qy	721	TKTQCRVIATKATEEPIVDPDKAQDRVKLAGISAGILVILLIILVFKSKLA	780		
Db	721	TKTQCRVIATKATEEPIVDPDKAQDRVKLAGISAGILVILLIILVFKSKLA	780		
Qy	781	KKRKDAMGNTROEMTMVNAMDRSYADOSTLHAEDPLSTTMDONFSPRYENHATAES	840		
Db	781	KKRKDAMGNTROEMTMVNAMDRSYADOSTLHAEDPLSTTMDONFSPRYENHATAES	840		
Qy	841	SRLLDVPRYLCEGTEPSYQTGOLHPATRVDLQHINLMKTSDFYGFKEEYESPFEGQSA	900		
Db	841	SRLLDVPRYLCEGTEPSYQTGOLHPATRVDLQHINLMKTSDFYGFKEEYESPFEGQSA	900		
Qy	901	SWDVAKDQNRAKRNRYGNLIAUDHSRVLQVYEDPSSDYNANYIDGYORPSHVIATQG	960		
Db	901	SWDVAKDQNRAKRNRYGNLIAUDHSRVLQVYEDPSSDYNANYIDGYORPSHVIATQG	960		
Qy	961	PVHETYYDFWRMWTIWOEQSACIYMTNLVEGRVYCKWPDDTFVYGDFFKTVCMEMPLA	1024		
Db	961	PVHETYYDFWRMWTIWOEQSACIYMTNLVEGRVYCKWPDDTFVYGDFFKTVCMEMPLA	1024		
Qy	1021	EYVVRFTLERRGCVNIREVKOFHETGMPDHGVPYHATSSLFIRVKLNSNPPSAGPIVV	1080		

Db	1021	BYVVRTFTLERRGNEIREVKQFHTFGWSDHGVYHATCULLSFRRVKLSNPSAGP1V	1080		DR PRINTS; PRO00700; PRTPHPHTASE.
Qy	1081	HCSAGAGRGCYIVDIMDMAEREGVVIYNCVKALRSRINNQTEQQYIFHDALLE	1140		DR SMART; SM00006; FN3; 3.
Db	1081	HCSAGAGRGCYIVDIMDMAEREGVVIYNCVKALRSRINNQTEQQYIFHDALLE	1140		DR SMART; SM000137; MAM; 1.
Qy	1141	AICLGETAIPVCEPKAAYDMIRDSQTNSHSLKDEFQTLNSVTPLQAEQDCSTAC1PRN	1200		DR SMART; SM00194; PTPC; 2.
Db	1141	AICLGETAIPVCEPKAAYDMIRDSQTNSHSLKDEFQTLNSVTPLQAEQDCSTAC1PRN	1200		DR PROSITE; PS50853; FN3; 1.
Qy	1201	HDXKRFMDMLPPDRCLPFLITIDESSNNINAALMDSYFQPAFIVTQPLPNTVKDFWR	1260		DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
Qy	1201	HDXKRFMDMLPPDRCLPFLITIDESSNNINAALMDSYFQPAFIVTQPLPNTVKDFWR	1260		DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
Db	1201	HDXKRFMDMLPPDRCLPFLITIDESSNNINAALMDSYFQPAFIVTQPLPNTVKDFWR	1260		DR PROSITE; PS50055; TYR_PHOSPHATASE_2.
		Glycoprotein. Hydrolase; Receptor.			KW
		SEQUENCE 1440 AA; B140BC621878586A CRC64;			SQ
Qy	1261	LVDYDGCTSIVMNLNEVDLQGCPQWPEGLRGPIQECMSMCDTIVNIFRICNL	1320		Query Match 99.5%; Score 7673.5; DB 2; Length 1440;
Db	1261	LVDYDGCTSIVMNLNEVDLQGCPQWPEGLRGPIQECMSMCDTIVNIFRICNL	1320		Best Local Similarity 99.7%; Pred. No. 0; Matches 1; Mismatches 1; Indels 1; Gaps 1;
Qy	1321	TRPQEGYLNVQFOQLGNASHREVPGSKRSFELKLILQVKEKWQBEWKEGRGRTIHCING	1380		Matches 1436; Conservative 1;
Db	1321	TRPQEGYLNVQFOQLGNASHREVPGSKRSFELKLILQVKEKWQBEWKEGRGRTIHCING	1380		1 MDITAAAALPAFAVALLLSPWPWLGSAQGSAGGCTPFDGPGACDHYHQDLYDDFEWTHV 60
Qy	1381	GRSGMFCAIGIIVVEMVKRNQVVDVFHAVTLLRNSKPNMVAPEQYRFYCVDALYELESS	1439		Db 1 MDITAAAALPAFAVALLLSPWPWLGSAQGSAGGCTPFDGPGACDHYHQDLYDDFEWTHV 60
Db	1381	GRSGMFCAIGIIVVEMVKRNQVVDVFHAVTLLRNSKPNMVAPEQYRFYCVDALYELESS	1439		61 SAQEPHILPPEMPQGSYNTIVDSSDHDPSEKARLQLQPTMKENDTHCIDFSYLLYSQKG1NP 120
Qy	1440	GTUNLIVRNVNGKPLANP1WNVTCFTGRWLRAIASFWPNPYQVITAEVGGRSGYI 180		Db 61 SAQEPHILPPEMPQGSYNTIVDSSDHDPSEKARLQLQPTMKENDTHCIDFSYLLYSQKG1NP 120	
Db	1440	GTUNLIVRNVNGKPLANP1WNVTCFTGRWLRAIASFWPNPYQVITAEVGGRSGYI 180		Qy 121 GTUNLIVRNVNGKPLANP1WNVTCFTGRWLRAIASFWPNPYQVITAEVGGRSGYI 180	
Qy	181	AIDDIQVLISYPCKSKPSHFLRLGDOEVNAGQNAFCQCIATGRDAVHNLWLQRNGEDIPV	240		Db 121 GTUNLIVRNVNGKPLANP1WNVTCFTGRWLRAIASFWPNPYQVITAEVGGRSGYI 180
Db	181	AIDDIQVLISYPCKSKPSHFLRLGDOEVNAGQNAFCQCIATGRDAVHNLWLQRNGEDIPV	240		Qy 181 AIDDIQVLISYPCKSKPSHFLRLGDOEVNAGQNAFCQCIATGRDAVHNLWLQRNGEDIPV 240
Qy	241	AQTKNINRRAFSRLOEVTKDQDLYRCVTOSERGSCVSNPAQLTVRBPPIPAPPOL 300		Db 181 AIDDIQVLISYPCKSKPSHFLRLGDOEVNAGQNAFCQCIATGRDAVHNLWLQRNGEDIPV 240	
Db	241	AQTKNINRRAFSRLOEVTKDQDLYRCVTOSERGSCVSNPAQLTVRBPPIPAPPOL 300		Qy 241 AQTKNINRRAFSRLOEVTKDQDLYRCVTOSERGSCVSNPAQLTVRBPPIPAPPOL 300	
Qy	301	LGVGPTTYLIQIQLNANSITGDGPILKEYRATISGSWTEHATAPTYKLWHDLPDTETB 360		Db 301 LGVGPTTYLIQIQLNANSITGDGPILKEYRATISGSWTEHATAPTYKLWHDLPDTETB 360	
Db	301	LGVGPTTYLIQIQLNANSITGDGPILKEYRATISGSWTEHATAPTYKLWHDLPDTETB 360		Qy 301 LGVGPTTYLIQIQLNANSITGDGPILKEYRATISGSWTEHATAPTYKLWHDLPDTETB 360	
Qy	361	IRVILTRDGEGGTGLPGPPLITRTKACPMRTPTKLKIAEQARRIAYDWESGYNITRC 420		Db 361 IRVILTRDGEGGTGLPGPPLITRTKACPMRTPTKLKIAEQARRIAYDWESGYNITRC 420	
Db	361	IRVILTRDGEGGTGLPGPPLITRTKACPMRTPTKLKIAEQARRIAYDWESGYNITRC 420		Qy 361 IRVILTRDGEGGTGLPGPPLITRTKACPMRTPTKLKIAEQARRIAYDWESGYNITRC 420	
Qy	421	HTFNFVTCIHYFRGHNESKADCLDMDPKAQHVNHLPYTNVSLKMILTNPEKESSE 480		Db 421 HTFNFVTCIHYFRGHNESKADCLDMDPKAQHVNHLPYTNVSLKMILTNPEKESSE 480	
Db	421	HTFNFVTCIHYFRGHNESKADCLDMDPKAQHVNHLPYTNVSLKMILTNPEKESSE 480		Qy 421 HTFNFVTCIHYFRGHNESKADCLDMDPKAQHVNHLPYTNVSLKMILTNPEKESSE 480	
Qy	481	TIIOTDDEVPGPVPKSLQGTSPENK1PLWKPLPDKPGLTQTYEISYSSIRFDPAVEV 540		Db 481 TIIOTDDEVPGPVPKSLQGTSPENK1PLWKPLPDKPGLTQTYEISYSSIRFDPAVEV 540	
Db	481	TIIOTDDEVPGPVPKSLQGTSPENK1PLWKPLPDKPGLTQTYEISYSSIRFDPAVEV 540		Qy 481 TIIOTDDEVPGPVPKSLQGTSPENK1PLWKPLPDKPGLTQTYEISYSSIRFDPAVEV 540	
Qy	541	AGPPQTISNLWISTHAYPMHLHPTGTTQFFIRASTVGKFGPATAINVTNNISAPTLPDYE 600		Db 541 AGPPQTISNLWISTHAYPMHLHPTGTTQFFIRASTVGKFGPATAINVTNNISAPTLPDYE 600	
Db	541	AGPPQTISNLWISTHAYPMHLHPTGTTQFFIRASTVGKFGPATAINVTNNISAPTLPDYE 600		Qy 541 AGPPQTISNLWISTHAYPMHLHPTGTTQFFIRASTVGKFGPATAINVTNNISAPTLPDYE 600	
Qy	601	GYDASLNETATTITVLLRPAQAKGAPASYQIVTELEPHRTKREAGAMECYOVTYVQN 660		Db 601 GYDASLNETATTITVLLRPAQAKGAPASYQIVTELEPHRTKREAGAMECYOVTYVQN 660	
Db	601	GYDASLNETATTITVLLRPAQAKGAPASYQIVTELEPHRTKREAGAMECYOVTYVQN 660		Qy 601 GYDASLNETATTITVLLRPAQAKGAPASYQIVTELEPHRTKREAGAMECYOVTYVQN 660	
Qy	661	AMGGAPYFYAASLPGNLPEPAFPFTVGDNRITYQFGNNPLAPRKGNIYFQAMSVERE 720		Db 661 AMGGAPYFYAASLPGNLPEPAFPFTVGDNRITYQFGNNPLAPRKGNIYFQAMSVERE 720	
Db	661	AMGGAPYFYAASLPGNLPEPAFPFTVGDNRITYQFGNNPLAPRKGNIYFQAMSVERE 720		Qy 661 AMGGAPYFYAASLPGNLPEPAFPFTVGDNRITYQFGNNPLAPRKGNIYFQAMSVERE 720	
Qy	721	TKTQCVRATKATEEEVIPPAKQTDRVVKIAGISAGLYVILLVLLVLLIVKSKL 779		Db 721 TKTQCVRATKATEEEVIPPAKQTDRVVKIAGISAGLYVILLVLLVLLIVKSKL 779	
Db	721	AKERKDAMGNTROEMTHVNANDRSYADOSTLHAEDPLSITFMQHNSPRYENHSATAE 839		Qy 721 AKERKDAMGNTROEMTHVNANDRSYADOSTLHAEDPLSITFMQHNSPRYENHSATAE 839	

Db	781	AKRKDAMGNTRQEMTHMNAMDYSADQSTLHAEDPLSITFMQDHNFSPRYENHSATAE	840	DR Pfam; PF00629; MAM; 1.
Qy	840	SSRLDVPRVLCGESPSYQTGQLHPAIRYADLQHINMKTSDDSYGFKEEYESSEFFEGS	899	DR Pfam; PF00103; Y_phosphatase; 2.
Db	841	SSRLDVPRVLCGESPSYQTGQLHPAIRYADLQHINMKTSDDSYGFKEEYESSEFFEGS	900	DR PRINTS; PR00020; MANDOMAIN.
Db	900	ASWDYAKDQDNRAKRYGNITAYDHSRVLIQPVEDPSSDYINANYIDGQRPHYIATQ	959	DR PRINTS; PR00700; PRTYPPHTASE.
Qy	901	ASWDYAKDQDNRAKRYGNITAYDHSRVLIQPVEDPSSDYINANYIDGQRPHYIATQ	960	DR SMART; SMM04099; FN3; 3.
Db	901	GPVHETVYDFWRMIVQEOSACIVMTNLVAGVRYCYKWPDDTEVYGFKEVTCYEMEPY	1019	DR SMART; SMM0137; MAM; 1.
Qy	960	GPVHETVYDFWRMIVQEOSACIVMTNLVAGVRYCYKWPDDTEVYGFKEVTCYEMEPY	1019	DR SMART; SMM0194; PTPC; 2.
Db	961	GPVHETVYDFWRMIVQEQSACIVMTNLVAGVRYCYKWPDDTEVYGFKEVTCYEMEPY	1020	DR PROSITE; PS50056; TYR_PHOSPHATASE; 1; 2.
Qy	1020	AEVYVRTFTLERGYNBIREVKQFETGMDPEGVYDLYNCYKAFLSRIRNNVQTEQYIYTHDAL	1079	DR PROSITE; PS50055; TYR_PHOSPHATASE; 2; 2.
Db	1021	AEVYVRTFTLERGYNBIREVKQFETGMDPEGVYDLYNCYKAFLSRIRNNVQTEQYIYTHDAL	1080	DR Glycoprotein; Hypothetical protein.
Qy	1080	VHCSAGAGRIGGYIVIDIMLDMAEREGVYDLYNCYKAFLSRIRNNVQTEQYIYTHDAL	1139	DR SEQUENCE 1440 AA; 162129 MW; 41BA5E4D6E0C0359 CRC64;
Db	1081	VHCSAGAGRIGGYIVIDIMLDMAEREGVYDLYNCYKAFLSRIRNNVQTEQYIYTHDAL	1140	Query Match Score 99.5%; Best Local Similarity 99.7%; Matches 1455; Conservative 1; Mismatches 0; Gaps 1;
Qy	1140	EACLGCTEAIPVCEFKAYAFDMIRIDSQNTSSHLDDEFOTLNSTVPRLOAEDCSTACLPR	1199	Qy 1 MDTTAAALPAFAVALLLSPWPLGLSAQGFSAGGCTFDGPGACDYHDLYDDFEWYHV 60
Db	1141	EACLGCTEAIPVCEFKAYAFDMIRIDSQNTSSHLDDEFOTLNSTVPRLOAEDCSTACLPR	1200	Db 1 MDTTAAALPAFAVALLLSPWPLGLSAQGFSAGGCTFDGPGACDYHDLYDDFEWYHV 60
Qy	1200	NHDKNRFMDMLPPDCICLPFLITIDESSESSNTYNAALMDSYSPQAFAITQYPLPLSTVKDWW	1259	Qy 61 SAQSPHYP LPPEMPQGSYMLVQDSSHDPGCEKARLQOPTMKENDTHCIDFSYLYSQKGJNLP 120
Db	1201	NHDKNRFMDMLPPDCICLPFLITIDESSESSNTYNAALMDSYSPQAFAITQYPLPLSTVKDWW	1260	Db 61 SAQSPHYP LPPEMPQGSYMLVQDSSHDPGCEKARLQOPTMKENDTHCIDFSYLYSQKGJNLP 120
Qy	1260	RLVYDYGCTSIVMLNEVDSLQSGCPQYVWPEGMRLYGPPIQVECMCSMDDCDVNRIFRICN	1319	Qy 121 GTANILVRNKGPLANP IWNVTGTTGRDWLRAELAVSFMPNEYQVIFRAEVSGRSRSGYI 180
Db	1261	RLVYDYGCTSIVMLNEVDSLQSGCPQYVWPEGMRLYGPPIQVECMCSMDDCDVNRIFRICN	1320	Db 121 GTANILVRNKGPLANP IWNVTGTTGRDWLRAELAVSFMPNEYQVIFRAEVSGRSRSGYI 180
Qy	1320	LTRPOFGYLMVQQFOYLGLWASHREVGSKRSFLKLQLQVKWQEEWKEGEGRTHICNG	1379	Qy 181 ADDDQVLISYPCDKSPHFLRLGDVBNAGONATFOCIATGRDAVHKCWLQRNGEDIPV 240
Db	1321	LTRPOFGYLMVQQFOYLGLWASHREVGSKRSFLKLQLQVKWQEEBEGRTIHCNG	1380	Db 181 ADDDQVLISYPCDKSPHFLRLGDVBNAGONATFOCIATGRDAVHKCWLQRNGEDIPV 240
Qy	1380	GGRSGMFCAIGIVVENVVKRQNVDYFHAKVTKLRSNSKPNTMVAECYRFCDVALEYLESS	1439	Qy 241 ACTKININHPRFAASFLRQEVTKTQDLYBCYTOSERGSGSVSNFAQLIVREPPTAPPQL 300
Db	1381	GGRSGMFCAIGIVVENVVKRQNVDYFHAKVTKLRSNSKPNTMVAECYRFCDVALEYLESS	1440	Db 241 ACTKININHPRFAASFLRQEVTKTQDLYBCYTOSERGSGSVSNFAQLIVREPPTAPPQL 300
Qy	301	LGVGETTYLJLQJLANSIIGDGPITIKEKEYRMGSWTETHANAPTYKLWHLDDTEYE	360	Qy 301 LGVGETTYLJLQJLANSIIGDGPITIKEKEYRMGSWTETHANAPTYKLWHLDDTEYE 360
Db	302	LGVGETTYLJLQJLANSIIGDGPITIKEKEYRMGSWTETHANAPTYKLWHLDDTEYE	360	Qy 361 IRVLLTRPGEFGGTGPGPPLIITRKYCAEPRTPKLTAETQARRIAVDWEISLGYNITRC 420
Qy	361	AC Q68DT8 PRELIMINARY; PRT; 1440 AA.		Db 361 IRVLLTRPGEFGGTGPGPPLIITRKYCAEPRTPKLTAETQARRIAVDWEISLGYNITRC 420
AC	Q68DT8			
DT	25-OCT-2004	(TREMBLrel. 28, Created)		
DT	25-OCT-2004	(TREMBLrel. 28, Last sequence update)		
DE	Hypothetical protein	DKEpp6632268;		Qy 421 HTFNTVTCYHYFRGHINESKADCLMDPDKAHOHQVYVNLPPYTNSKMLTNPGRKESEE 480
GN	Name=DKPZp86C2268;			Db 421 HTFNTVTCYHYFRGHINESKADCLMDPDKAHOHQVYVNLPPYTNSKMLTNPGRKESEE 480
OS	Homo sapiens (Human)			
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. NCBI TaxID=9606;			
OX				
RN	[1]	SEQUENCE FROM N.A. TISSUE=Endometrium carcinoma cell line;		Qy 481 TIIQDDEDYPGPVPKSLQGTSFENKIFLANKWEPLDPNGITQTYISYSSIRSFPAPVY 540
RP		The German cDNA Consortium; Oettawaelder B., Deutschenbaur S., Schaiapp A., Newes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2004) to the ENBIL/GenBank/DBJ databases.		Db 481 TIIQDDEDYPGPVPKSLQGTSFENKIFLANKWEPLDPNGITQTYISYSSIRSFPAPVY 540
RG		EMBL; CR749277; CAH18132.1; -		Qy 541 AGPPOTVSNIWNSTHVFMLHPGTYQFPIRASTVKGFSPATAINVNTNISAPLPLDYE 600
RA		InterPro; IPR003961; FN III.		Db 541 AGPPOTVSNIWNSTHVFMLHPGTYQFPIRASTVKGFSPATAINVNTNISAPLPLDYE 600
RL		InterPro; IPR008957; FN III-like.		Qy 601 GVDASLINEATTITVLLPRAQAKGAPISAYQVYELPHRTKREAGAMYCYOVPVTYQN 660
DR		InterPro; IPR003599; Ig.		Db 601 GVDASLINEATTITVLLPRAQAKGAPISAYQVYELPHRTKREAGAMYCYOVPVTYQN 660
DR		InterPro; IPR007110; Ig-like.		Qy 661 AMSGGAPYYPAEELPGNPLPEPAPTVGDNRTYQGFWNPLAPRKGYNIFYQAMSVKE 720
DR		InterPro; IPR000998; MAM.		Db 661 AMSGGAPYYPAEELPGNPLPEPAPTVGDNRTYQGFWNPLAPRKGYNIFYQAMSVKE 720
DR		InterPro; IPR003595; PTPC motif.		Qy 721 TKTQCVRIATK-AATEPEV1PDPKQTDDEVVKLAGISAGILVFLLLLWVILVTKSKL 779
DR		InterPro; IPR000242; Tyr_PP.		Db 721 TKTQCVRIATKAAATEEPEV1PDPKQTDDEVVKLAGISAGILVFLLLLWVILVTKSKL 780
DR		PFam; PF00041; fn3; 2.		

Beta-catenin may be a substrate for the catalytic activity of prp-2	
7800 AKGRKDAMNTQEMTHNMNDRSYADOSTLHADPLSITMDQHNFSPRYENHSATAE	839
781 AKRKDAMNTQEMTHNMNDRSYADOSTLHADPLSITMDQHNFSPRYENHSATAE	840
8400 SSSLILDPVRYLCBEGTESPYOTGOLHPAIVADLQHTNMKTSIDSYGFKEYESSEFFEGS	839
· 841 SSSLILDPVRYLCBEGTESPYOTGOLHPAIVADLQHTNMKTSIDSYGFKEYESSEFFEGS	900
9000 ASNDYAKCKQNRAKRNKGNTIAYDHRSVRLQPVEDDPSSTYDINAYTGYQRSHYIATQ	959
901 ASNDYAKCKQNRAKRNKGNTIAYDHRSVRLQPVEDDPSSTYDINAYTGYQRSHYIATQ	960
9600 GPVHETVDFWRM1TWOEQACIYTWNLVBGVRYCKWKPDDTEVYGDVKTCVEMEP1	1019
· 961 GPVHETVDFWRM1TWOEQACIYTWNLVBGVRYCKWKPDDTEVYGDVKTCVEMEP1	1020
1020 AEYVVRFTFLERRGYNETREVKOFHETGWDGHGVYPAHGTVLGLSPFIRRKVLSNPPSAQDV	1079
1021 AEYVVRFTFLERRGYNETREVKOFHETGWDGHGVYPAHGTVLGLSPFIRRKVLSNPPSAQDV	1080
10800 VHCSAGAGRTGCYTVIDM DMALEREGTYDIVYC KVALSR RRRRNNMVQEYQFTHDNL	1139
· 1081 VHCSAGAGRTGCYTVIDM DMALEREGTYDIVYC KVALSR RRRRNNMVQEYQFTHDNL	1140
1140 AEACIGETAIPIVCEFKAAVFDMDIRDSQNSHLLKDEFDTLNSTVTPRQAEDCSIACIPLR	1199
1141 AEACIGETAIPIVCEFKAAVFDMDIRDSQNSHLLKDEFDTLNSTVTPRQAEDCSIACIPLR	1200
1200 NHDKNRNFMDMLPPDRCLPFLITIDGESSNYINALMDSYTROPAFAVITYQPLPNTVQDFW	1259
12201 NHDKNRNFMDMLPPDRCLPFLITIDGESSNYINALMDSYTROPAFAVITYQPLPNTVQDFW	1260
1260 RLVDYDGCTSIYMLNEVDLISQGPQWMEBGMRYGPQVECMCSMDODVNRIFRICN	1319
1261 RLVDYDGCTSIYMLNEVDLISQGPQWMEBGMRYGPQVECMCSMDODVNRIFRICN	1320
1320 LTRPQEGLMVQQEYLGWASHREVPGSRSFLKLQEVKNOBEVGEGRTIHCLNG	1379
13221 LTRPQEGLMVQQEYLGWASHREVPGSRSFLKLQEVKNOBEVGEGRTIHCLNG	1380
1380 GGRSGMFCAGIGIVVEMYKQVQNYDVFHAWKTLRNSKPNMVAEBOQRCYDALEYLESS	1439
1381 GGRSGMFCAGIGIVVEMYKQVQNYDVFHAWKTLRNSKPNMVAEBOQRCYDALEYLESS	1440
RESULT 4	
PTPK_MOUSE	STANDARD;
ID	PRT; 1457 AA.
AC	P35822;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Receptor-type protein tyrosine phosphatase kappa precursor (BC 3..1..3..48) (R-PTP-kappa).
EN	Name=Prpk; Synonyms=Peplk; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10990;
DC	[1]
DC	SEQUENCE FROM N.A.
DN	STRAIN=R1; TISSUE=Brain;
DN	MEDLINS=93243655; Published=8474452;
DN	Jiang Y.P., Wang H., D'Eustachio P., Musacchio J.M., Schlessinger J., Sap J.; Cloning and characterization of R-PTP-kappa, a new member of the receptor protein tyrosine phosphatase family with a proteolytically cleaved cellular adhesion molecule-like extracellular region.; Mol. Cell. Biol. 13:2342-2351(1993).
DN	-1- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/polakoglobin
CC	"
CC	Beta-catenin may be a substrate for the catalytic activity of prp-2
CC	kappa.
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: High levels in liver and kidney. Lower levels in lung, brain and heart. Not seen in spleen and testis.
CC	-1- DEVELOPMENTAL STAGE: Developmentally regulated with highest expression found in areas capable of developmental plasticity.
CC	-1- PTM: This protein undergoes proteolytic processing.
CC	-1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC	-1- Receptor class 2B subfamily.
CC	-1- SIMILARITY: Contains 4 fibronectin type III domains.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC	-1- SIMILARITY: Contains 1 MAM domain.
CC	-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
CC	EMBL; L10106; AAA0021.1; -.
DR	PIR; A48066; A48066.
DR	HSSP; P28822; 1RPM.
DR	MGD; MGJ:103310; Ptprk.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR008937; FN_III-like.
DR	InterPro; IPR003589; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR009388; MAM.
DR	InterPro; IPR003987; TYR_phosphatase.
DR	InterPro; IPR000242; Tyr_PP.
DR	Pfam; PF00041; fn3; 2.
DR	Pfam; PF00047; ig; 1.
DR	Pfam; PF00623; MAM; 1.
DR	Pfam; PF00102; Y_phosphatase; 2.
DR	PRINTS; PR00020; MANDORIN.
DR	SMART; SM00060; FN3; 3.
DR	SMART; SM00409; Ig; 1.
DR	SMART; SM00137; MAM; 1.
DR	SMART; SM00194; PtPc; 2.
DR	PROSITE; PS50583; FN3; 4.
DR	PROSITE; PS50835; Ig_LIKE; 1.
DR	PROSITE; PS00740; MAM; 1; 1.
DR	PROSITE; PS5060; MAM; 2; 1.
DR	PROSITE; PS00383; TYR_PHOSPHATASE; 1; 2.
DR	PROSITE; PS50056; TYR_PHOSPHATASE; 2; 2.
KW	Glycoprotein_Hydrolate; Immunoglobulin domain; Protein phosphatase.
KW	Receptor; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 25
FT	CHAIN 26 1457
FT	DOMAIN 26 752
FT	TRANSMEM 753 774
FT	DOMAIN 775 1457
FT	DOMAIN 3 193
FT	DOMAIN 195 280
FT	DOMAIN 290 382
FT	DOMAIN 388 484
FT	DOMAIN 489 588
FT	DOMAIN 589 688
FT	DOMAIN 922 1158
FT	DOMAIN 1218 1452
FT	ACT_SITE 1100 1100
FT	ACT SITE 1394 1394
CC	Phosphocysteine intermediate (By sambo).

FT	DISULFID	215	269	similarity).	Db	780	AKKRKDAMGNTRQEMTHVNAMDRSYADQSTLHAEDPLSLTLPNMDPLVPT	839
FT	CARBODY	100	100	Potential.	Qy	832	--- ENHSATAESRLLDPYRLCEGTESPYQTGQLPAIRVADLQHNLNMKTSDSYGF	887
FT	CARBODY	139	139	N-linked (G1cNAc. . .) (Potential).	Db	840	AVLDENHSATAESRLLDPYRLCEGTESPYQTGQLPAIRVADLQHNLNMKTSDSYGF	899
FT	CARBODY	210	210	N-linked (G1cNAc. . .) (Potential).	Qy	888	KEEYESFFRGQSASWDAVKDNRKRNRYGNIAYDHSRVILQFEDDPSSDYINANYI-	946
FT	CARBODY	415	415	N-linked (G1cNAc. . .) (Potential).	Db	900	KEEYESFFRGQSASWDAVKDNRKRNRYGNIAYDHSRVILQFEDDPSSDYINANYID	959
FT	CARBODY	423	423	N-linked (G1cNAc. . .) (Potential).	Qy	947	--- DGYORPSHYATQCPVHETYDFRMIMQEQSACIVMNTLVEGRVCKYKYWPD	1001
FT	CARBODY	435	435	N-linked (G1cNAc. . .) (Potential).	Db	960	IWLXRDGYQRPSHYATQCPVHETYDFRMVMQEQSACIVMNTLVEGRVCKYKYWPD	1019
FT	CARBODY	461	461	N-linked (G1cNAc. . .) (Potential).	Qy	1002	DTEYQDFKWTCVMEPLAYVWRTFTLERRGNEIREVKQFHFTGPDHGVPTATGLL	1061
FT	CARBODY	551	551	N-linked (G1cNAc. . .) (Potential).	Db	1020	DTEYQDFKWTCVMEPLAYVWRTFTLERRGNEIREVKQFHFTGPDHGVPTATGLL	1079
FT	CARBODY	585	585	N-linked (G1cNAc. . .) (Potential).	Qy	1062	SFIRRKLSNPPSAGPTVYHCASAGAGRGCYIVIDIMLDMAEREGVVDIYNCVAKLRSRR	1121
FT	CARBODY	589	589	N-linked (G1cNAc. . .) (Potential).	Db	1080	SFIRRKLSNPPSAGPTVYHCASAGAGRGCYIVIDIMLDMAERGVVDIYNCVAKLRSRR	1129
FT	CARBODY	606	606	N-linked (G1cNAc. . .) (Potential).	Qy	1122	INMYCTBEQQYIPHDAILFACLGCTAIPVCEPKAYEDFMIRIDSQTNSSHLKDFOFLN	1181
FT	CARBODY	689	689	N-linked (G1cNAc. . .) (Potential).	Db	1140	INMYCTEEQYIFHDAILFACLGCTAIPVCEPKAYEDFMIRIDSQTNSSHLKDFOFLN	1199
SEQ	SEQUENCE	1457	AA;	164185 MW; 19D4B9B7EC68605 CRC64;	Qy	1182	SVTPRLQAEQDCSIACLPRHDKQRFDMLIPPDRCPLFLITIDGESSNYNAALMSYRQP	1241
Query Match		98.2%	Score 7571;	DB 1; Length 1457;	Db	1200	SVTPRLQAEQDCSIACLPRHDKQRFDMLIPPDRCPLFLITIDGESSNYNAALMSYRQP	1259
Best Local Similarity		97.3%	Pred. No. 0;		Qy	1242	AATIVTOYPLNPTYKDFWFLVYDGCISVMLNEVDLSSOCGPOYWEQMLRYGPQVEC	1301
Matches 1419;	Conservative	13;	Mismatches 6;	Indels 20;	Db	1260	AATIVTOYPLNPTYKDFWFLVYDGCISVMLNEVDLSSOCGPOYWEQMLRYGPQVEC	1319
Matches 1419;					Qy	1302	MSCSMDCDVINRIPICNLTROPQEGYLMTQFQVLYGWASHREVPGSKRSFLKLJLQVEKW	1361
Db	1 MD-VAAAALPAFAVLLISMPILLASQGQSAGGCTFDPGACDHYKQLYDDDEFTWY	60			Db	1320	MSCSMDCDVINRIPICNLTROPQEGYLMTQFQVLYGWASHREVPGSKRSFLKLJLQVEKW	1379
Qy	1 MDTTAAALPAFAVLLISMPILLASQGQSAGGCTFDPGACDHYKQLYDDDEFTWY	60			Qy	1362	QEENWEGEGRTITHLNGGRSGMCAIGIVVNVRKQNVVDVFHAVKTLRNSKPNVVEA	1421
Db	1 MD-VAAAALPAFAVLLISMPILLASQGQSAGGCTFDPGACDHYKQLYDDDEFTWY	59			Db	1380	QEENWEGEGRTITHLNGGRSGMCAIGIVVNVRKQNVVDVFHAVKTLRNSKPNVVEA	1439
Qy	61 SAQEPHYLPPMPQGSYMIDPSIDHPGKARLOPPTMENDTHC1DFSYLLYSQRGLNP	120			Qy	1422	PEOYRFCDYVALEYLESS	1439
Db	60 SAQEPHYLPPMPQGSYMIDPSIDHPGKARLOPPTMENDTHC1DFSYLLYSQRGLNP	119			Db	1440	PEQIRFCYDVALEYLESS	1457
Qy	121 GTLNILVRVNGKPLANPIWNTYGTGDRDMLRAELAVSTFWPEYQVIFAEVGSGRSYI	180						
Db	120 GTLNILVRVNGKPLANPIWNTYGTGDRDMLRAELAVSTFWPEYQVIFAEVGSGRSYI	179						
Qy	181 ADDIQVLSYPCDKSPHFLRIGDVENAGONATFQCIATRDVANKWILQRNGEDIY	240						
Db	180 ADDIQVLSYPCDKSPHFLRIGDVENAGONATFQCIATRDVANKWILQRNGEDIY	239						
Qy	241 AQTQNINHRFAASPFRLQEVTKTDQDLRYCUTKTDQDLRYCUTQSERGSYNSNFAOLIVRPPR1APPOL	300						
Db	240 AQTQNINHRFAASPFRLQEVTKTDQDLRYCUTKTDQDLRYCUTQSERGSYNSNFAOLIVRPPR1APPOL	299						
Qy	301 LGVGPTYLQLQUNANSTIGDGPILKEVYRMTGKPSWTHETAQNAPTYKLWHLDPDTYE	360						
Db	300 LGVGPTYLQLQUNANSTIGDGPILKEVYRMTGKPSWTHETAQNAPTYKLWHLDPDTYE	359						
Qy	361 IRLVLTTRGECTGJLGPPLTRTKCAEPMTPTKTLKIAETQARIAVWESLGYNITRC	420						
Db	360 IRLVLTTRGECTGJLGPPLTRTKCAEPMTPTKTLKIAETQARIAVWESLGYNITRC	419						
Qy	421 HTFNTVICHYFRGHNESRACLDMDPKAPOPHVNHLPPTVNSLKMILTNPEGKESSE	480						
Db	420 HTFNTVICHYFRGHNESRACLDMDPKAPOPHVNHLPPTVNSLKMILTNPEGKESSE	479						
Qy	481 TIIQTDVEDPGPVPVKSLQGTSFENKIFLAWKEPLDNGITOTYBYSYSSRSFDPAVPV	540			DT	01-DBC-1992	(Rel. 24, Created)	
Db	480 TIIQTDVEDPGPVPVKSLQGTSFENKIFLAWKEPLDNGITOTYBYSYSSRSFDPAVPV	539			DT	01-DBC-1992	(Rel. 24, Last sequence update)	
Qy	541 AGPPQTVSNLNSTHVNMLHPTGTYQFTRASTVKGFPATAINTNTISAPLDPDE	600			DT	25-OCT-2004	(Rel. 45, Last annotation update)	
Db	540 AGPPQTVSNLNSTHVNMLHPTGTYQFTRASTVKGFPATAINTNTISAPLDPDE	599			DE	(R-PTP-mu)	Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)	
Qy	601 GVDASLINEATTITVILRPAQKAPISAYQIVVVELHPRHTKREGAMECYQPVFTYQ	660			DE	(R-PTP-mu)		
Db	600 GVDASLINEATTITVILRPAQKAPISAYQIVVVELHPRHTKREGAMECYQPVFTYQ	659			GN	Name=PTPM;	Synonyms=PTPRL1;	
Qy	661 AMSGGAPYYFAAELPPGNLPEPAPFTVGDNRTYQCFWNPLAPRKCYNTYFOAMSVEKE	720			OS	Homo sapiens (Human).		
Db	660 ALSGGGAPYYFAAELPPGNLPEPAPFTVGDNRTYQCFWNPLAPRKCYNTYFOAMSVEKE	719			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
Qy	721 TKTQCVRIATK-AATTEPEVITDPAQKTFDQYKINGISAGILVFLILVILIKKSKL	779			OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Db	720 TKTQCVRIATKAAATEPEVITDPAQKTFDQYKINGISAGILVFLILVILVIVTKSKL	779			OX	NCBI_TaxID=9606;		
Qy	780 AKKRKDAMGNTRQEMTHVNAMDRSYADQSTLHAEDPLSLTLPNMDPLVPT	831			RN	[1]	SEQUENCE FROM N.A.	
					RP		Medline=200844; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;	
					RX		Gebbia M.F. B.G., van Etten I., Heteboer G., Suijkerbuijk R.,	
					RA		Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;	
					RA	"Cloning, expression and chromosomal localization of a new putative receptor-like protein-tyrosine phosphatase.",		
					RT	FEMS Lett. 291:123-130 (1991).		
					RL	[2]		
					RN	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.		
					RP	MEDLINE=98010572; PubMed=9346878; DOI=10.1074/jbc.272.44.27505;		
					RX			

RA	Hoffmann K.M., Tonks N.K., Barford D.; receptor protein-tyrosine phosphatase mu."	RT "The crystal structure of domain 1 of receptor protein-tyrosine phosphatase mu."	RT J. Biol. Chem. 272:27505-27508(1997).	RT -!- FUNCTION: May play a key role in signal transduction and growth control.	RT -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.	RT -!- SUBCELLULAR LOCATION: Type I membrane protein.	RT -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.	RT -!- SIMILARITY: Contains 4 fibronectin type III domains.	RT -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.	RT -!- SIMILARITY: Contains 1 MAM domain.	RT -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - use by non-profit institutions is allowed as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	PTR; S17669; S17669.	DR PDB; 1RPM; X-ray; A/B=87-1156.	DR GeneW; XAA:3675; PTPRM.	DR MIM; 176888; -.	DR GO; GO:005887; C:integral to plasma membrane; TAS.	DR GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. . . ; TAS.	DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.	DR InterPro; IPR033961; FN_III.	DR InterPro; IPR008937; FN_III-like.	DR InterPro; IPR008979; Gal_bind_like.	DR InterPro; IPR033599; Ig.	DR InterPro; IPR007110; Ig-like.		
CC	PRINTS; PR000098; MAM.	DR InterPro; IPR000387; TIR_phosphatase.	DR InterPro; IPR000242; Tyr_PP.	DR Pfam; PF000041; Fn3; 3.	DR Pfam; PF00047; Ig; 1.	DR Pfam; PF00639; Mam;	DR Pfam; PF00102; Y_phosphatases; 2.	DR PRINTS; PR00020; MAMDOMAIN.	DR SMART; SM00060; Fn3; 3.	DR SMART; SM00409; Ig; 1.	DR SMART; SM00137; Mam; 1.	DR SMART; SM00194; PTPC; 2.		
CC	PROSITE; PS50853; Fn3; 3.	DR PROSITE; PS50835; Ig_LIKE; 1.	DR PROSITE; PS00740; MAM; 1; 1.	DR PROSITE; PS50060; Ig; 1.	DR PROSITE; PS50383; TYR_PHOSPHATASE_1; 2.	DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.	DR PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.	KW 3D-structure; Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.	FT SIGNAL_1; 20	Receptor-type protein-tyrosine phosphorylase mu.	Extracellular.	FT DOMAIN_21; 1452		
FT	TRANSMEM	21	742	FT DOMAIN	743	764	FT DOMAIN	765	1452	Cytoplasmic (Potential).	MAM.	FT DOMAIN	765	1452
FT	CARBOHYD	72	92	FT CARBOHYD	92	92	FT CARBOHYD	131	131	N-linked (GlcNAc. . .)	N-linked (GlcNAc. . .)	FT CARBOHYD	131	131
FT	DISULFID	260	249	FT CARBOHYD	249	249	FT CARBOHYD	249	249	N-linked (GlcNAc. . .)	N-linked (GlcNAc. . .)	FT CARBOHYD	249	249
FT	ACT_SITE	1095	1095	FT ACT_SITE	1389	1389	FT ACT_SITE	1389	1389	Phosphocysteine intermediate (By similarity).	Phosphocysteine intermediate (By similarity).	FT ACT_SITE	1389	1389
FT	DISULFID	260	406	FT CARBOHYD	406	406	FT CARBOHYD	414	414	Potential.	Potential.	FT CARBOHYD	414	414
FT	CARBOHYD	72	454	FT CARBOHYD	454	454	FT CARBOHYD	534	534	N-linked (GlcNAc. . .)	N-linked (GlcNAc. . .)	FT CARBOHYD	534	534
FT	CARBOHYD	92	544	FT CARBOHYD	544	544	FT CARBOHYD	598	598	N-linked (GlcNAc. . .)	N-linked (GlcNAc. . .)	FT CARBOHYD	598	598
FT	CARBOHYD	92	651	FT CARBOHYD	651	651	FT CARBOHYD	681	681	N-linked (GlcNAc. . .)	N-linked (GlcNAc. . .)	FT CARBOHYD	681	681
FT	CARBOHYD	92	905	FT TURN	905	905	FT TURN	916	916	884	884	FT TURN	916	916
FT	STRAND	880	926	FT HELIX	882	882	FT HELIX	921	921	931	931	FT TURN	921	921
FT	SPRAND	930	936	FT HELIX	930	936	FT HELIX	936	936	941	941	FT TURN	936	936
FT	SPRAND	946	947	FT TURN	946	947	FT TURN	949	949	952	952	FT STRAND	949	952
FT	STRAND	953	961	FT TURN	953	953	FT TURN	962	962	963	963	FT STRAND	953	953
FT	STRAND	964	971	FT HELIX	964	971	FT HELIX	976	976	978	978	FT STRAND	964	971
FT	HELIx	979	988	FT TURN	979	988	FT TURN	989	989	990	990	FT TURN	979	988
FT	TURN	993	996	FT STRAND	993	996	FT STRAND	1001	1002	1002	1002	FT TURN	993	996
FT	TURN	1003	1004	FT STRAND	1003	1004	FT STRAND	1005	1005	1004	1004	FT TURN	1003	1004
FT	STRAND	1005	1016	FT TURN	1005	1016	FT TURN	1015	1016	1016	1016	FT STRAND	1005	1016
FT	STRAND	1020	1021	FT HELIX	1020	1021	FT HELIX	1022	1022	1032	1032	FT STRAND	1020	1021
FT	STRAND	1032	1034	FT TURN	1032	1032	FT TURN	1033	1033	1034	1034	FT STRAND	1032	1034
FT	STRAND	1044	1044	FT HELIX	1044	1044	FT HELIX	1045	1045	1044	1044	FT STRAND	1044	1044
FT	STRAND	1045	1058	FT TURN	1045	1058	FT HELIX	1071	1071	1083	1083	FT STRAND	1045	1058
FT	STRAND	1058	1136	FT HELIX	1083	1083	FT TURN	1086	1086	1094	1094	FT HELIX	1086	1086
FT	HELIX	1110	1118	FT STRAND	1110	1118	FT STRAND	1120	1120	1121	1121	FT HELIX	1110	1118
FT	HELIX	1112	1133	FT TURN	1112	1133	FT HELIX	1123	1123	1133	1133	FT TURN	1123	1133
FT	HELIX	1123	1136	FT AA;	1123	1136	FT AA;	1135	1135	1136	1136	FT AA;	1135	1136
FT	SEQUENCE	1452	1452	Score 62.4%; Best Local Similarity 60.8%; Matches 206; Conservative 889; Gaps 8;	Score 4807; DB 1; Pred. No. 6..8e-33; Matches 326; Indels 42; Gaps 8;	Query Match 4 TAAALAPFAVLLSPWPLLSAQGOPSAGGTQDLYDDPFGACDYPQLDYLTDPSYLGTLFVSSKGNSPPGIL 123	Query Match 55 TRPTSDPMPGSGSLMLYNASGRPEQRHLAQLPKENDTHCIDLPHYFVSSKGNSPPGIL 114	Query Match 124 NILVRWKGPPLANPIWNTGFRGDMLRAELAVSTFWNEQVIEAEVGGRSGSYIAID 183	Query Match 115 NYVVKVNGPLGPINNISGDPTTRWRAELAISTWFENYQVIEEV-ITSGHQGLYLAID 173	Query Match 184 DIOVLYSPCDKSBDHFLRLGQDVENVAGONATFOCIATGRDAVNLKLWLRRGEDIPVAQT 243				

174	EVKVGLHPCTRPHFLRIONVEVNAGQFATFQCSAIGRTYAGDRILWQDVRDAPLKEI	233	QY	1296	P1QVECMNSCMGDCDVIRIFRICNLTFRQEGTMVQOFQYGLNASHREVPGSKRSFLKL1	1355		
244	KINHRRFAASFRILQEVTKTDDQLYRCVTOSEERSGSVSNPAOLIVREPPRPIAPPOLLGV	303	QY	1309	P1QVEFTSADLEDIIRIFRIFTYNAARPDQGRMVMQOFOPLGNPMDYRTPVRSRSLKL1	1368		
234	KVTSSRRFTASENVNTTRDAGYCRCMIRTEGGVGSNTAELVKEPPVPIAPPOLASV	293	Db	1309	P1QVEFTSADLEDIIRIFRIFTYNAARPDQGRMVMQOFOPLGNPMDYRTPVRSRSLKL1	1368		
304	GPTTLLIQNANSIIGDPILIKEVYRMTSGSWTETHAVNAPTYKLWILDPTDEYEIRV	363	QY	1356	LQVEKNGQEWKEGEGRITIHCLNGGSGMFCAIGIUYYEMVKRNQVVDVFHAVKTLRNSK	1415		
294	GATLWLQNLNANSINGDPIVAREYCTAGSNSNDROPYTSKIGHLDPTDEYEISV	353	Db	1369	RQYDKNGQEWYNGEGRPTVHCINGGSGTFCASIVCEMLRHORTVDFHAVKTLRNNK	1428		
364	LUTRPGEGGTGLCPPLTRKCAAPMRTPKTLKIAEIQRARIAYDWESLGYNTRCHTF	423	QY	1416	FNNVEABQYRQPCYDVALEYLES	1438		
354	LUTRPGEGGTGSPGPALRTKCADPMGRGKLEVEVKSQRIITRWEPPGYNTRCHSY	413	Db	1429	PNMVDLQYKCFEVALBEYLN5	1451		
424	NTVTCYHYFRGHNESKAD - CLDMDPKAPOHVVNHLPPYTNTVSLKMLTNPBGRKESHEET	481	RESULT 6					
414	NLTTHYCQVGQECQREEVSDTENSHPQHTTINLSPTVNVSKVLANPBGRKESQEL	473	Db	BT TPM	MOUSE	STANDARD;	PRT;	1452 AA.
482	IIOQDDEVGPVPSLOGTSFENKIFLAWKEPLDNGITIOTYESYSSRSFADAVPA	541	QY	AC	28878;			
474	IVQTIDELGCAVPTESIQGSTEEFKIPLREPIOTYGVITLYETIKYAVSFDEIDL5	533	Db	DT	01-DEC-1992	(Rel. 24, Created)		
542	GPPOTVSNLWNISTHIVFMLHLPGTYOFFIRASTYKFGPATATAINTTNISAPTLPDYEG	601	QY	DE	01-DEC-1992	(Rel. 24, Last sequence update)		
534	NQSGRVSKLGNETHLFFGJYPGTYSFSTRASTAXGFGPATNOPTKISAPSNPAYE-	592	Db	DE	05-JUL-2004	(Rel. 44, Last annotation update)		
602	VDA5LNETATTITVLLRPAOKGAPISAYQIVVTEELHPHTKREGAMECYQVPTYQNA	661	QY	DE	Receptor-type protein-tyrosine phosphatase mu precursor (BC 3.1.3.48)			
593	LETPLNQTONTVWMLKPAHSGRAGPVSQVQIVVTEEBRPTKTTBILKCYCPVPLHFQNA	652	Db	DE	(R-PTP mu).			
662	MGGGAPYYFAAELPPGNLPPAPFVQGDNRTYQGFWNPPLAPRKYNIYQAMSYVEKET	721	QY	DE	Name=ptpm;			
653	SLLNSQQYFAAEFPADSLQRAQPFTGDNKTYGTYWNTPLPYKSYRIVQAASRANGEI	712	Db	DE	Mus musculus (Mouse).			
722	KTCQCYRIATAKEPEVITDPAKOTDRTVYTAGISAGAILVFLILLVILVKSKLAK	781	QY	DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
713	KIDCQVATKGAA-TPKVPEBEPKQDHTVYAGTAGIYVFLGVVLMVKRKLA	771	Db	DB	Beijersbergen R.; Geurts van Kessel A.; Moolenaar W.H.;			
782	KRKDAMGNTTROEMTMVNAMDHSYADQSTLHAEDPLSITMDQHNSPRY-----	831	QY	DB	"Cloning, expression and chromosomal localization of a new putative receptor-like protein tyrosine phosphatase";			
772	KRKETMSSTROEMTMVNNSDKSYAEQGTCDE--AFSPMDTHNLNGRSYSSPSSFTMK	828	Db	DB	FEBS Lett. 290:123-130 (1991).			
832	- - - - - ENHSATAESBLLDVKY - LCEGTEPSYQTGQLPAIRVADLQH	875	QY	CC	-I- FUNCTION: May play a key role in signal transduction and growth			
829	TINTLSTSVPNSYYPBETHIMASDTSSLVQSHSTYKKREPADVPSYQGQLHPRVADLQH	888	Db	CC	-I- CONTROL:			
876	INLMKTKSDSYGKFKEYESPFEGOSASWDYKDNRAKORYGNITIAYDHSRVILOPEDD	935	QY	CC	-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
889	ITQMKCAEGFGKKEYESPFEGOSASWDYKDNRAKORYGNITIAYDHSRVILOPEDD	948	Db	CC	tyrosine + phosphate.			
936	PSSDYINANYIDGQYRPSHYIATGPHVHETYDWRMIWQOSACIYMTVNLVEGRVKC	995	QY	CC	CC -I- SUBCELLULAR LOCATION: Type I membrane protein.			
949	TNSDINGNYDGTHERPNHYTATGOMQETYDFWRMVWHNTASIMTVNLVEGRVKC	1008	Db	CC	CC -I- TISSUE SPECIFICITY: Most abundant in lung, less in brain and			
996	YKWDDTTEYVGDVKVTCVNEPLAAYVRFTRTBERGYNLIREVKQFHFTGPDHGVFY	1055	QY	CC	CC -I- heart.			
1009	CKYWDDTTEYKDIKVLTIELTTELLAYVIRTFAVERGVHIREIYQFHFTGPDHGVFY	1068	Db	CC	-I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
1056	HATGLLSFTIRVKLSNPPSAGPIVHCSAGAGRITGCYVIIIDIMLMAEREGYVDLYNCVK	1115	QY	CC	CC -I- Receptor class 2B subfamily.			
1069	HATGLLGIVYQVKQSPPSAGPIVHCSAGAGRITGCYVIIIDIMLMAEREGYVDLYNCVK	1128	Db	CC	CC -I- SIMILARITY: Contains 4 fibronectin type III domains.			
1116	ALRSRRINMYCTEQYIFINHAILECLCGETAIPCEKFAYDMIRIDSQTNSSSHLD	1175	QY	CC	CC -I- SIMILARITY: Contains 1 immunoglubulin-like C2-type domain.			
1129	ELRSRRINMYCTEQYVTPHAKTLEACLGTSVSPASQVRLYYDKNLDPOTNSSIIKE	1188	Db	CC	CC -I- SIMILARITY: Contains 1 MAM domain.			
1176	EFQTLNSVTIRKLQAEQDCSIALCPNEDKNRNDMPLPDRCPFLTIDGESNSYINAALM	1235	QY	CC	CC -I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.			
1189	EFRILNMVTPTRVEDCSIALPRTHEKNTCDILPPDRCPFLTIDGESNSYINAALM	1248	Db	CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
1236	DSYRQPAFTYQYPLPNTYDFWRLVYDYCTSTIYLNVEYDLSQSGCPYMEEGMLRYG	1295	QY	CC	CC	CC		
1249	DSYKPSAFIYQHPLNFTYDFTWRLVYDCTSTIYLNVEYDLSQSGCPYMEEGMLRYG	1308	Db	CC	CC	CC		
			DR	DR	DR	DR	DR	DR
			PIR	PIR	PIR	PIR	PIR	PIR
			S17670	S17670	S17670	S17670	S17670	S17670
			P28827	P28827	P28827	P28827	P28827	P28827
			1RPM	1RPM	1RPM	1RPM	1RPM	1RPM
			MGI:102694	MGI:102694	MGI:102694	MGI:102694	MGI:102694	MGI:102694
			InterPro: IPR0033961	InterPro: IPR0033961	InterPro: IPR0033961	InterPro: IPR0033961	InterPro: IPR0033961	InterPro: IPR0033961
			InterPro: IPR008979	InterPro: IPR008979	InterPro: IPR008979	InterPro: IPR008979	InterPro: IPR008979	InterPro: IPR008979
			InterPro: IPR0035359	InterPro: IPR0035359	InterPro: IPR0035359	InterPro: IPR0035359	InterPro: IPR0035359	InterPro: IPR0035359
			InterPro: IPR007110	InterPro: IPR007110	InterPro: IPR007110	InterPro: IPR007110	InterPro: IPR007110	InterPro: IPR007110
			InterPro: IPR00998	InterPro: IPR00998	InterPro: IPR00998	InterPro: IPR00998	InterPro: IPR00998	InterPro: IPR00998
			InterPro: IPR00387	InterPro: IPR00387	InterPro: IPR00387	InterPro: IPR00387	InterPro: IPR00387	InterPro: IPR00387
			InterPro: IPR000422	InterPro: IPR000422	InterPro: IPR000422	InterPro: IPR000422	InterPro: IPR000422	InterPro: IPR000422
			PF00041	PF00041	PF00041	PF00041	PF00041	PF00041
			PFam: 3	PFam: 3	PFam: 3	PFam: 3	PFam: 3	PFam: 3
			DR	DR	DR	DR	DR	DR
			PF00047	PF00047	PF00047	PF00047	PF00047	PF00047
			19	19	19	19	19	19

QY	DR PRam; PFO0629; MAM; 1.	323 IILKEVEYRMTSGSMWTEHVNAPTYKLWHLDPDPEYEIRVLLTRPGEGETGGLPPPLIT 382
Pfam;	PFO0629; Y_phosphatase; 2.	
Pfam;	PFO0102; Y_phosphatase; 2.	
PRINTS;	PR00020; MAMDOMAIN.	
PRINTS;	PR00700; PTYDHPHPTASE.	
SMART;	SMART0049; FN3; 1.	
SMART;	SMART00137; MAM; 1.	
SMART;	SMART00194; PTPC; 2.	
PROSITE;	PS500853; FN3; 3.	
PROSITE;	PS500835; IG_LIKE; 1.	
PROSITE;	PS500740; MAM; 1; 1.	
PROSITE;	PS500660; MAM; 2; 1.	
PROSITE;	PS500670; TYR_PHOSPHATASE_1; 2.	
PROSITE;	PS50056; TYR_PHOSPHATASE_2; 2.	
PROSITE;	PS50055; TYR_PHOSPHATASE_PTP; 2.	
Glycoprotein; Hydrolase;	Immunoglobulin domain; Protein phosphatase;	
Receptor; Repeat;	Signal; Transmembrane.	
SIGNAL	1	20
CHAIN	21	1452
DOMAIN	21	742
TRANSHEM	743	764
DOMAIN	765	1452
DOMAIN	765	184
DOMAIN	186	277
DOMAIN	281	371
DOMAIN	379	477
DOMAIN	482	581
DOMAIN	589	671
DOMAIN	923	1153
DOMAIN	1213	1447
ACT_SITE	1095	1095
ACT_SITE	1389	1389
DISULFID	206	260
CARBODY	72	72
CARBODY	92	92
CARBODY	131	131
CARBODY	249	249
CARBODY	406	406
CARBODY	414	414
CARBODY	454	454
CARBODY	534	534
CARBODY	544	544
CARBODY	598	598
CARBODY	651	651
CARBODY	681	681
SEQUENCE	1452 AA;	163594 MW;
		F990FC67922CF1 CRC64;
Q	Query Match	Score 4791; DB 1; Length 1452;
	Best Local Similarity	61.3%; Pred. No. 8..1e-312;
Matches	885; Conservative	205; Mismatches 320; Indels 34; Gaps 7;
Y	23 LIGSAQGFSAGGCTFDIGPGACDYDHDFFEWIVSAQEEPHLPPEMPOGSYMTVD 82	
Y	14 LLTAAGETFSGCCFLDEPYSTCGYSQADDENWEQNTLKP7SDWMPSCSFMLVN 73	
Y	83 SDHPGKEKRLQLPTMKENDTCIDFESVLYSOKGLNGFTNLIVRYNGKPLANPINTV 142	
Y	74 SKCPGEQRAHLJPOLCNDTCIDFESVLYSOKGLNGFTNLIVRYNGKPLANPINTV 133	
Y	143 GPTGRDMLRRAELAVSTWPNEYQVIFAEAVSGGRSGTIAIDIQVLISYPDKSPHFORLG 202	
Y	134 GDPTRTWRHAELAISTWPNFQVIFEV-VTSVGHQYLAIDEVKVLGHPCTRPHFLRI 192	
Y	203 DVEVNAGNQATFOCIATGRDAVENKWLQRRNGEDIPVATQTKNINHFRFAASRLOEVTK 262	
Y	193 RVEVNAQFATQCSA.GRTVAGDRLWQGDPIKEIKVTSRRIASPVNNTV 252	
Q	263 TDQDLYRCVTQSERGSVSNFQOLIVREPPIAPPOLLGIVSPYTLJQLNANSIIGDGP 322	
Db	313 IVAREVEYCTASGSWNDRQEVDSYKIGLDPDPEYEIVSLLTREGEGETGGSPEPALRT 372	
Db	383 RTKCAEPMTPKLIAE_QARRIAWDWESLGLQVTRCHFENVTCYHYGRHNNSRDR- 441	
Db	373 RTKCDPMPGPKLEVEYKSROITIRWEFGYNTRCHSYNLTTHYQVGQBOQVREE 432	
QY	442 -CLMDPKAQPHVYNHLPPTNVSKLMLTNPGRKESEETIQTDBDVPVPKYKSLOG 500	
Db	433 VSWDDDNDSFHFOHTITINSPITVSKLILMNPEGKESQILTVDQDLDLGAVPESIQG 492	
QY	501 TSFENKIEFLANKWKEPDLPNGLITOYHSYSSIRSFSNPAPVAGPPQTVSNLWNSTHHVFMH 560	
Db	493 SAFREKFLQWREPQTYGIVTLYITYKAVSSPFSRKLGNETHFLFFG 552	
Db	432 VSPEDDNTSHFADLQHPTTITLRLPDIQEGVDAISLNETATTITLRLP 620	
QY	561 LHPGTQKPIRASTVKGGPATANINVNTISAPLDPDIEGVDAISLNETATTITLRLP 671	
Db	553 LYPGTTYSFPIRASTAKGCPATNOFTKISASSMPAYE-FETPINOTDNTVTLKPA 611	
QY	621 QAKGAPIASAYQIVVYELPHPTKREAGAMECYQVPTVYONAMSGGAPYPPAELPGGNLP 680	
Db	612 QSRAPVSYQIVVHEBTERPRTKTEIILCPVLFHQNASLINSQYAAEFADSLQ 671	
QY	681 EPAPPTVGDNRITYQQPMNPPLAPKGNYXIFOAMSVEKEKTKTQCVRIATAEPEPEVI 740	
Db	672 AAQPFITGDNKTYGNYWMTPLPKSYRYYQOASRANGEKTKIDCVRATKGAV-TPKPV 730	
QY	741 PDPAKOTDVKLAGISAGLVFLVLLIVYKSLAKKRKUAMGNTROEMTMVNA 800	
Db	731 PEPEKOTDVTKLAGIVGILFVTFIYLGVLVNNKVKRLAKKRKETMMSSTRQEMTMVWN 790	
QY	801 MDRSYAQDSTLHAEDPLSITEMDODHNSPFRY-----ENHS 835	
Db	791 MDKSYAEQGINCDE --AFSMGTHINLNGRSVSSDSSPSITVSNSYIDDETHT 847	
QY	836 ATAESSRLLDVPVR-YLCEGTESPYGTCGOLHPAIRADLQHINLMKTSDSYGGKEYESEF 894	
Db	848 MASDQSSLQPHTYKCREAADVPQTCGOLHPAIRADLQHITQNKCAEGYGGKEYESEF 907	
QY	895 FEGGASWDVAKQDQNRAKRYGNTIAYDSRVLQFEDPSSYIINANIDGQRPSH 954	
Db	908 FEGGASPDASAKDENRMCNRYGNIAYDHSRVRLQMLBGDNNSYIYNGYTDGTHRPNH 967	
QY	955 YIATQGPWETVYDFWRFMIWIQEACIVMVTNLYEVGRYTCYKWPDDPTEVYDGFKVTCV 101	
Db	968 YIATQGPWETVYDFWRFMIWIQEACIVMVTNLYEVGRYTCYKWPDDPTEVYDGFKVTCV 102	
QY	1015 EMEPLAEVYVTPFLYERRGYNEIREVKQFHPTGHPDGHGPYHATCGLLSFTRVUKLSNPPS 107	
Db	1028 DTEILAAEVYVTPFLYERRGYNEIREVKQFHPTGHPDGHGPYHATCGLLSFTRVUKLSNPPS 108	
QY	1075 AGPTVHCSAGAGRTGCYIVIDMLDMAREGVVDIYNCVYKALRSRIRNVOEQYIFI 113	
Db	1088 AGPLVHCSAGAGRTGCPIVIDMLDMAREGVVDIYNCVYKALRSRIRNVOEQYIFI 114	
QY	1135 HDALAEACLGCTEAIPVCERKFAAYFDMTRIDSONSSHUKDEFOTLNSTPRLQABDCSI 119	
Db	1148 HDALAEACLGCTEAIPVCERKFAAYFDMTRIDSONSSHUKDEFOTLNSTPRLQABDCSI 120	
QY	1195 ACPLRNHDKNRENDMILPPDRCLPFLITDGESSIONYINALMDSYRQPAFIVTOYPLNT 125	
Db	1208 ALLPRNHEQRNDMILPPDRCLPFLITDGESSIONYINALMDSYRQPAFIVTOPLNT 126	
QY	1255 VDFWFLWYDYGCTSIVMNEUDVSQGCPQWPEGMRYGPIOVEFCMSMDCVINRI 131	
Db	1268 VDFWFLWYDYGCTSIVMNDVBAQLCQWPMGNGVHRHGPQIEFVSDLEEEIIISRI 132	
QY	1315 FRICNLTRFQEGYLMVOOFOYLGNASHRPGSKRSPLKLILOVEKQWEKGGRFTII 137	
Db	1328 FRIYNAFSEQDGHRMVOQFQFLGPMYRDTPVSKRFLKLIRQDVQWOBYNGGPFVV 138	
QY	253 RDAGKFCRMICBEGGVTSYNAELVWKEPVYPTAPPOLASVATYIWMOLNANSINDGP 312	

Qy	1375	HCLNGGRSGMFCAGIVVEMVKRONVVDFHAYKTLRNSKPNVVEAPPQYRFCCYDVALE	1434	DR PROSITE; PS00740; MAM 1; 1.
Db	1388	HCLNGGRSGMFCAGIVVEMVKRONVVDFHAYKTLRNSKPNVVEAPPQYRFCCYDVALE	1447	DR PROSITE; PS00783; TIR_1PHOSPHATASE 1; 2.
Qy	1435	YLES 1438		DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
Db	1448	YLES 1451		DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
				KW Glycoprotein.
				SQ SEQUENCE 1486 AA; 167143 MW; 3698067AD522D01A CRC64;
RESULT 7				Query Match 62.1%; Score 4784; DB 2; Length 1486;
Q68PM4		PRELIMINARY;	PRT; 1486 AA.	Best Local Similarity 60.1%; Pred. No. 2.5e-311; Index 319; Gaps 7;
ID Q68PM4;				Matches 887; Conservative 205; Mismatches 319;
AC Q68PM4;				
DT 25-OCT-2004 (TREMBUREL. 28, Created)				
DT 25-OCT-2004 (TREMBUREL. 28, Last sequence update)				
DE Ptpm protein.				
Name=Ptpm;				
OS Mus musculus (Mouse).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OC NCB1_TaxID=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
STRAIN=C57BL/6; TISSUE=Brain;				
Pubmed=1247932; DOI=10.1073/pnas.242603899;				
RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA Klausner R.D., Collins F.S., Wagner L., Sheenmen C.M., Schulter G.D.,				
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,				
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,				
RA Fahey J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,				
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,				
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,				
RA Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human				
RT and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RL [2]				
RP SEQUENCE FROM N.A.				
STRAIN=C57BL/6; TISSUE=Brain;				
Director MGC Project;				
Submitted (AUG-2004) to the EMBL/GenBank/DDJB databases.				
RL EMBL; BC019621; AAH9621.1; -.				
DR InterPro; IPR003961; FN III.				
DR InterPro; IPR008957; FN III-like.				
DR InterPro; IPR008979; Gal_bind_like.				
DR InterPro; IPR003599; Ig.				
DR InterPro; IPR007110; Ig-like.				
DR InterPro; IPR000998; MAM.				
DR InterPro; IPR003595; PTPC motif.				
DR InterPro; IPR000387; TYR_Diphosphatase.				
DR InterPro; IPR000242; tyr_PP.				
Pfam; PF00041; fn3; 3.				
DR SMART; SM00060; FN3; 3.				
DR SMART; SM00409; IG; 1.				
DR SMART; SM0137; MAM; 1.				
DR SMART; SM00194; PTPC; 2.				
DR SMART; SM00404; PTPC motif; 2.				
DR PROSITE; PS500835; IG_LIKE;				

Db	909	QLHPAIRVADLQHITQMCAGYGFKEEYESTFEGQSAPWDSAKKDERMKARYGNTIA	968	RT "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Qy	922	YDHSSVILQEVEDDSDTINANTIDGYCPSPHTATQCPVHETTYDFRMIFDQEOSACI	981	RL [2] SEQUENCE FROM N.A.
Db	969	YDHSSVRLQMLLEGDNNSDINGNTDGHPRPHYATQCPMQTITYDFRMWHEENTASI	1028	RC TISSUE=Brain;
Qy	982	VMTNLVEGRVKCYKWPDDTEYGFVKTVCVEMEPABYVVTFTLERRGYNENIREWK	1041	RA Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
Db	1029	IMTVNLVEGRVKCYKWPDDTEYGFVKTVCVEMEPABYVVTFTLERRGYNENIREWK	1088	DR EMBL; BC051651; AAH51651.1; -.
Qy	1042	QFHFGWPDHGPVPHATGLISPIRVKLSNPPSAGPIVTHCSAGAGRCCYIVTDIMD	1101	DR HSSP; P28827; 1RPM.
Db	1089	QFHFGWPDHGPVPHATGLISPIRVKLSNPPSAGPIVTHCSAGAGRCCYIVTDIMD	1148	DR GO; GO:0016020; C:membrane; IEA.
Qy	1102	AERESVVDIYCNVKALESRSRINNQTYEBOYTFINDAILLACLCBTATEVCEFKAYFM	1161	DR GO; GO:0016787; F:hydrolase activity; IEA.
Db	1149	AERESVVDIYCNVCALESRSRINNQTYEBOYTFINDAILLACLCBTATEVCEFKAYFM	1208	DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
Qy	1162	IRPSQTNSSHLKDDEFOTLNSTVPLRQARDCSTACLPKRHDKNRFMDMLPPDRCLPFLTT	1221	DR InterPro; IPR003961; FN_III.
Db	1209	NKLDPQTNSQIKBEFRTRINMVTPLRVEDCSTAILPRHEKORCMDIIPPDRLPFLTT	1268	DR InterPro; IPR008957; FN_III-like.
Qy	1222	IDGESSNNYNAALMDSYRQPAAFIVTOYDPLNTYKDFWFLVYDYGCTSTMALNEVDLSQG	1281	DR InterPro; IPR008979; GaII_bind_like.
Db	1269	IDGESSNNYNAALMDSYKPSAFIVTOYDPLNTYKDFWFLVYDYGCTSTMALNEVDLSQG	1328	DR InterPro; IPR007110; Ig-like.
Qy	1282	CPOQWPEERGKQYIPIQVBMCSNDCDYVTRPOGYLMQQFOYOLGWASH	1341	DR InterPro; IPR000387; TYR_phosphatase.
Db	1329	CPOQWPEERGKQYIPIQVBMCSNDCDYVTRPOGYLMQQFOYOLGWASH	1388	DR InterPro; IPR002412; Tyr_PP.
Qy	1342	REVPGSKRSFLKLTLQVKEQEWKEGEGRITLHCLNGGRGSMFCATGIVYVMVKRNQN	1401	DR Pfam; PF00041; fn3; 2.
Db	1389	RDTFVSKRFKLJRQDVWQEYNGBGRTRVHCLNGGRGSGTCFAJSIVCEMLRHORT	1448	DR Pfam; PF00044; 19; 1.
Qy	1402	VDVFHAVKTLRNSKPNMVAPEAQKFYCDALEYLES	1438	DR SMART; SM00194; 1G_LIKE; 1.
Db	1449	VDVFHAVKTLRNSKPNMVAPEAQKFYCDALEYLES	1485	DR PROSITE; PS50835; IG_LIKE; 1.
SQ				DR PROSITE; PS00740; MAM_1; 1.
				DR PROSITE; PS50060; MAM_2; 1.
				DR PROSITE; PS00183; TYR_PHOSPHATASE_1; 2.
				DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
				DR PROSITE; PS50055; TYR_PHOSPHATASE_2PTP; 2.
				KW Glycoprotein; Hydrolase.
				SEQUENCE 1390 AA; 156936 MW; D8173543CDD979 CRC64;
				Query Match 61-3%; Score 4726; DB 2; Length 1390;
				Best Local Similarity 62-2%; Pred. No. 1_7e-307;
				Matches 867; Conservative 202; MisMatches 292; Indels 34; Gaps 7;
				Qy 72 MPQGSPYMIYDSSHDPGKARLQPLTMKENDTHCIDFXYLLPSQKGKNGPNTNLVRNPK 131
				Db 1 MPQGSPYMIYDSSHDPGKARLQPLTMKENDTHCIDFXYLLPSQKGKNGPNTNLVRNPK 60
				Qy 132 GPLANPIMNVGTGFTGRDYLIRAEELAVSTFWPNEQVIFEAEVSGGRSGYTAIDDIQVLISYP 191
				Db 61 GPLGNPINTNISGDPARTVNRAELIASTWNPNTQVIFEV-ITSQHGYLAIDEVKVLGHP 119
				Qy 192 CDKSPHFLRLGQDVBNVAGNATPQCIAIGRDVAHNKWLQRNGEDIPVAQTKNINHHRP 251
				Db 120 CTRTPHFLRIONVBNVAGQFATQCSAIGRTYAGDRLWMLQGIDVRAQPLKEIRVTSRRP 179
				Qy 252 AASFRLQEVTKTIDQDLTVCVTSERGVSNFQQLTREPPRTAAPOLLGCGPTYLJLQ 311
				Db 180 IASFNVNNTKRDAGKRCMRITEGGVSNTAELVVKBPYPVIAAPPPLASVATYLMIQ 239
				Qy 312 LNANSIIGDGPTILKEYEYRMTGSWIEETHANAPTYKLWHLDPDTSEKIRVLTTRPGBG 371
				Db 240 LNANSIINGDGPTILKEYEYRMTGSWIEETHANAPTYKLWHLDPDTSEKIRVLTTRPGBG 299
				RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Loqueland N.A., Peters C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soberon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.; McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton R., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimewood J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnierer A., Schein J.E., Jones S.J., Marrs M.A.;
				Qy 372 GRGLGPPLITRTRKACAFMRTPKTLKABIQARRIADVWSLGYNTRCHTFNNTICHY 431
				Db 300 GRCSGPALRTRTKCADPMGRPKLKVEEVKSQRTISWEPGCVNTTRCHSINTLVHNYCY 359
				Qy 432 FRGHNEISKAD--CLDMDEKAPOHVNLLEPPYTINVSILMNTPEBGRKESBETIQTQDDV 489
				Db 360 QveGQEVREEVSWDTENSHPORTINTLSPYTNVSXLLMNPEBGRKESQELVQTDSDL 419

Qy	490	PGPVVKSLQGTSFENKIFANKEPLDINGLITQYEISSSIRSFDPAVEVAGBPQTVN	549	DT 05-JUL-2004 (TREMBUREL, 27, Created)
Db	420	PGAVPTESTIQSSTFERKIFLLOWFRTQYITLYEITYKAVSSDPEDLSNGSGRVSX	479	DT 05-JUL-2004 (TREMBUREL, 27, Last sequence update)
Qy	550	LWNSTHVFMLHPGTTYQFPIRASTVKGFGPATAINVTINISAPTLPDYEGVDAISLNST	609	DT 05-JUL-2004 (TREMBUREL, 27, Last annotation update)
Db	480	LGNETHEFLGGTYSFTIRASTAKGFGPATNQFTKISAFSMPAYE-LTLPNQT	538	DB Receptor tyrosine phosphatase.
Qy	610	ATTIILRLRAQKAPISAYQIVWEELHPRTBAGAMECQYDPTVQAMSGGAPY	669	OS Gallus gallus (Chicken).
Db	539	DNTVTVMKCPAHSRGAPVSYQIVVTEEEERRRTKCTTELKCYPPHFQNASLNSQTY	598	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Gallinidae; Phasianinae; Gallus.
Qy	670	FAAELEPPGNIPEPAPEPTVGDNRTYQFMNPPLAPRKGYNTYQAMSSVVERETKDCVQA	658	OC NCB_ TaxID=9031;
Db	599	FAAEFPDSLQAQPFTIGDNTKINGWNTPLPLPKSYRIYFQASRANGEETKDCVQA	658	OX RN [1]
Qy	730	TKAAIEBPEVIPDPAKOTDRVKLAGISAGILVFILLIYVILIVKSKLAAKKRDKAMGN	789	RP SEQUENCE FROM N.A.
Db	659	TKGAA-TPKVPEPEQTDTVKIAKVGIAFLFTIFLGLVYMKKRLAKGERKETMSS	717	RA Arrte B.; Stoker A.; Ish-Horowicz D.; Submitted (SB-2002) to the EMBL/GenBank/DBJ databases.
Qy	790	TQEMTMVNAAMDRTADQSTLHAEDPLSITFMDPQHNFSPY	831	RL AY147868; AAN38300.1; -.
Db	718	TQEMTMVNMNSMDKSYAEGTNCDE--AFAESMDTHNLNGRSVSSPSSFTMKTNLSTS	774	DR DR HSSP; P18031; LAST.
Qy	832	-----ENHSATAECSRLLDVPYR-LCEGEESPYQTQGHPATRVADLQIHTQMKAC	883	DR GO; GO:0016028; Cimembrane; IEA.
Db	775	PNSYYDPDETTMASDTSLLSVQSHTYKKREPADVQTQGHPATRVADLQIHTQMKAC	834	DR GO; GO:0016781; F; hydrolyase activity; IEA.
Qy	884	SYGFKEEYESPFEQGOSASWYDAAKDDONRAKRYGNNTIAVDHSRVILQPVYDPPSSADYINA	943	DR GO; GO:0004875; F; protein tyrosine phosphatase activity; IEA.
Db	835	GYGFKEEYESPFEQGOSAWPDSSAKGENRMRNKGNNRQYGNNTIAVDHSRVLQTLEDGTNSDING	894	DR GO; GO:0006470; F; receptor activity; IEA.
Qy	944	NYIDGYQRPSHMIATQPHQHETVYDWRMIWQEQSACIWMNTLVEVGURKCYKXWPDTI	1003	DR GO; GO:0006470; F; protein amino acid dephosphorylation; IEA.
Db	895	NYIDGTHRPNHYIATQPMQETIYDWRMWHENTASILWNTLVEVGURKCCXCYWPDDT	954	DR DR InterPro; IPRO03962; FNIII sub.
Qy	1004	EYVGDPEKTVCEMPELALEYVVRTFTLBRGRYNEIREVKOPFHTGPDPHDGHVYPYHATGLLSP	1063	DR DR InterPro; IPRO03961; FNIII.
Db	955	EYVGDPEKTVCEMPELALEYVVRTFAVERGYTHEIREIRQHFTGPDPHDGHVYPYHATGLC	1014	DR DR InterPro; IPRO08957; FN III-like.
Qy	1064	IRRVKLNSPPSAGATPVHCSAGAGRTGCYTVIDIMDMAREGQVYDYNCKALSRRAIN	1123	DR DR InterPro; IPRO03959; GaT_bind_like.
Db	1015	VRQVKSKPSPPSAGPLVHCSAGAGRTGCYTVIDIMDMAREGQVYDYNCKVRELSRRVN	1074	DR DR InterPro; IPRO03599; 19-like.
Qy	1124	MVQEEOQJFHDAILNCGCTAIPVCEKAAYEDMIRDQSNTSSHKEFOTINSV	1183	DR DR InterPro; IPRO07110; 19-like.
Db	1075	MVQTEECQVFHDAILCAUCGDTSYVSPAQS0VSLYDMKLDPQNTSSQIKEEPTLNKV	1134	DR DR InterPro; IPRO0998; MAM.
Qy	1184	TPLRQAEDCSIACLPNHDKNRFMDMLPDRCLFLITIIGESSNYINAALMDSYRQPA	1243	DR DR InterPro; IPRO00387; TYR_Phosphatase.
Db	1135	TPLTIVEDCSTALLPNHNRKCMDLPPBCLFLITIODESSNNINAALMDSYKQPA	1194	DR DR InterPro; IPRO0242; TYR_PP.
Qy	1244	FIVTOYPLPTVKDFWRLVYDGCTSIWVLINEVDSLQGKPCOYWPBEGMLRYGPIOVECMS	1303	KW DR InterPro; IPRO00629; MAM; 1.
Db	1195	FIVTOQBLPNVTKDFWRLVYDQHCTSWMLNDVDPQLCPWPGVHRHGPJOVEFYS	1254	DR DR Pfam; PF00040; IGI; 1.
Qy	1304	CSDMDCDVINRIFRICLUTRQPGQLMQOFQVQIWHASHRTPGSXRSPEFLKLQIWERKQE	1363	DR DR Pfam; PF00119; Y_Phospha
Db	1255	ADLEEDISRLFRYNAARPDQGYRNVQOFQFLGNPMYRDTPVSKRSFELLKLIRODVKWQE	1314	DR DR PRINTS; PR00014; FNTYPE; II.
Qy	1364	EWREGEBRTRIHCLNGGGRSGMFCATGIVVEMVKRONVVDFHAVKTLRNSKPNVNEAPE	1423	DR DR PRINTS; PR00020; MAMDOMAIN.
Db	1315	FIVTOQBLPNVTKDFWRLVYDQHCTSWMLNDVDPQLCPWPGVHRHGPJOVEFYS	1274	DR DR PRINTS; PR00700; PTYPHEPTASE.
Qy	1424	QYRCYDVALEYLES 14 38		DR SMART; SM00066; FN3; 3.
Db	1375	QYKFCYEALEYLNS 13 89		DR SMART; SM00040; IGI; 1.
Qy				DR SMART; SM00137; MAM; 1.
Db				DR SMART; SM00194; PPBC; 2.
Qy				DR SMART; SM00404; PPBC motif; 2.
Db				DR PROSITE; PS50053; PN3; 3.
Qy				DR PROSITE; PS50335; IG_LIKE; 1.
Db				DR PROSITE; PS50060; MAM; 1; UNKNOWN_1.
Qy				DR PROSITE; PS50040; MAM; 2; 1.
Db				DR PROSITE; PS00183; TYR_Phosphatase; 1; 2.
Qy				DR PROSITE; PS50056; TYR_Phosphatase; 2; 2.
Db				DR PROSITE; PS50055; TYR_Phosphatase; PTP; 2.
Qy				KW Glycoprotein; Hydrolase; Receptor.
Db				SQ SEQUENCE 1434 AA; 161678 MW; 4.9E0E609BA4055SCS CRC64;
Qy				Query Match 60.9%; Score 4697.5; DB 2; Length 1434;
Db				Best Local Similarity 61.4%; Pred. No. 1.5e-305; Matches 870; Conservative 216; Mismatches 870; Gaps 11;
Qy				33 AGGCTT-C-DPGGACDHYDOLYPDPEWHVSAQEPHYPPEMQSYMIVDSSDHDPGEK 90
Db				Db 24 SAGCTTTEDDLNQCBYSQBEDDDGWLRSYMPHLTADLPHESYLWNASQHAQGR 83
Qy				91 ARLOQPTMKENDTHCIDESTLIXYQSKGLNGPTLNLYVNRKGLPANPINVTGFTGRDWL 150
Db				84 AHLFQALSNDTICLQFSYFMSDGHSPCTLSAYVRMGGPVSAVWNASGSGRWNH 143
Qy				Db 151 RAELAVSTPNEYCVTFEARBVSGRSGYTAIDQVLSYPCDKSPKPHPLRIGDVYNAGQ 210
Db				Db 144 QAEIQLSFLFPSEYQVLFEAVISSERGRYGLDILLNAPSKSPKSFPSRIGDVYNAGQ 203
Qy				Qy 211 NATFOCIATGRDVAHNKLWLRQRNGEDIPVQATQINHRRFAASPRLQEVTKTDDOLYC 270
Db				Db 204 NATFQVAAGAAEERFLNMQRSSEVPAVSKHSHRFLATQLDVEISKGDQLYRC 263
Qy				271 VTOQSERGSVSNPAOLIVREPRPAPPOLLGVGPTYLJLQLNANSIIGDGPILKEVEY 330

RESULT 9
Q6Y148
ID Q6Y148
AC Q6Y148,
PRELIMINARY
PRT; 1434 AA.

b	264	VTQSSRGSGVSNPAELIVKEKPTTAPPOLLRRAGGSTYL1IQLNTNS1IIGDPIVREKEY	323	
Y	331	RMTSSWWTETHAVNAAPTYKLWHLDDPTEYEIVRLTRPGEGGTGLPGPLITRTRCAEPM	390	
b	324	RMTSSPWSETHAVNACTYKLWHLDDPTEYEIVRLTRPGEGGTGLPGPLISRTCAEPM	383	
b	391	RTPKTLKIAZQARIADWESLGNITRCHTNVTCYHF--EGHNEKSAADCIDMDPK	448	RESULT 10
b	384	RAPKGELAFSEOSRQITLQNEPLGNYLTRCHTYSYSLCYLVGGSLNQFRECKXKMER	443	Qy 000197 PRELIMINARY; PRT; 1436 AA.
b	449	AQPHVNHLPPTYNSLKMILTNPEGRKESETI1QTDDEDVPGPVVKPSLQGTSPENKIF	508	Db 000197 ID 000197; PRELIMINARY; PRT; 1436 AA.
b	444	ANRITKINLPPYRNHVKLISNPNGRKKEGVTTQDDEDPGGTASESLLTPEDMIF	503	AC 000197 ID 000197; PRELIMINARY; PRT; 1436 AA.
b	509	LWKPLDPNGLITTYEISYSSIRSFDPAVPGPOTVSNLNSTHNVFMHLHGTTYQ	568	DT 01-JUL-1997 (T-EMBLrel. 04, Created)
b	504	LKWEPVPEPNGLITTYEISYQIESSDPAVNPGRRTWSKLNRNTYHESNLHGTTYI	563	DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
b	569	FFIRASTVKGFGPATINTNISAPTLPDYEQDASLNETATTIVLRLPAQKAPIS	628	DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
b	564	FSVRARTGKGFGQTALEITINNISAPTPE-DYGDMSPLGESESTITVLLRPAQKAPIS	622	DB Receptor protein tyrosine phosphatase hPTP-J precursor.
b	629	AQVITVEELPHRTKREAGAMECYQPVTYQANMSGAPYFAAELPPGNLPEPAFPFTVG	688	OS Homo sapiens (Human); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleoscomi;
b	623	TYQVIVEDEPKRIRKRELGQECFPVPLTEDAMSRGSVTFGAELPASSLETEAMPFVTG	682	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
b	689	DNRTYQGFWMNPPLAPRKGNMYFOAMSSEVKETKQCVRIATKAATEPVEIPDAKQT	748	OX NCBI_TaxID-9606; NCBI_TaxID-1;
b	683	DNQTSGYWNPPLEPKAYLIYFOAMSNLKGETRINCIRLARKACKESRPLETSQHSE	742	RN [1]
b	749	RVKTAGISA-GILVFILLVLVILVKSKLAKRKDKANGNTROSMTHVNAMDSYAD	807	RP SEQUENCE FROM N.A.
b	743	: EMGLIGICAGGLVVILLLGAIIVVTRKGKPVNNTK-ATINYRHEKTHIMMSAIRSFTD	801	RC TISSUE-Skeletal muscle;
b	808	QSTLHAEDPLSFTMDQHNSSPRHNSA-ESSRLL-DVPRVLCETGESPYQYQQLHP	865	RX MEDLINE=97234402; PubMed=2070223; DOI=10.1006/bbr.1997.6004;
b	802	QSTLQDERIGLSFDTANYSNRGQRSVSNESLLGGSPPRQRGRKSPPHYQQLHP	861	RA Wang B.; Kishihara K.; Zhang D.; Hara H.; Nomoto K.;
b	866	AIRYBDLQHINLMTSDSYGFKEYESFFEGQASSWDYAKKDRNQKRYGNLYIAYDHS	925	RT Molecular cloning and characterization of a novel human receptor protein tyrosine phosphatase gene, hPTP-J: down-regulation of gene expression by PMA and calcium ionophore in Jurkat T lymphoma cells.;
b	917	RVKLHPPLGPNSDYINANYIDGTRSRNHFIAITQCPQKQEMVYDFTRMVOEHCSSIVMIT	916	RT Biochem Biophys Res Commun. 231:77-81(1997).
b	862	AVRYBDLQHINQMTAEGYGFQKYESFFEG-- -WDA SKRK-KIKTKGRQDHYSTYDRH	916	RL BMBL; U73127; AAB51343.1; -.
b	926	RVILQVEDDPSSDVINANYIDGKQPHSYIATQGPVHETVYDFTRMVOEQSACIYVMT	985	DR PIR; JC5220; JCS290;
b	917	KLVEGRVICKSKWDDSENGDIXLTYKSEMLEYARTFALLRRGYSARHETQFH	1036	DR HSSP; P28827; 1RPM.
b	1046	TGWPDHGVPYTHATGLSFTRVKLSNPPSAGPIVTHCSAGAGRTSCYIVIDIMDMAERE	1105	DR GO; GO:0016200; C:membrane; IEA.
b	1037	1097 GVDIYNCVKLCSRINM1QTEQYIPIHDALLEACLGCTTSIDBMLDMAECE	1096	DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
b	986	1116 SQTNSSHLDKDEFOTLNSVTPRLLOADCSTACLPRHDKNRFDMLPPDRCLPFLJTIDGE	1225	DR GO; GO:004872; F:receptor activity; IEA.
b	977	1106 GVDIYNCVKLCSRINM1QTEQYIPIHDALLEACLGCTTSIDBMLDMAECE	1165	DR GO; GO:006470; P:protein amino acid dephosphorylation; IEA.
b	1097	1107 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR InterPro; IPR031962; FnIII sub.
b	1166	1117 SQTNSSHLDKDEFOTLNSVTPRLLOADCSTACLPRHDKNRFDMLPPDRCLPFLJTIDGE	1225	DR InterPro; IPR031961; Fn-III.
b	1106	1117 GVDIYNCVKLCSRINM1QTEQYIPIHDALLEACLGCTTSIDBMLDMAECE	1165	DR InterPro; IPR008979; GaI_bind_like.
b	1097	1107 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR InterPro; IPR03599; Ig-.
b	1166	1117 GVDIYNCVKLCSRINM1QTEQYIPIHDALLEACLGCTTSIDBMLDMAECE	1156	DR InterPro; IPR007110; Ig-like.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR InterPro; IPR00998; MAM.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR InterPro; IPR00387; TYR_phosphatase.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR InterPro; IPR000242; Tyr_PP.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR InterPro; IPR00041; fn3; 3.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Pfam; PF00629; MAM; 1.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Prints; PR000102; Y_phosphatase; 2.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Prints; PR00014; ENTPPELI.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Prints; PR00020; MANDOMAIN.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Prints; PR00056; TYR_phosphatase; 2.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Prints; PR00056; TYR_phosphatase; 2.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	DR Glycoprotein; Hydrolase; Receptor; Signal; Potential.
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	FT SIGNAL 1 18
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	FT CHAIN 19 1436
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	SQ SEQUENCE 1436 AA; 161092 MW; C05B865F7A9412D9 CRC64;
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	Query Match 60.1%; Score 4632; DB 2; Length 1436;
b	1117	1117 TSWPHGVPYTHATGLAFTRVKASTPPDAGPVIVHCASGTGRTSCYIVDMLDMAECE	1156	Best Local Similarity 60.1%; Fred. No. 3.6e-301; Matches 867; Conservative 211; Mismatches 339; Indels 26; Gaps
b	1343	EVPGSKRSFLKLIQLOVEKHOEWKEGEFRGTRHNGGRSGMFCAIGIVVEMYKRQNVY	1402	6 AAALPAVALLILSPWPLGGSAQGOFSGAGCTTFD---DGPAGCDYHDLYYDFEWVHSV
b	1343	DTPDKRKSFHLLAVVERWKE---SGDGRVWVCHNGGRSGTYCASTILEMKCHNN 1394		4 RQALVIALTFLFCAP-----ETEPAAAGCTFEASDPAVCEYSAQYDFQWEQVY

Qy	63	QEPHYLPPMFGSYMIVMDSSDHDPGEKARILQLPTMKENDTHC1DFSYLYSQKGILNPET	122	Qy	1138	IIEACLCGETAIPIVCEFKAAKFDMIRIDSQTNSSHLDKEFQTLNSVTPLQAOEDOSIACL	1197		
Db	57	HPGTRAPADLHRGSTMVNTSQHACQRALIVIHQSLNQDQYRNGEDIPVHQ	242	Db	1131	IIEACLCGETTIPSEFATYKEMRIDPQNSQSLQDVECSIAL	1190		
Qy	123	LNLIVRNKGPLANPIWNTGFTGRDWLRAELAVSTFWNEYOIYEAEVSGGRSGYIAI	182	Qy	1198	PRNHDKNRFMDLPPDRCLPFLITDGESSNYINAALMDSYROPAFTVTOYPLPNTVKD	1257		
Db	117	LGVVYRNNGPLGSATWNMTGSHGRQWQAEELAVSTFWNEYOIYEAEVSGGRSGYIAI	176	Db	1191	PRNRDKNRSMDVLPPDRCLPFLISTGDSDNNYINAALTDYSYRASFATVTLHPLQSTPD	1250		
Qy	183	DDIQVLYSPCDKSPHPLRLGDEVAGONATFOCIATGRDAVHNKLWLRQRNGEDIPIVHQ	242	Qy	1258	FWRLVYDGCSTIMLNEVDLSQG--CQYWDEGMFRYGPLOVECMCSMCDVNR	1314		
Db	177	DDILLISYPCKAKPHPSRLSDEVAGONASFOCMAAGRAEAERFLQGALVPAG	236	Db	1251	FWRLVYDGCSTIWLQNQNSNSAWPCLQYWPGRQYGLMEBFMSGTADEDLVARY	1310		
Qy	243	TKNINHRRFAASFRILQEQVTKTDQDLYRCVTSQSERPVGVSNAFOIIVREPPRTPAPOOLG	302	Qy	1315	FRCNLULTRQBGYLMQQOQLGYASHREVPGSKRSPFLKLILQVEKWQEWKEGBGRITII	1374		
Db	237	VRHSIRFLFLAVSRAEQLYRCSQAPRAGVSFAELIVKEPTPIAPPQLR	296	Db	1311	PRVQNSRQEGHMLVYRHFQFLRMSAYRTDPSKAFHLILAEVDKWQE--SGDGRITV	1368		
Qy	303	VGPTYLQIQLQNLANSITLGDPPLILKEVYRMTSGSWTETHAWAPTYKLNWHLDPOTEYER	362	Qy	1375	HCLNGGGRSGMFCATGIVYVMKRQNVYDFHAYTTLRNSKPNNVEAPEQYRFCDYVALE	1434		
Db	297	AGPTYLIQLQNLANSITLGDPPLILKEVYRMTSGSWTETHAWAPTYKLNWHLDPOTEYER	356	Db	1369	HCLNGGGRSGTFCACATVLEMIRCHNLVDFPAAKTLRNYKPNNVETMDQYHFCYDVALE	1428		
Qy	363	VLLTRIGEGTGTPGPPLITPTKCAEPMPRPTKTLKAEIARRIADVLSGLNTRCHT	422	Qy	1435	YLE	1437		
Db	357	VLLTRIGEGTGTPGPPLISPKCAEPMPRPTKTLKAEIARRIADVLSGLNTRCHT	416	Db	1429	YLE	1431		
Qy	423	FNVTICHHYFRG--HNEKADCLMDPKAPKAPOHVNNHLPPTVNLKMLITNPEGRKESSE	480	RESULT 11.					
Db	417	YTVSLCYHYTIGSSHHQTIRSCVKRBEQGSYYTINLPLPVRVNLPEGRKGE	476	Q92850	PRELIMINARY;	PRT;	1436	AA.	
Qy	481	TIIQTDDBDVGPPVPUKSLQGTSENKIFLWKKEPLDNGLITQYBISYSSIRSDFPAPVY	540	ID	Q92850;				
Db	477	VTFQTDDEDPVSGIAAESLTTFPLEDMIFLKMEEPQEPNGNGLITQYBISYQTESSDPAVV	536	AC	Q92850;				
Qy	541	AGPPQTVNSLWLNSTHIVFMHJHPGTYQFFTRASTVKGFDATANVTVNISAPPLDYE	600	DT	01-FEB-1997	(TREMBrel.	02,	Created)	
Db	537	PGPRTTSKLNETHVFSNLHPGTYLFSYSTRAPICKGFQQAALTETITNISASF-DYA	595	DT	01-FEB-1997	(TREMBrel.	02,	Last sequence update)	
Qy	601	GVDASLINEATTATITVLLPRAOGKAPTAQSYAQVVEELHPIRKREGAMECYQEVPTYQ	660	DT	01-OCT-2003	(TREMBrel.	25,	Last annotation update)	
Db	596	DMPSPGESENITIVLLPAGRGAPSIVCVIVEERARLRLREGQQCPVPLTFA	655	DE					
Qy	661	AMSGGAPYFAAELPFGNLPPEPAPFTYGDNRTYQOFVNPLAALKGYNNTYQFQAMSSVKE	720	DR					
Db	656	656 ALARGLVHYFGRAELAASSLSPAMPFTYGDNQTYGRFWNPPLPEPKRAYLTYFQAASHLKGD	715	DR					
Qy	721	TKTCVYRATAATEPEVIPDPKQTDVVKIAGISA-GILVFILLVLLVLYIKSKL	779	DR					
Db	716	716 TRLNCCRIRAAKCKSKRPLEVQSEMEYLGLGICAGLVLIGLIGATIVLIRKGKP	775	DR					
Qy	780	AKKRKDAMGNTRQEMTHMVNADMRSYADQSLTHAEDPLSITFMDORNFSPRYNS--AT	837	DR					
Db	776	VNMTR-ATVNQRQETHMMSAVDRSTQDQSLQDERRGLSFMDFTHYSTQDQRSGGT	834	DR					
Qy	838	AESSRLIDVPRYLCETGTESPYOTQGQHPATRADLQHINLMKTSQDSYGFKEYEYESFFEG	897	DR					
Db	835	BASSLUGGSPZRPCKRGKGSPTHTQGLHPAVRDLQHINOMKTAEGYGPQEYESFFEG	894	DR					
Qy	898	QASASWDYAKDQDNRAKRYGNLIAYDHSRVLQVVEDPSSDYINANYIICYQRSHYIA	957	DR					
Db	895	---WDATKKDKVKGSSRQEEMPAYRHRVYKLHPMLGDPNADYINANYIICYHRSHYIA	950	DR					
Qy	958	TGQPVHETVDFWRMIWQEQSACIVMNTLYEVGRYKCYKWPDDTVEVYGBFKTCVEME	1017	DR					
Db	951	TQGPKPMMVDFWRMWWQHECGSIWVTKLVEVRYKCSRWPEDDTGDIKIMVKE	1010	DR					
Qy	1018	PLAEXYVVRTRFTLERRGYNEIREVKQFHFTGMDHGVPYHATGLLSFTRVYKLNSNPPSAGP	1077	KW					
Db	1011	1011 TLAEXYVVRTRFALERRGYSARHVRQFHFTAWPERHGTVYHATGLLAFTRVKASTPDAGP	1070	SQ					
Qy	1078	IVTHCSAGAAGRTGCVYIDIMDMAEGRVYDINCYKALSRRIIMVQTEQYFIIHDA	1137	Query Match Score: 60.0%; Best Local Similarity: 60.0%; Matches: 866; Conservative: 210; Mismatches: 341; Indels: 26; Gaps: 10;					
Db	1071	IVTHCSAGTGTGCVYIDIMDMAECEGVYDINCYKTLCSRRVNMVQTEQYFIIHDA	1130	6 AAALPAFVALLLSSPWPLIGSAQGGQFSAGGCTFD--DGPAGCDYHQDLYDDFEVWVHVS	62				

Db	4	AQALVLALTFFQLCAP-----ETETPAAGCTFEAASDEPAVPCYSOAOYDDFQWEQVRI	56	
Qy	63	QEPhYLPPMPOQSSYIVDSSDHDPGEKARLQLPTMKENDTHCIDSFLYLSOKGLNPGT	122	
Db	57	HPGTRAPADLPHGSYLMNTSQAHPGQRHAFQSLSENDTHCVQFSYLSRDGHSPGT	116	
Qy	123	LNLFLVRVNGPLPLANPIWNTGFTGRDWIAELAELAVSTFWNEYCFTFEAVSGSGSGTIA	182	
Db	117	LGvTVRVNGPLGSAVNNTGSHGRWQAEELAELAVSTFWNEYCQLFEEALISPDGRGNGL	176	
Qy	183	DDICOLSYSPCDKSPEFLRLIGDVEVNAGONATFOCIATGRDAVINKLWLRNRGEDIPIVAQ	242	
Db	177	DBLLLSTFCAKAHFSRSGDVEVNAGONASFOCMAAGRAAEALERFLIQRSQSLALVPAQ	236	
Qy	243	TKNINHRPFAASPLQFETTKTDOLYRCUTOSERGSCGVSNPAOLIVRPPRTPAPPOLLG	302	
Db	237	VRIHSRRLETFPLAAVSRAEQLDYRCVSQLPRGAGTSNPAELIVEKEPPTIAPPOLR	296	
Qy	303	VGPTYLLQIQLNANSIIGDOPILIKKEVEVMTSSWTEHAANAPTYKUWHLDDETEYER	362	
Db	297	AGPTYLIQLQNTSIIIGDOPIVRKETIEVMARGEWAETHAVSLOTYKUWHLDDETEYIS	356	
Qy	363	VLLTRPGEFGTGLPGPPLTRTKCAEPMPPTPKTLKIAEQARRTAVIDWESLGYNITRCHT	422	
Db	357	VLLTRPGEFGTGRGPPLSRTKCAEPMPPTPKTLKIAEQARRTLQWEPGQYNTVRCHT	416	
Qy	423	ENTYCYYFRG-HNESKADCLDMDPKZPQHVVNHLPPTYNLSKMLTNPBGRKSEEE	480	
Db	417	YTDSLCHYHTLGSNNOTIRECYKTCYEGSRYTICNLPYRNVHVRVLTNPGRKCEKE	476	
Qy	481	TIQTDDEDPGPVYEVKSLGTSSENFKINPWRDPLDNGNITTOYEISYSIRSFDPAVY	540	
Db	477	VTFOTDVEDPGSIIAESLTTPLDMDIFKWKWEEQEPNLQIYEISYSIESSDPAVN	536	
Qy	541	AGPFQTWSNLWNSTHVTMPLHPLHPGTTQFIRASTVKGFPATAINYNTNISAPTLPYE	600	
Db	537	PGPRTISLERNETHVFEFLNHPETTYLSVSRATGKGFQGAALTEITNISAPSFP-DYA	595	
Qy	601	GVDAISLNETATTITVLLRPAQACAPISAYQIVTYEELMHPRTREAGAMECYQYPVYQN	660	
Db	596	DMPSPPLGESENTITVLLRPAQRGAPISVQVIVEEFAARRLREPGQQDFPVPLTFFA	655	
Qy	661	AMSGCAGPYFAAELPGPNLPEPAPFTVDNRYTQFVGNPLAPRKGTNTYFOAMSSVKE	720	
Db	656	ALARGLVHVFGAELAASSIPEAMPTVGDNQTRGFNWPPLERKATLYFOQASHLKGE	715	
Qy	721	TKTQCVRIATKAATEEPVTPDPAKOTDRVVKTAGISA-GILVFLILLVILVKSKL	779	
Db	716	TRUNCIRLARKAACKEKSPPLEVSQRSEEMGLIGAGLAVLILLGAIITVIRKGKP	775	
Qy	780	AKERKDAMCTRQEMTMNAMRSYAAQSTLHAEDPLSITEMDQNESPRVENHS-AT	837	
Db	776	VNTIK-ATVNYRQEKTWMMSAVDRSFTQDQSTLQEDERLGSFMNDTHGTSSTRGQRSGET	834	
Qy	838	AESERLLDPRYLCGEGTESPYOTCQLHPAIRDALLQHINLMTKSDSYGKKEYEYESFFG	897	
Db	835	EASSLLGGSPRRPGRKGSPPYHTCQLHPRVADLQHINQMTAEGYFKQYESFFG	894	
Qy	898	QGASWDVAKKDNONRAKNTYGNLTAYDHSRVLQFVEDDPSDYINANITYGKORPSHYIA	957	
Db	895	---WDATKKDKDVKTGSRQDPMPPADYHRKLGHEMLGDENADYNTDGYRSNHFIA	950	
Qy	958	TGQPVHETYIDFWRMIWQEQSACIUMVTNLVEBGRVKCXYWPPDDTEVYDGFKVTCVME	1017	
Db	951	TQGKPKEMYDFNRMWQBEHCSSIVMPLKVEGRVKCSRYWEDSDTYD1KIMLYKTE	1010	
Qy	1018	PLAFYVVRFTLERRGYNBIREYQFHFTGPDPGVYHTATGLLSFTRVKLSNPPSAGP	1077	
Db	1011	TLAFYVVRFTALERGYSARHVEYQFHFTAWPBRGVYHTATGLLAFLRKVASTPPDG	1070	
Qy	955	TOGPVHETYIDFWRMIWQEQSACIUMVTNLVEBGRVKCXYWPPDDTEVYDGFKVTCVME	1017	
Db	956	PFAFVYRFTLERRGYNBIREYQFHFTGPDPGVYHTATGLLSFTRVKLSNPPSAGP	1077	
Qy	1078	IVYHCSAGAGRGTGCVYIDIMDMAEAREGVDIYNCVKALESRRINMVQTEEQYIFHDA	1137	
Db	1071	IVHCSAGTGRGTGCVYIDIMDMAECEGVDVYDNCVTKLCSRVMQTEEQYIFHDA	1130	

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

[4] SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
 RP Mizuta M., Bergman B., Miki T., Hutton J.C.;
 RT "Molecular cloning and functional characterization on mouse receptor-
 like protein tyrosine phosphatase, mPrPPrho, which mediates cell-cell
 adhesion of pancreatic beta cells.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 [5]
 RN TISSUE SPECIFICITY.
 RP MEDLINE=98146229; PubMed=98146229;
 RX DOI=10.1002/(SICI)1096-9861(19980222)391:4<444::AID-CNEB3>3.0.CO;2-0;
 RA McAndrew P.E., Frostholm A., Evans J.E., Zdilar D., Goldowitz D.,
 RA Chiu I.-M., Burges A.H.M., Rotter A.;
 RT "Novel receptor protein tyrosine phosphatase (RPrPPrho) and acidic
 fibroblast growth factor (FGF-1) transcripts delineate a rostrocaudal
 boundary in the granule cell layer of the murine cerebellar cortex.";
 RT J. Comp. Neurol. 391:444-455(1998).
 -!- FUNCTION: May be involved in both signal transduction and cellular
 adhesion in the CNS. May have specific signaling roles in the anterior
 tyrosine phosphorylation/dephosphorylation pathway in the anterior
 compartment of the adult cerebellar cortex.
 CC CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 CC SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=5;
 Name=1;
 IsoId=Q99M80-1; Sequence=Displayed;
 CC Name=2;
 IsoId=Q99M80-2; Sequence=VSP_007803; VSP_007806;
 CC Name=3; Synonyms=RPrPPrho2;
 IsoId=Q99M80-3; Sequence=VSP_007803; VSP_007804;
 CC Name=4; Synonyms=RPrPPrho1;
 IsoId=Q99M80-4; Sequence=VSP_007803;
 CC Name=5;
 IsoId=Q99M80-5; Sequence=VSP_007803; VSP_007805;
 CC -!- TISSUE SPECIFICITY: Expression is restricted to the CNS.
 CC -!- DISTRIBUTED THROUGHOUT THE BRAIN AND SPINAL CORD.
 CC -!- DEVELOPMENTAL STAGE: Exceptionally high levels found in the cortex
 and olfactory bulbs during perinatal development and are down-
 regulated during postnatal week 2. Expression in the cerebellar
 cortex is restricted to the granule cell layer of lobules 1-6.
 CC Anterior and posterior compartments become discernible only during
 postnatal weeks 2 and 6.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 MAM domain.
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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 DR EMBL; AP12556; AAD3158.4; -;
 DR EMBL; AY026861; AAK18741.1; -;
 DR EMBL; AY026862; AAK18742.1; -;
 DR EMBL; AY026863; AAK18743.1; -;
 DR EMBL; AF244125; AAF4712.1; -;
 DR EMBL; AF1622856; AAF23400.2; -;
 DR EMBL; AF1622857; AAF82401.1; -;
 DR HSSP; P10586; LLAR.
 MGD: MGI:1321152; Prpt.
 InterPro; IPR003961; PN-III.
 InterPro; IPR008957; FN-III-like.
 InterPro; IPR003599; Ig-
 InterPro; IPR007110; Ig-like.

DR InterPro; IPR000998; MAM.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR00212; Tyr_PP.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00629; MAM; 1.
 DR Pfam; PF01022; Y_phosphatase; 2.
 DR PRINTS; PR00040; MAMDOIIN.
 DR PRINTS; PR00700; PTYPPTHTASE.
 DR SMART; SMD0086; FN3; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS000383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Alternative splicing; Glycoprotein; Hydrolase; Immunoglobulin domain;
 KW Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 29
 FT DOMAIN 3.0 1454
 FT DOMAIN 3.0 770
 FT TRANSMEM 771 791
 FT DOMAIN 792 1454
 FT DOMAIN 3.4 195
 FT DOMAIN 197 288
 FT DOMAIN 292 383
 FT DOMAIN 390 484
 FT DOMAIN 485 588
 FT DOMAIN 670 767
 FT DOMAIN 902 1156
 FT DOMAIN 1188 1450
 FT ACT_SITE 1097 1097
 FT ACT_SITE 1391 1391
 FT DISULFID 217 271
 FT CARBOHYD 82 82
 FT CARBOHYD 102 102
 FT CARBOHYD 141 141
 FT CARBOHYD 212 212
 FT CARBOHYD 425 425
 FT CARBOHYD 514 514
 FT CARBOHYD 551 551
 FT CARBOHYD 605 605
 FT CARBOHYD 658 658
 FT CARBOHYD 688 688
 FT VARSPlic 731 749
 FT VARSPlic 731 749
 FT VARSPlic 794 794
 FT VARSPlic 794 794
 FT VARSPlic 1007 1007
 FT CONFLICT 13 16
 FT CONFLICT 21 21
 FT CONFLICT 34 37
 FT CONFLICT 87 87
 FT CONFLICT 254 254
 FT CONFLICT 266 266
 FT CONFLICT 602 602
 FT CONFLICT 822 822
 FT CONFLICT 825 825
 FT CONFLICT 844 845
 FT CONFLICT 1016 1016
 FT CONFLICT 1049 1049
 FT CONFLICT 1050 1050

R->V (In Ref. 1).
 R->P (In Ref. 1).
 GGCS -> RGVP (In Ref. 1).
 A->T (In Ref. 4; AAF82401).
 S (In Ref. 4; AAF82401).
 I->V (In Ref. 4; AAF82401).
 T->S (In Ref. 4; AAF82401).
 A->T (In Ref. 4; AAF82401).
 G-S (In Ref. 4; AAF82401).
 TD->N (In Ref. 4; AAF82401).
 D->A (In Ref. 4; AAF82401).
 Y->H (In Ref. 1).
 H->N (In Ref. 4; AAF82401).

/FTId=VSP_007806.

Missing (In Ref. 1).

R->V (In Ref. 1).

R->P (In Ref. 1).

R->RNNAYSYSTYL (In isoform 3).

/FTId=VSP_007804.

R->RNNAYSYTSLQR (In isoform 5).

/FTId=VSP_007805.

R->RHPAHTVGATLGRAASPPGM (In isoform 2).

/FTId=VSP_007803.

R->V (In Ref. 3).

R->P (In Ref. 3).

R->RNNAYSYTSLQR (In isoform 5).

R->RHPAHTVGATLGRAASPPGM (In isoform 2).

FT	CONFLICT	1076	L -> V	(in Ref. 4; AAF82401).	Db	892	TQNKRGQGYGFKEEYALPEQQTASWDTAKEDENRKNQFNGNIIISYDHSVRVLLYLGDGP	951
FT	CONFLICT	1103	R -> K	(in Ref. 1).	Db	937	SSPYTINANYTDGKQRPHSYIATQCPVHETTYDQPRMIQEQSACVMTNLVEGRVKCV	996
FT	CONFLICT	1125	P -> L	(in Ref. 4; AAF82401).	Qy	952	HSPYTINANYTDGTHPRPHYIATQCPMOTVKDFPRMIQENSASTVMTNLVEGRVKCV	1011
FT	CONFLICT	1266	L -> I	(in Ref. 4; AAF82401).	Db	997	KWPDPDTEVYGPKVTCYMEPLAAYVVRTFTLERGTYNEIREYQFHFTGPWDGIVPYH	1055
FT	CONFLICT	1269	T -> S	(in Ref. 4; AAF82401).	Db	1012	RWPDPDIEVYGDIKVLTIEPLAAYVIRTPTVQKGKHYIRELRLFHFTSPWDGVPCY	1077
SQ	SEQUENCE	1454	AA:	163012 MW: C60467FB423F848 CRC64;	Qy	1057	ATGLLSPFIRRVLCLSNPPSAGATVHCSAGAGRGTGCTYVIDIMDMAEREGVVDIYCNVKA	1111
Qy	1	MDTAAAALPAFAVALLLSSPPWPLIGSAOGQSAGGCTEDPGGACTDYHQL-YDDFEWYH	59	Qy	1072	ATGLGFTPRQVKELNPPEAGPIVHCSAGAGRGTGCFIAIDTMLDNAENEGVVDIYCNVRE	1113	
Db	1	MGSJGLALCLLRLRLGLRPLPAGAGASAAGCSDPHYSNCYVALGTINGTWEQ	60	Db	1117	LSRRRINMVVOTEBOYIIFHDIALEACLGCBETAPVCEPKAYEDMIRDSQTNSHKLDE	1177	
Qy	60	VSAQPHYLPEPMQGSYMIVDSSDHDPGEKARLQLOPTMKENDTHCIDFPLLYSQKGLN	119	Qy	1117	LSRRRINMVVOTEBOYIIFHDIALEACLGCBETAPVCEPKAYEDMIRDSQTNSHKLDE	1177	
Db	61	INTWCKPMDPAVTGSEPMVNNSSGRASGKKAHLJLPLTKENDTHCIDFPHYFSERDRSS	120	Db	1132	LRAQRVNVLVOTEQQVYVHDIALEACLCCLNTSRDQTNSSQIKDE	1119	
Qy	120	PGLTILYRVNKGPLANPIWNTGFTGRDWLRAELAVSTWPNEYQVIFPAEVSGGRSGY	179	Qy	1177	FOTLNSUTPRLQABDCSACLPNHDKORFMDMLPDRCLPFLITIDGESSNYINNALMD	1231	
Db	121	PGALNVYVKGNGFQGNPWNVNGVTVTGEVKAELAISTWPHFTQVIFFESVSLKGHPGY	180	Db	1192	FOTLNTVTPRVPEPDCTSGLLPNHDKRSMDVLPLDRCLPFLISVGDESSNYINNALMD	1255	
Qy	180	IADDIVOLSYPCUDCKSPHFLRGLGVENVAGQONATEQCIACTGRDAYHNKMLQLQRNGEDIP	239	Qy	1237	SYROPAAFIVTOYPLPNTYKDFWRLVYDGCTSLVMLNEVDLSCOPYOMPEEGMLRYGP	1299	
Db	181	IADDEVRLAHPCXKAAPHFLRQLQNVEVNGQONATEQCIACTGRDAYHNKMLQLQRNGEDIP	240	Db	1152	SHKQPAAFVVTOPPLPNFTADFWRLVFDNCSSVMNEMDTAQCMQWPKEKTSGYCP	1311	
Qy	240	VAQTQNNINHRFAASFRLOEVTKTDDLYRCVTSBERGSSVSNAQOLIVEBPPRDIAPPQ	299	Qy	1297	IQEYCMSCSMIDCDVINRIFRICNLTRPQEGLYVQOFQYLGASHREVPCSKRSKSFKLIL	1355	
Db	241	LMYTRVNRFRSATVSVATDQSISKYCVTISDGGSVSUNASYELITYEPPTTIAAPE	300	Db	1312	IQEYFWVSADIDEIILHRLFRICNMARPQDGYRIVQHQLQYGPWARYDTPPSKRSLKVV	1377	
Qy	300	LLAVGPTYLLIQNANSITGGDTPLKILKEVYRMTSGSWTHAYNAPTYKLWHLDPDTYE	359	Qy	1357	QVERWWEEWKEGGRITIHCLNGGRSGMFCAIGIVVENVKRONVVDVFHAVKTLRNSKP	1411	
Db	301	LLAVGATLWIKPANASIIGDGPILKILKEVYRTTGWATHIVDSPNPKLWHLDPDTYE	360	Db	1372	RLEKWWOYDREGRTVYHCLNGGRSGTFCALCSVCCEMIQQNIDVHFHVKTIRNIKS	1433	
Qy	360	EIRVLLTRPGEKGSTGLPGPPLITRTKCARMRTPKTLKLAELIQARRIAVTDWESLYNTR	419	Qy	1417	NNVEAAPCYRFYCVDALEYLES	1438	
Db	361	EIRVLLTRPGEKGSTGLPGPPLITRTKCADVHGPONVETDIRARQLTGWEPFYAVTR	420	Db	1432	NNVETLEQYKFVYEALEYSS	1453	
Qy	420	CHTPNVTCYHYFRGNESKADCLMDPKPAQHVNWHLPPTYNLSKMLTNPEGRKESE	479	RESULT	15			
Db	421	CHSYNLTQYQXY--ENQQYBAAEVICTSQHSHYTLURGEPLFPMTRLRLISNPBERMSE	478	P78399	PRELIMINARY,	PRT,	1439 AA.	
Qy	480	ETLIQTDDBVPGPYPVKSLQGTSFENKLFILANWKBEPLDPNGITTOYESYSSIRSFDPAVE	539	ID	P78399			
Db	479	ELWQTEEDVPGAVPLESTQGGPPEEKYYIOWKOPENETINGVILYEINTKAVGSLDPSAD	538	AC	P78399;			
Qy	540	VAGQPQTYSNLWNSTHYEMHLHPGTTYOFIRASTVKFCGPATAINTVNISAPTLPY	599	DT	01-MAY-1997	(TREMBLrel.	03 ; Last sequence update)	
Db	539	LSSORGKVEKLRNETHLFLVGLYFGTTYSFTIKASTAKGFPVTRIATKISAPSMPY	598	DT	01-MAY-1997	(TREMBLrel.	03 ; Last sequence update)	
Qy	600	EGYDASLINEATTITVLLRPQAQKAPISAYQIYVVEELHHRTRKEAGAMEBCYQPVTVQ	659	DT	01-OCT-2003	(TREMBLrel.	25 ; Last annotation update)	
Db	599	D-ADTPNEDDTITVLLRPQAQKAPISAYQIYVVEELHHRTRKEAGAMEBCYQPVTVQ	657	DE		"Characterization and chromosomal localization of pipro, a novel protein tyrosine phosphatase receptor omicron.		
Qy	660	NAMSGGAPYFAAELPGPGLNLPAPPFYGDNRITYFOAMSSVKEK	719	DN		Name=pipro;		
Db	659	NASNLDLHYFAAELPKSNLPLVTOFTVSDNKTQNGWPLSPLKSYSYFQALSKANG	717	OS	Homo sapiens (Human).			
Qy	760	ILVFILLLIVLIVKSKLAKKGDAMNTRQEMTHMYNAMDSYADQSTLHADPLS1	819	DR	Metaxoa;			
Db	777	LAMFILLLIVLIVKSKLAKKGDAMNTRQEMTHMYNAMDSYADQSTLHADPLS1	819	DR	Chordata;			
Qy	777	LAMFILLLIVLIVKSKLAKKGDAMNTRQEMTHMYNAMDSYADQSTLHADPLS1	819	DR	Vertebrata;			
Db	718	ETKINCVRLATKGAPMGSAQQTPTPLCLLTTASTQNSNTV-EPEKQVNDTVKMGAVTQ	776	DR	Buteleostomi;			
Qy	760	ILVFILLLIVLIVKSKLAKKGDAMNTRQEMTHMYNAMDSYADQSTLHADPLS1	819	DR	Mammalia;			
Db	777	LAMFILLLIVLIVKSKLAKKGDAMNTRQEMTHMYNAMDSYADQSTLHADPLS1	819	DR	Eutheria;			
Qy	820	TFMDQHNFSPRYENHSATAESSRLDV--PRVLCEGTESPYOTQCOLHPAIRVADLQH	876	DR	Primates;			
Db	836	SSODDVNGT---DGSRGELSQPQTLTQHPRYTCDFPMSYPRDQFQPAIRVADLQH	891	DR	Catarrhini;			
Qy	877	NLMKTSDSYGEKEYSEPEQGASASWYDKDQNBKQYGNITADHGRVILQFVEDP	936	DR	Hominidae;			

DR InterPro; IPR003599; Ig-
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR00014; PNTYPEI11.
PRINTS; PR00020; MANDOMAIN.
PRINTS; PR00700; PRTPHPTASE.
SMART; SM00560; FN3; 3.
SMART; SM00409; IG; 1.
SMART; SM00137; MAM; 1.
SMART; SM00194; PTPC; 2.
PROSITE; PS50853; FN3; 3.
PROSITE; PS00740; MAM; 1.
PROSITE; PS50060; MAM_2; 1.
PROSITE; PS50063; TYR_phosphatase_1; 2.
PROSITE; PS00383; TYR_phosphatase_2; 2.
PROSITE; PS50056; TYR_phosphatase_PTP; 2.
PROSITE; PS50055; TYR_hydroxylase_Receptor.
KW Glycoprotein; Hydrolase; Receptor.
SEQUENCE 1439 AA; 161655 MW; 99E88D14D7C965D CRC64;

Query Match Score 4581.5; DB 2; Length 1439;
Best Local Similarity 59.6%; Pred. No. 8.9e-298;
Matches 863; Conservative 212; Mismatches 339; Indels 35; Gaps 13;

Qy 6 AAALPAFAVALLSPWPLGLSAQGOFSSAGGTCTD--DGGACDYHDLYDDFENVHSA 62
Db 4 AQALVIALTFOICAP-----ETEPAAAGTCFEASDPAVCEPSQAQYDDFOEQVRI 56

Qy 63 QEPHYLPEMPOGSYMIVDSSDHDPGEKAROLQPTMKENITHCIDEFSYLJSOKGLNPCT 122
Db 57 HPGTRAPADLPHGSYLMNTQSQAPEQRAYVIFOSLSENDTHCVQFSYFLYSRDGHSPGT 116

Qy 123 LNLIVRVNGKPLANPIWNVTGPTGRDLRAELAVSTFWPEYQVTFEAEVSGGSYIAI 182
Db 117 LGVYVRVNGGIGLSAWNNVTSQSHGQWHAELAVSTFWPEYQVTFEAEVSGGSYIAI 176

Qy 183 DDIQVLSPCDKSPHFLRGDDEVNNGQATNQFCIATGRDAVHNKLWLRNNGEDIPVAQ 242
Db 177 DDLIISYCPAKAHPSRLGDDEVNNGQNAASQCMAGRAAEARFLQQSGALVPAAG 236

Qy 243 TKNINHPRFAASRFQEVTKDQDLYBCATQOSERGSGVSNSAQLJYREPPRPIAPPQJG 302
Db 237 VRHISRRRELATPLAIVSRAEQLYRCVSQAPRGAVSNPAELTVKEPPPIAPQLJR 296

Qy 303 VGPYLLIQLQANSLTGDPILKEVEYRTMGSWTETHAVNAPYKLWLDPTDEYEIR 362
Db 297 AGPTYLIQLQANSLTGDPILKEVEYRTMGSWTETHAVNAPYKLWLDPTDEYEIS 356

Qy 363 VLLTRPGEGGTOLPGPPLLITRTKCAEFMRPTKTLKIAEIQOARRIAYDWESLGYNITRCHT 422
Db 357 V_LSRPDDGGTORPGPPLIISRTKCAFMRAXKGЛАЕIQRQLAQWEPLGYNTRCHT 415

Qy 423 FNVTCIYHFRG--HNEKSAKCLDMDFKAPOHVVNLHPYTNVSKMLTNPEGRKESSE 480
Db 416 YTVSLCYHTYLGSSSHNOTIRECVKTEGGSVTYKLNLYPYNVHLRPTVNLPEGKECKE 475

Qy 481 TIIQTDDBDVGPPVPUVSLOGTSFENKLFLNKEPLDNGNLTQYETSYSSSTRSFDAVPV 540
Db 476 VTFQQTBDVPSQGTAEEAESTTFTPLEDMFLKVEEPQPNNLTQYETSYQESSUPAVV 535

Qy 541 AGPPQTVSNLNSTHAYFHMLHGTTYQFFRASYTGFGDATAINTVNTISAPTLPDYE 600
Db 536 PGPRRTISKLNRNETHYFNSNLHPTTYLFSSTARTGKGFOALBITNISAPSF-DYA 594

Qy 601 GVDASINETATITVILRPAQKQAPISAYQVVEELHPRHTKREAGMECYQPVPTYQN 660
Db 595 DMPSPLBESNTITVILRPAQRGAPISVYQVIVEBRARLURREGQDFPVPVLFTEA 654

Qy 661 AMSGGAPYYFAAEELPPGNLPEPAPFTVGDNRTYQGFVNPLAPRKSYNTFQAMSSVEKE 720

Db 655 ALARGLVHYFGAELAASSLPEAMEPFTVGDNQTYRGFWNPLPEKAYLIYFQASHLKGSE 714

Qy 721 TKTCQVTRIATAATEPEVPIPDPAKQTDRVVKZAGISA_GILVFILLLVILVTKKSKL 779
Db 715 TRLNQIATARKAACKESKRPLEYSQRSBEMGLIIGCAGLAVLILVILGAIIVTRKGKP 774

Qy 780 AKKRIDAMGNTRQEMTHNMVAMDYSADOSTLHAEDPLSDMDQHNFSPRYENH--SAT 837

Db 775 VRMTK-ATVNYRQEKTTHMSAVDSTFDOSTLQEDBERGLSFDMDTGTSTGRDGWGVY 833

Qy 838 AECSRLLDVPRYLCGETESPYOTCQLHPAIRVADLQHINLMKTSDSYGFKEEYESPFEG 897

Db 834 EASSLGSSPRRGKGSQHSTCQLHPAVRVALQHINQMKTAEGTGFQKEYESPFEG 893

Qy 898 QSASWDVAKKDQNEAQNRYGNIJAYDHSRVLQPDPSDYNANYID----GYOR 951
Db 894 ----WDATEKKDKVKGSRQEPMPAYDRTRVCLHFMGLGNDADYNANYIDIRINREGYHR 949

Qy 952 PSHYTATQGPVHETTYDFPWRMIWQBSACIVMVTNLVEGRVRCYKWMDDTBYGDFKV 1011

Db 950 SNHFTATQCPKPENYDFPWRMIVQHBCSSIVMITKLVEGRVCKSRYWEDSDTYGDKI 1009

Qy 1012 TCYEMEPLAEXYVVRTFTLERRGYNEIREVKQFHTGPDPDHGVPTATGILLSFIRRKVLNSN 1071

Db 1010 MLVKTETLAEXYVVRTFALERRGTSARHEVRQFHTAWPHGVPTATGLLAFTTRVKASt 1069

Qy 1072 PPSACPIVHCAGAGRTGTYIVDIDM DMAERGQVDTIYNCVKA LSRINMVQTEEQY 1131

Db 1070 PPDAQPIVHCAGTGTGTYIVDIDM DMAECGGVDTIYNCVKTLC SRRVNMQTEEQY 1129

Qy 1132 IFIHDAILEACLGETEATPVCPEKAYFDMIRIDSQTNSHLLKDFQTLNSVTERLOAED 1191

Db 1130 IFIHDAILEACLGETTIVSEFKAFTYKEMIRIDPQSNSQLREFQTLNSVTPPLDVE 1189

Qy 1192 CSIACLPRNHDKNRFMDMLPPDRCIPLPFLITDGESSNYTNAALMDSYRQPAFTVTOYPL 1251

Db 1190 CSIAALLPRNRDKNRSMDVLPFDRCIPLFISTSDGDSNNYTNAALTDSYTSRRAFTVLHPL 1249

Qy 1252 PNTVDFWRLVYDGCSTS1VMLNEVDSLQG--CPOYWDEBGMURYGPQVECMCSMDC 1308

Db 1250 QSTTFDWFRLVYDGCSTS1VMLQUNONNSAWPCLQYWBPGRCQYGLMEVEFNSGTADE 1309

Qy 1309 DVNRFIRICNLTRFQEGLTMVQFQYLGWSHREVPGSRSRFSFLKLLOVEKWOEWKEG 1368

Db 1310 DLVANVFRVONISR-EGHLLVRHIFQFLNSAYRTDPSKKAFLHLLAENVDKWQDE-SG 1365

Qy 1369 EGRTLTHCLNGGGRGGMFCAGIGTVEMVKRQNIVYDFHAVKTURSKPNVNEA PFOYRFC 1428

Db 1366 DGRTLVHCLNGGGRGSGTFCRCAVLEIIRCHNLVDFFAAKTLNRYKPNVETMDQYHFC 1425

Qy 1429 YDVALEYL 1437

Db 1426 YDVALEYL 1434

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